

GENE PRECURSOR-SEQUENCE P-SEQID GENE-SEQ G-SEQID FOLDED PRECURSOR

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GAM15 ACCTCTTTCTGATGGAGTCG 1 TGATGGAGTC 350 TTTCT- T TC AAG CT TC TCTTC
T CTCACAA

 TAAAAAAGTTTTATCTCTTT GTAAAAAAGT C GA GGAG GTAAAA TTTTAT CTT TC GA
GGT A
 CTCTCTTCGATGGTCTCACA TTTA | ||||| ||||| ||||| || |||||
 AAAATATTAAACCTCTTTCT G CT TCTC TATTTT AAAATG GAG AG CT CCA A
 GATGGAGTCGTAAAAAAGTT CTTCTCT T -- GAA CT GT TCTTT - AATTATA
 TTATCTCTTTCTCCTTCGAT
 GGT

GAM16 ACCTCTTTCTGATGGAGTCG 2 TGATGGAGTC 351 TTTCT TG TC AAG CT TC TCTTC
T CTCACAA

 TAAAAAAGTTTTATCTCTTT GTAAAAAAGT TC GA GAG GTAAAA TTTTAT CTT TC GA
GGT A
 CTCTCTTCGATGGTCTCACA TTTA || || ||| ||||| ||||| || |||||
 AAAATATTAAACCTCTTTCT AG CT TTC TATTTT AAAATG GAG AG CT CCA A
 GATGGAGTCGTAAAAAAGTT CTTCT CT TC GAA CT GT TCTTT - AATTATA
 TTATCTCTTTCTCTCTTCGA
 TGGT

GAM17 ACCTCTTTCTGATGGAGTCG 3 TGATGGAGTC 352 TTTCT TG TC AAG CT TC TCTTC
T CTCACAA

 TAAAAAAGTTTTATCTCTTT GTAAAAAAGT TC GA GAG GTAAAA TTTTAT CTT TC GA
GGT A
 CTCTCTTCGATGGTCTCACA TTTA || || ||| ||||| ||||| || |||||
 AAAATATTAAACCTCTTTCT AG CT TTC TATTTT AAAATG GAG AG CT CCA A
 GATGGAGTCGTAAAAAAGTT CTTCT CT TC GAA CT GT TCTTT - AATTATA
 TTATCTCTTTCTCTCTTCGA
 TGGT

GAM18 ACCTCTTTCTGATGGAGTCG 4 TGATGGAGTC 353 TTTCT TG TC AAG CT TC TCTTC
T CTCACAA

 TAAAAAAGTTTTATCTCTTT GTAAAAAAGT TC GA GAG GTAAAA TTTTAT CTT TC GA
GGT A
 CTCTCTTCGATGGTCTCACA TTTA || || ||| ||||| ||||| || |||||
 AAAATATTAAACCTCTTTCT AG CT TTC TATTTT AAAATG GAG AG CT CCA A
 GATGGAGTCGTAAAAAAGTT CTTCT CT TC GAA CT GT TCTTT - AATTATA
 TTATCTCTTTCTCTCTTCGA
 TGGT

GAM19 ACCTCTTTCTGATGGAGTCG 5 TGATGGAGTC 354 TTTCT TG TC AAG CT TC TCTTC
T CTCACAA

 TAAAAAAGTTTTATCTCTTT GTAAAAAAGT TC GA GAG GTAAAA TTTTAT CTT TC GA
GGT A
 CTCTCTTCGATGGTCTCACA TTTA || || ||| ||||| ||||| || |||||
 AAAATATTAAACCTCTTTCT AG CT TTC TATTTT AAAATG GAG AG CT CCA A
 GATGGAGTCGTAAAAAAGTT CTTCT CT TC GAA CT GT TCTTT - AATTATA
 TTATCTCTTTCTCTCTTCGA
 TGGT

GAM20 ACCTCTTTCTGATGGAGTCG 6 TGATGGAGTC 355 TTTCT TG TC AAG CT TC TCTTC
T CTCACAA

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|-------------------------------|----------------|-------|----|-----|--------|--------|-----|-------|-----------|
| TAAAAAAGTTTTATCTCTTT | GTAAAAAAGT | TC | GA | GAG | GTAAAA | TTTTAT | CTT | TC | GA |
| GGT A | | | | | | | | | |
| CTCTCTTCGATGGTCTCACA | TTTA | | | | | | | | |
| AAAATATTAAACCTCTTTCT | | AG | CT | TTC | TATTTT | AAAATG | GAG | AG | CTCCA A |
| GATGGAGTCGTAAAAAAGTT | | CTTCT | CT | TC | GAA | CT | GT | TCTTT | - AATTATA |
| TTATCTCTTTCTCTCTTCGA | | | | | | | | | |
| TGGT | | | | | | | | | |
| GAM21 ACCTCTTTCTGATGGAGTCG 7 | TGATGGAGTC 356 | TTTCT | TG | TC | AAG | CT | TC | TCTTC | |
| T CTCACAA | | | | | | | | | |
| TAAAAAAGTTTTATCTCTTT | GTAAAAAAGT | TC | GA | GAG | GTAAAA | TTTTAT | CTT | TC | GA |
| GGT A | | | | | | | | | |
| CTCTCTTCGATGGTCTCACA | TTTA | | | | | | | | |
| AAAATATTAAACCTCTTTCT | | AG | CT | TTC | TATTTT | AAAATG | GAG | AG | CTCCA A |
| GATGGAGTCGTAAAAAAGTT | | CTTCT | CT | TC | GAA | CT | GT | TCTTT | - AATTATA |
| TTATCTCTTTCTCTCTTCGA | | | | | | | | | |
| TGGT | | | | | | | | | |
| GAM22 ACCTCTTTCTGATGGAGTCG 8 | TGATGGAGTC 357 | TTTCT | TG | TC | AAG | CT | TC | TCTTC | |
| T CTCACAA | | | | | | | | | |
| TAAAAAAGTTTTATCTCTTT | GTAAAAAAGT | TC | GA | GAG | GTAAAA | TTTTAT | CTT | TC | GA |
| GGT A | | | | | | | | | |
| CTCTCTTCGATGGTCTCACA | TTTA | | | | | | | | |
| AAAATATTAAACCTCTTTCT | | AG | CT | TTC | TATTTT | AAAATG | GAG | AG | CTCCA A |
| GATGGAGTCGTAAAAAAGTT | | CTTCT | CT | TC | GAA | CT | GT | TCTTT | - AATTATA |
| TTATCTCTTTCTCTCTTCGA | | | | | | | | | |
| TGGT | | | | | | | | | |
| GAM23 ACCTCTTTCTGATGGAGTCG 9 | TGATGGAGTC 358 | TTTCT | TG | TC | AAG | CT | TC | TCTTC | |
| T CTCACAA | | | | | | | | | |
| TAAAAAAGTTTTATCTCTTT | GTAAAAAAGT | TC | GA | GAG | GTAAAA | TTTTAT | CTT | TC | GA |
| GGT A | | | | | | | | | |
| CTCTCTTCGATGGTCTCACA | TTTA | | | | | | | | |
| AAAATATTAAACCTCTTTCT | | AG | CT | TTC | TATTTT | AAAATG | GAG | AG | CTCCA A |
| GATGGAGTCGTAAAAAAGTT | | CTTCT | CT | TC | GAA | CT | GT | TCTTT | - AATTATA |
| TTATCTCTTTCTCTCTTCGA | | | | | | | | | |
| TGGT | | | | | | | | | |
| GAM24 ACCTCTTTCTGATGGAGTCG 10 | TGATGGAGTC 359 | TTTCT | TG | TC | AAG | CT | TC | TCTTC | |
| T CTCACAA | | | | | | | | | |
| TAAAAAAGTTTTATCTCTTT | GTAAAAAAGT | TC | GA | GAG | GTAAAA | TTTTAT | CTT | TC | GA |
| GGT A | | | | | | | | | |
| CTCTCTTCGATGGTCTCACA | TTTA | | | | | | | | |
| AAAATATTAAACCTCTTTCT | | AG | CT | TTC | TATTTT | AAAATG | GAG | AG | CTCCA A |
| GATGGAGTCGTAAAAAAGTT | | CTTCT | CT | TC | GAA | CT | GT | TCTTT | - AATTATA |
| TTATCTCTTTCTCTCTTCGA | | | | | | | | | |
| TGGT | | | | | | | | | |
| GAM25 ACCTCTTTCTGATGGAGTCG 11 | TGATGGAGTC 360 | TTTCT | TG | TC | AAG | CT | TC | TCTTC | |
| T CTCACAA | | | | | | | | | |
| TAAAAAAGTTTTATCTCTTT | GTAAAAAAGT | TC | GA | GAG | GTAAAA | TTTTAT | CTT | TC | GA |
| GGT A | | | | | | | | | |
| CTCTCTTCGATGGTCTCACA | TTTA | | | | | | | | |
| AAAATATTAAACCTCTTTCT | | AG | CT | TTC | TATTTT | AAAATG | GAG | AG | CTCCA A |
| GATGGAGTCGTAAAAAAGTT | | CTTCT | CT | TC | GAA | CT | GT | TCTTT | - AATTATA |

TTATCTCTTTCTCTCTCGA
 TGGT
 GAM26 ACCTCTTTCTGATGGAGTCG 12 CGTAAAAAAG 361 TTTCT TG TC AAG CT C TTC--
 T CTCACAA
 TAAAAAAGTTTTATCTTTCT TTTTATCTTT TC GA GAG GTAAAA TTTTAT TTCT TC GA
 GGT A
 CTCTTCGATGGTCTCACAAA CTCT || ||| ||||| ||||| ||| || |||
 AATATTAAACCTCTTTCTGA AG CT TTC TATTTT AAAATG GAGG AG CT CCA
 A
 TGGAGTCGTAAAAAAGTTTT CTTCT CT TC GAA CT T TCTTT - AATTATA
 ATCTCTTTCTCTCTTCGATG
 GT
 GAM27 GATGGAGTCGTAAAAAAGTT 13 TGATGGAGTC 362 T TC AAG -- T TCCTTC T
 CTCACAA
 TTATCTCTTTCTCCTTCGAT GTAAAAAAGT GA GGAG GTAAAA TTTTAT CTCT TC GA GGT
 A
 GGTCTCACAAAAATATTTAA TTTA ||||| ||||| ||||| ||| || |||
 CCTCTTTCTGATGGAGTCGT CT TCTC TATTTT AAAATG GAGG AG CT CCA A
 AAAAAAGTTTTATCTCTTTC T -- GAA CT T TCTTT- - AATTATA

 GAM28 GATGGAGTCGTAAAAAAGTT 14 TGATGGAGTC 363 T TC AAG -- T TCCTTC T
 CTCACAA
 TTATCTCTTTCTCCTTCGAT GTAAAAAAGT GA GGAG GTAAAA TTTTAT CTCT TC GA GGT
 A
 GGTCTCACAAAAATATTTAA TTTA ||||| ||||| ||||| ||| || |||
 CCTCTTTCTGATGGAGTCGT CT TCTC TATTTT AAAATG GAGG AG CT CCA A
 AAAAAAGTTTTATCTCTTTC T -- GAA CT T TCTTT- - AATTATA

 GAM29 GATGGAGTCGTAAAAAAGTT 15 TGATGGAGTC 364 T TC AAG CT TC TCTTC T
 CTCACAA
 TTATCTCTTTCTCTCTTCGA GTAAAAAAGT GA GGAG GTAAAA TTTTAT CTT TC GA GGT
 A
 TGGTCTCACAAAAATATTTAA TTTA ||||| ||||| ||||| ||| || |||
 ACCTCTTTCTGATGGAGTCG CT TCTC TATTTT AAAATG GAG AG CT CCA A
 TAAAAAAGTTTTATCTCTTT T -- GAA CT GT TCTTT - AATTATA
 C

 GAM30 GATGGTCTCATAAAAAAGT 16 ATAAAAAAG 365 G TCATAAAA TTTTAC ATTCT-
 CTCTCTT TG
 TTTACAAAAATATTTTTATT TTTTACAAAA AT GTC AAAG AAAAATATTTTT CTTT
 TGA G
 CTCTTTCTCTCTTTGATGGT ATAT |||| ||| ||||| ||||| ||| |||
 CTCATAAAAAAAGTTTTACA TG TAG TTTC TTTTATAAAAA GAAA ACT /
 AAAATATTTTTATTCTCTTT G TTTCTCTC TCTTA- CATTTT AAAAT-- CT
 CTCTCTTTGATGGTC

 GAM31 GGAGTCATAAAATATTTTTA 17 TAAAATATTT 366 TC A T- T TCTCTTC T CTCACAA
 TTCTCTTTCTCTCTTCGATG TTATTCTCTT GGAG ATAAAAT TTTTAT CTCT TC GA GGT
 A

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|----------------------|------|------------------------------|-----------|
| GTCTCACAAAAATATTAAC | TCTC | | |
| CTCTTTCTGATGGAGTCGTA | | TCTC TATTTTG AAAAATG GAGG AG | CT CCA A |
| AAAAAGTTTTATCTCT | -- | A CT T TCTTT-- | - AATTATA |

GAM32 TTAAACCTCTTTCTGATGGA 18 TGATGGAGTC 367 CTTTCT TG TC AAG -- T TCCTTC
T CTCACAA

| | | | | |
|----------------------|------------|------------------------------|----------------|---------|
| GTCGTAAAAAAGTTTTATCT | GTAAAAAAGT | GA GAG GTAAAA | TTTTAT CTCT TC | GA |
| GGT A | | | | |
| CTTTCTCCTTCGATGGTCTC | TTTA | | | |
| ACAAAAATATTAACCTCTT | | CT TTC TATTTT AAAATG GAGG AG | CT CCA | A |
| TCTGATGGAGTCGTAAAAAA | | TCTTTC CT TC GAA | CT T TCTTT- - | AATTATA |
| GTTTTATCTCTTTCTCCTTT | | | | |
| CTCACAAAAA | | | | |

GAM33 TTAAACCTCTTTCTGATGGA 19 TGATGGAGTC 368 CTTTCT TG TC AAG -- T TCCTTC
T CTCACAA

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|----------------------|------------|------------------------------|----------------|---------|
| GTCGTAAAAAAGTTTTATCT | GTAAAAAAGT | GA GAG GTAAAA | TTTTAT CTCT TC | GA |
| GGT A | | | | |
| CTTTCTCCTTCGATGGTCTC | TTTA | | | |
| ACAAAAATATTAACCTCTT | | CT TTC TATTTT AAAATG GAGG AG | CT CCA | A |
| TCTGATGGAGTCGTAAAAAA | | TCTTTC CT TC GAA | CT T TCTTT- - | AATTATA |
| GTTTTATCTCTTTCTCCTTT | | | | |
| CTCACAAAAA | | | | |

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|---|-----------|------------------------|-------|--------------|
| GAM34 TTTTCTTTGGTACAAAATT 20 TCTTTGGTAC 369 | T | TT CACAA | ---- | CA A |
| TCACACAAGTTTTTATACAG | AAAATTTAC | TTTTTCTT GGTACAAAA | TCA | GTTTT TATA |
| GACAA T | | | | |
| ACAAATTCTTGTCCATATAT | ACAA | | | |
| TTTAAACATTGACTTTTGT | | AAAAAGAA TCATGTTTT AGT | CAAAA | ATAT CTGTT T |
| ACTAAGAAAAA | - | C- TA--- | TTTT | AC C |

GAM35 AGAGATAAACTTTTTTACG 21 TGAGACCATC 370 -- AC ----- A A AAGA A T
ACTCCATCAGAAAGAGGTTT GAAGGAGACT AGAGATA AAACTTTTTT GA CTCC TC GA
GTTTT ATA T

| | | | |
|----------------------|------|--------------------|---------------------|
| AATATTTTTGTGAGACCATC | CCAT | | |
| GAAGGAGACTCCATCAGAAA | | TTTTTAT TTTGGAGAAA | CT GAGG AG CT CCAGA |
| TGT T | | | |
| GAGGTTTAATATTTTT | AA | GA ACCTCA | A - A--- G T |

| | | |
|--|------------------|--------------------------------|
| GAM36 ATAAAAATATTTTTGTAAAA 22 AATATTTTTG 371 | AAAA | A-- GA |
| CTTTTTTATGAGACCATCA | TAAAACTTTT | ATAAAAATATTTTTGT CTTTTTT TGA C |
| AAGAGAGAAAGAGAATAAAA | TTTA | |
| ATATTTTTGT | TGTTTTTATAAAAATA | GAAAGAGA ACT / |
| | AGA- | GAA AC |

| | | |
|--|------------|--------------------------------|
| GAM37 ATAAAAATATTTTTGTAAAA 23 AATATTTTTG 372 | AAAA | A-- GA |
| CTTTTTTATGAGACCATCA | TAAAACTTTT | ATAAAAATATTTTTGT CTTTTTT TGA C |
| AAGAGAGAAAGAGAATAAAA | TTTA | |

GAAGAGAG

GAM43 CTTTTTTACGACTCCATCAG 29 CATCAGAAAG 378 A CTCCA G G T A G GACCA -
AAAGA
AAAGAGGTTTAATATTTTTG AGGTTTAATA T CGA TCA AAAGA GTT AAT TTTTT TGA TCG
AAGAGAG G
TGAGACCATCGAAGAGAGAA TTTT | ||| ||| |||| ||| |||| ||| ||| |||||
AGAGATAAACTTTTTTACG A GCT AGT TTTTT TAA TTG AGAAA ACT AGC TTTTTTC
A
ACTCCATCAGAAAGAGGTTT - ACCAG G A T G G ACCTC A AAAAT
AATATTTTTGTGAGACCATC
GAAGAGAG

GAM44 CTTTTTTACGACTCCATCAG 30 CATCAGAAAG 379 A CTCCA G G T A G GACCA -
AAAGA
AAAGAGGTTTAATATTTTTG AGGTTTAATA T CGA TCA AAAGA GTT AAT TTTTT TGA TCG
AAGAGAG G
TGAGACCATCGAAGAGAGAA TTTT | ||| ||| |||| ||| |||| ||| ||| |||||
AGAGATAAACTTTTTTACG A GCT AGT TTTTT TAA TTG AGAAA ACT AGC TTTTTTC
A
ACTCCATCAGAAAGAGGTTT - ACCAG G A T G G ACCTC A AAAAT
AATATTTTTGTGAGACCATC
GAAGAGAG

GAM45 CTTTTTTACGACTCCATCAG 31 CATCAGAAAG 380 A CTCCA G G T A G GACCA -
AAAG
AAAGAGGTTTAATATTTTTG AGGTTTAATA TT CGA TCA AAAGA GTT AAT TTTTT TGA TCG
AAGAGAG A
TGAGACCATCGAAGAGAGAA TTTT || ||| ||| |||| ||| |||| ||| ||| |||||
AGATAAACTTTTTTACGAC AA GCT AGT TTTTT TAA TTG AGAAA ACT AGC
TTTTTTC T
TCCATCAGAAAGAGGTTTAA - ACCAG G A T G G ACCTC A AAAA
TATTTTTGTGAGACCATCGA
AGAGAG

GAM46 GTGTGCCTGAATCGTTCGAT 32 TGAATAGAGT 381 C TTCGAT C C CAA
TAACCCTACTCATCCAATTT TATCGATTCA GTGTG CTGAATCG TAAC CTA TCATC T
CAGATGAATAGAGTTATCGA GACA |||| ||||| ||| ||| ||||
TTCAGACACAC CACAC GACTTAGC ATTG GAT AGTAG T
A T----- A A ACT

GAM47 TCAGAAAGAGGTTTAATATT 33 AGAGGTTTAA 382 AAA GTTT-- GAGACCA- GA
TTTGTGAGACCATCGAAGAG TATTTTTGTG TCAG GAG AATATTTTTGT TC A
AGAAAGAGAATAAAAAATATT AGAC |||| ||| ||||| ||| ||
TTATGACTCCATTGA AGTT CTC TTATAAAAATA AG /
AC- AGTATT AGAGAAAG AG

GAM48 TTTTATGAGACCATCAAAGA 34 AGAGAGAAAG 383 ACCA AAG AGA- AAAA A-
- GA
GAGAAAGAGAATAAAAAATAT AGAATAAAAA TCA AGAGAAAG ATAAAAATATTTTTGT
CTTTTTTT TGA C
TTTTGTAAACTTTTTTTAT TATT ||| ||||| ||||| ||||| ||||| |||

GAGACCATCAAAGAGAGAAA AGT TTTTTTC TGTTTTTATAAAAATA GAAAGAGA
 ACT /
 GAGAATAAAAATATTTTTGT CCAG A-- AAAA AGA- GAA AC
 AAAACTTTTTTTTATGAGACC
 ATCAAAGAGAG
 GAM49 TTTTATGAGACCATCAAAGA 35 GAAGAGAGAA 384 ACCA AAG AGA- AAAA---
 - A
 GAGAAAGAGAATAAAAATAT AGAGAATAAA TCA AGAGAAAG ATAAAAATATTTTTGT
 CTTTTTTTG TG G
 TTTTGTAAACTTTTTTTGT AATA ||| ||||| ||||||||| ||||| ||
 GAGACCATCGAAGAGAGAAA AGT TTTTTTC TGTTTTTATAAAAATA
 GAGAGAAGC AC A
 GAGAATAAAAATATTTTTGT CCAG A-- AAAA AGAGAAA T C
 AAAACTTTTTTTTATGAGACC
 ATCAAAGAGAG
 GAM50 TTTTCTTAGTACAAAAGTC 36 TCAATGTTTT 385 A- G- AT--- AAAA G
 AATGTTTTAAAATATATGGA AAAATATATG TTTTCTT GTACAAA TCA GTTTT
 TATATGGACAA A
 CAAGAATTTGTCTGTATAAA GACA ||||| ||||| || ||| |||||||
 AACTTGTGTGAAATTTTGTA AAAAGAA CATGTTTT AGT CAAAA ATATGTCTGTT A
 CCAAAGAAAA AC AA GTGTT ---- T

 GAM51 ATGTAGTAATCGTTGTCGTG 37 ATGGTTCTTT 386 C TG GTGTTCC-- TCC TTCTCC -
 T TTCT
 TTCCTGTTTCCTACTTCTCC CCGTACAACA AT GT TC TGTT TAC AATCAT
 ATAGATATT TCT A
 AATCATATAGATATTTTCTT TACT ||| || ||| ||| ||||| ||||| |||
 TCTATCATGGATAATATTG TATA AG ACAA ATG TTGGTA TGTTTATAA AGG /
 TAATGGTTCTTTCCGTACAA - GT ATTTGTCAT C-- CCTTTC A T TACT
 CATACTGTTTAGATGATATT
 GCGCAT
 GAM52 GAATGACTCGTCCCTTAATA 38 TGA CTGCTCC 387 GA G TAATA AGTAG - TCT
 GGCAGTAGGCTAGTATCTTT CTTAATAGGC GAAT CTC TCCCT GGC GCTA GTA T
 TTTACGTAGTAATCGTCGTA AGTA ||| ||| ||| ||| ||| |||
 GGGAGAGAATTC CTTA GAG AGGGA CTG TGAT CAT /
 A- - TG--- CTAA- G TTT

 GAM53 GAGATTGTATCAGTTTCGTA 39 GATTGTATCA 388 -- - T TA TGA G T
 GTCTTGAGTATTGGTATTAC GTTTCGTAGT GAGATTGTA TC AGT TCG GTCT GTATTG TAT A
 TATATAGTATATAGATGTCG CTTG ||||| || ||| ||| ||||| |||
 ACGCTAGATATACAGTCTC CTCTGACAT AG TCG AGC TAGA TATGAT ATA C
 AT A C TG TA- - T

 GAM54 GGCAAATCTTATCATTGGTC 40 TAACATCGAT 389 CTT - --- TG- TTGCTTT
 GGTGTTTGGTCTTGCTTTGT TCCCATATGA GGCAAAT ATCAT TGG TCGGTGTT GTC G
 GACTTTGATAATAACATCGA TGTT ||||| ||||| ||| ||||| |||
 TTCCCATATGATGTTTGT TTGTTG TAGTA ACC AGCTACAA TAG /

--- T CTT TAA TTTCAGT

GAM55 AGTATGTTGTACGGAAAGAA 41 TGATTGGAGA 390 -- A GAAAGAA ATTACAAA A- TG--
- AAGA

CCATTACAAATATTATCCAT AGTAGGAAAC AGTA TGTTGT CG CC TATT TCCA
ATAGA A
GATAGAAAGAAAATATCTAT AGGA ||| ||||| || || ||| ||| ||||
ATGATTGGAGAAGTAGGAAA TCAT GCAACA GC GG ATGA AGGT TATCT /
CAGGAACACGACAACGATTA TA - ACAA--- ACAAAGG- AG TAGTA ATAA
CT

GAM56 AAAATCGATTCCGTCCAAGA 42 TCGATTCCGT 391 C CCAAG AAAAACA
TGATAAAACATTTACCGGC CCAAGATGAT AAAAT GATTCCGT ATGAT T
ATCATAAACACGGAGTTTAT AAAA |||| ||||| ||||
TTT TTTTA TTGAGGCA TACTA T
T CAAA- CGGCCAT

GAM57 CATGGAGATACTTTATTACT 43 TAATGTCCTG 392 ----- T TAAATA
CCATTAAATAATTTATCATG TTTCATTTGT CATGGAGAT AC TTATTACTCCAT A
GAGTGATAATGTCCTGTTTC TTCC ||||| || |||||
ATTTGTTTCCATG GTACCTTTG TG AATAGTGAGGTA /
TTTACTTTGTCC T CTATTT

GAM58 ACTGTATGCTCCTAGCGGAG 44 TGTATGCTCC 393 A - A AATCCTTCG T
TTAATCCTTCGTTGTTTCTA TAGCGGAGTT ACTGT TGCTC CT GCGGAGTT TTGT T
CAAAGTCTCTCGACTCCGCG AATC |||| |||| || ||||| |||
AGAGAGTAACAGT TGACA ATGAG GA CGCCTCAG AACAC
- A G CTCTCTGA- T

GAM59 ATACGGAATATCTACGTCCA 45 TCATCGGGTG 394 C C----- GT - T T
TGTCATTATTGTCATCGGGT TATTCTCATT ATA GGAATAT TAC CC ATG CA T
GTATTCTCATTATATTCTC CATA ||| ||||| ||| || ||| ||
TAT TAT TCTTATA ATG GG TAC GT A
C CTTACTCTT TG C T T

GAM60 GCAATACTTCTGGTCTCGGA 46 TTCTGGTCTC 395 ACTTC A ----- C
TTAGGCGTCGTTACGTATAT GGATTAGGCG GCAAT TGGTCTCGGATT GG CGT G
ATCCACCAATCCGAGACCAT TCGT |||| ||||| ||| |||
TGATTGC CGTTA ACCAGAGCCTAA CC GCA T
GTT-- - ACCTATATAT T

GAM61 GCTTTGCAAATTGTATATTA 47 ATCGATCATA 396 TT ATT TAT C C CCGC AAT A
TTT
TTGACATCGACCGCGTAATA TCTATATCAT GCT GCAA GTATAT TGA AT GA GT ATAGT
GAG T

| | | |
|----------------------|------|--|
| TAGTAGAGTTTTATTCTCAT | CCAT | |
| TATCGATCATATCTATATCA | | TGA CGTT CATGTA ACT TA CT TA TATTA CTC / |
| TCCATGTACTTGCTTAGT | | TT --- CCT A T ATAC GC- - TTA |

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|-------|-------------------------|----------------|-----------------------------|
| GAM62 | GTCGTTCTCGTTCAGAATCT 48 | TTGAAGACTC 397 | T GTTC A TCG - G G |
| | TTCCGAGAGAC | GTCGT CTC | AGA TCTT CAGC ATAAGTA TAT T |
| | TCGATATACTTATCGTTGAA | GAT | |
| | GACTCTTCCAGAGACGAT | TAGCA GAG | TCT AGAA GTTG TATTCAT ATA C |
| | - ACCT C --- C - G | | |

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|-------|-------------------------|-------------------|--------------------------|
| GAM63 | TAACAATATATTATTAGTTT 49 | TTAATAATAT 398 | ----- TA |
| | ATATTACTGAATTAATAATA | AAAATTCCCA | TAACAA TATATTATTAGTTTA T |
| | TAAATTCCCAATCTTGTTA | ATCT | |
| | ATTGTT | ATATAATAATTAAGT T | |
| | CTAACCCCTTAAA | CA | |

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|-------|-------------------------|-----------------|----------------------------|
| GAM64 | TCTCAATAAGAAGATTAACG 50 | TGGGGTACT 399 | C AA AACGAT-- CTA |
| | ATTTCCATGTCTACATTATA | CTAAATCGCT | TCT AATAAG GATT TTCCATGT C |
| | TGGGGTACTCTAAATCGCT | TGTT | |
| | TGTTTAGA | AGA TTGTTC CTAA | GGGGTATA / |
| | T G- ATCTCATT | TTA | |

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|-------|-------------------------|-----------------|---|
| GAM65 | TGTATTCAGTCAGACAATGT 51 | TTAGTAGCGT 400 | A - AA TGACGTCG G C G |
| | CTGACGTCGGCCACGGTATT | GGCAATGACA | TGT TTCAGT CAGAC TGTC GCCACG TATT |
| AGG A | | | |
| | CAGGGAGTCCTTAGTAGCGT | GGGT | |
| | GGCAATGACAGGGTCTGAAC | | ACA GGGTCA GTCTG ACAG CGGTGC ATGA TCC G |
| | TGGGCACA | C A GG TAA----- | G T T |

| | | | |
|-------|-------------------------|----------------|--|
| GAM66 | TTGATATTACTTATAATAAC 52 | TTAATTGTAA 401 | T T--- CG -TG -- TT T |
| | GATTTGTTTAATTTTTAGTT | ATGATATTAT | TTGATA TACTTA AATAA AT T TTTA ATT TAGT T |
| | TATACTATTAATTGTAAATG | TATT | |
| | ATATTATTATTTTTTTAAGT | | GACTAT ATGAAT TTATT TA A AAAT TAA ATCA A |
| | ATTATCAG | T | TTTT AT TGT GT TT T |

| | | | |
|-------|-------------------------|----------------|---------------------|
| GAM67 | TTTAAACTTTGGCATATACA 53 | AGATAACATA 402 | CTT CATATACAA-- ACT |
| | AGTCTATACTTTTAGTAGAT | CCACACCATT | TTTAAA TGG GTCTAT T |
| | AACATACCACACCATTTTTT | TTTT | |
| AAA | | AAATTT ACC | TAGATG / |
| | TTT ACACCATACAA | ATT | |

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|-------|--------------------------|----------------|-------------------------------|
| GAM68 | TTTCTTTTTCACGATGCATCT 54 | ATAAGTGGAC 403 | TC- GA- ----- GA CGT |
| | TATTGAATGACGTTTTCTCA | ATATAGATGC | TTTCTTT AC TGCACT TATT ATGA T |

TAAGTGGACATATAGATGCA AGAA ||||| || ||||| ||| |||
GAAGTAATGAAGAAA AAAGAAG TG ACGTAGA GTGA TACT /
TAA AAG TATACAG A- CTT

GAM69 TCGATGATACATGTATTAAA 55 TGATACATGT 404 A--- TGTA T TCC
ATACTTTCCGAATAAGTCTT ATTAAAATAC TCG TGATACA TAAAA ACTT G
TTAAATATTGTATTAATTAT TTTC ||| ||||| ||||| |||
GA AGT ATTATGT AATTTT TGAA /
ATTA TATA C TAA

GAM70 TGATAATACTTAAAAAATA 56 TAAAAATTAA 405 A AAAAA ATCATTAC AA A
ATAATATCATTTACAATTAA ACAAATCGTT TGATA TACTT ATAATAAT AATT TAGT T
TAGTATAAACTAAAAATTAA ATTA ||||| ||||| ||| |||
ACAAATCGTTATTATAAGTA ACTAT ATGAA TATTATTG TTAA ATCA A
ATATCA A ----- CTAAACAAA AA A

GAM71 AGCAGCGAACAACAACATCA 57 ATGGATTCTG 406 AACAAAC T TAT CA
GATATTTTCATCGACATTTTT TGTTTATGCT AGCAGCG AACACAGA TTCATCGA T
GATGGATTCTGTGTTTATGC GTT ||||| ||| ||| |||||
TGTT TTGTCGT TTGT GTCT AGGTAGTT /
AT---- - T-- TT

GAM72 TAACAAGATTGGGAATTTTA 58 TAATATAAAC 407 GATTGGGAAT- AA
TATTATTAATTCAGTAATAT TAATAATATA TAACAA TTTATATTATT T
AAACTAATAATATATTGTTA TTGT ||||| ||||| |||||
ATTGTT AAATATAATGA /
ATATAATAATC CT

GAM73 TACATGCTGACATCTAATGC 59 TCTCTAGCGT 408 C ATCTAATGCC AA -- C- T
AATA
CTGTATAACCATGAGAGCAT GGATACAGTC TACATG TGAC TGTAT CCATG AGAG ATC
AC C
CTACAATACATACCGTCGAT ACCG ||||| ||| ||||| ||| ||| |||
ATCTCTAGCGTGGATACAGT ATGTGC ACTG ACATA GGTGC TCTC TAG TG A
CACCGTGTA C ----- -- GA TA C CCAT

GAM74 TCCGTTTTTATCAGTATGTA 60 TATCAGTATG 409 T----- TGTA- C AT T
TATCTATATTAACGTCGTCG TATATCTATA TCCGTTTT ATCAGTA TAT TAT TAACG C
TTGTAGTGAATAGTAGTTAT TTAA ||||| ||||| ||| ||| |||
TGATCTATTATATGAAACGG AGGCAAAG TAGTTAT ATA GTG GTTGC G
A TATATTATC TGATG A AT T

GAM75 TGCTAAATATGCGATGTATC 61 TATTATACAA 410 A- - T TCTAT A T- AACAAATAC

TATGTTATTTGTATTTATCT AAATTTTSTA TGCT AATATGC GA GTA GTT TTTGTAT TATCTA
 C
 AAACAATACCTCTACCTCTA TTTC ||| ||||| || ||| || ||||| |||||
 GATATTATACAAAAATTTT ATGA TTATACG CT TAT TAA AAACATA ATAGAT /
 TATTTGAGCATATTAAAGTA AA A T TTTT- - TT CTCCATCT

GAM76 TTTTGATTACGATGTTATAA 62 TATAACATCG 411 ATGT TTAATT TG GAT
 GAATGTAGTTAATTGATGTA TAATCAAAA TTTTGATTACGATGTTATAAGA AG GA TAT G
 TGATGTTAATGTGTCCTCTT ||||| ||||| || |||
 TCCTCTTATAACATCGTAAT AAACTAATGCTACAATATTCT TC CT GTA /
 CAAAA CCTT TC---- GT ATT

GAM77 GATTTTGTGATTTTCTTCC 63 ATAGTTAGAT 412 TTTT TTT TC A A
 TAACTGTTTACGTAAATAG AGAATATTCA GA GTGA TTCT CTAA CTGTTT C
 TTAGATAGAATATTCATTAG TTAG || ||| ||| ||| |||||
 TTC CT TACT AAGA GATT GATAAA G
 TGAT TAT TA - T

GAM78 GCGTCAAATATTTCCCGTTT 64 TGGTATGTTT 413 CAA- CC TTA- GTCAAGA
 AATATCGCATTGTGCAAGAT ACGATAAGTA GCGT ATATTT CGT ATATCGCATT T
 AATAATAGAGTGTGGTATGT TAAT ||| ||||| || |||||
 TCACGATAAGTATAATAACG CGCA TATGAA GCA TATGGTGTGAG /
 C ATAA TA CTTG ATAATAA

GAM79 TATCTTTTAAGAATTGTGGA 65 TCTTTTAAGA 414 C A GATAT GA TA
 TATTAGGATATTATTACGTA ATTGTGGATA TAT TTTTA GAATTGTG TAG TAT T
 AACTATTACACAATTCTAAA TTAG ||| ||||| ||||| ||| |||
 ATATA ATA AAAAT CTTAACAC ATC ATG T
 T - ATT-- AA CA

GAM80 ATTTAGACTGATGTATGGGT 66 TTCTCATCAT 415 GA T T - GTTT
 AATAGTGTGTTGAAGAGCTCG CAGAATAAAT ATTTA CTGATG ATGGG AAT AGT G
 TTCTCATCATCAGAATAAAT |||| ||||| ||||| ||| |||
 TAAAT GACTAC TACTC TTG TCG /
 AA - - C AGAA

GAM81 AGCCGCTGAGTGGTAAACAA 67 CCGCTGAGTG 416 C ---- CAACA- AG
 CAGAACAGATAGTTTATTAT GTAAACAACA AGC GCTGAG TGGTAAA GAAC A
 CTTTACCAACACCCTCAGCC GAAC ||| ||||| ||||| |||
 GCT TCG CGACTC ACCATTT TTTG /
 C CCACA CTATTA AT

GAM82 GACTAGATCCGTTAGTTTAA 68 CGTTAGTTTA 417 CCGTT T T CATC- TA

| | | | | | | | | |
|----------------------|------------|----------|---------|---------|------|-------|-------|---|
| TATCCTCAGTCATCTTGTCT | ATATCCTCAG | GA | CTAGAT | AGTTTAA | ATCC | CAGT | TTGTC | G |
| AGAATGGCAAATCTAACTGC | TCAT | | | | | | | |
| GGGTTTAGGCTTTAGTTTAG | | TTGATTTG | TCGGATT | TGGG | GTCA | AACGG | A | |
| TT | ATT-- | - | C | ATCTA | TA | | | |

| | | | | | | | | |
|-------|----------------------|----|------------|--------|----------|--------|------------|---------|
| GAM83 | GGATGTAAAATGTTGATGAT | 69 | TTGATGATAT | 418 | AAAAT | A | CTACATCGTT | TTT |
| | ATCTACATCGTTTGGATTTT | | CTACATCGTT | | GGATGT | GTTG | TGATAT | TGGAT T |
| | TATGTATCCACTTTAATAAT | | TGGA | | | | | |
| | ATCATAGCTGTAACATCC | | | CCTACA | CGAT | ACTATA | ACCTA | A |
| | | | ATGT- | - | ATAATTC- | TGT | | |

| | | | | | | | | | | |
|-------|-----------------------|----|------------|------|-----|------|--------|-----|--------|-------|
| GAM84 | GTCCGTATCCAGTCAACACT | 70 | TAGCTTTCAC | 419 | C | CC | C | CA | TA | T |
| | ATGTTAGCATTCTGTGCGAT | | TCATATGAC | | GTC | GTAT | AGT | AA | CTATGT | GCA T |
| | ATAGCTTTCACATCATATGAC | | | | | | | | | |
| | | | CAG | TATA | TCA | TT | GATATA | TGT | T | |
| | | | - | C- | C | TC | GC | C | | |

| | | | | | | | | | | |
|-------|----------------------|----|------------|--------|---------|---------|-----------|-----------|------|----|
| GAM85 | TAGCTTTCATAGTTAGATAC | 71 | CAGAAGTAGG | 420 | ---- | GTCTCA- | --- | T | A | CT |
| | ATGGTCTCAGAAGTAGGATT | | ATTATGTAAC | | AGTTAG | ATACATG | GAA | GTAGGATTA | | |
| | GTAAC TCAG TCG A | | | | | | | | | |
| | ATGTAACATCAGCTTCGATA | | ATCA | | | | | | | |
| | AAATGACTGGGTTATTTAGT | | | TCAATT | TATGTAC | CTT | CATTCTGAT | TATTG | GGTC | |
| | AGT A | | | | | | | | | |
| | CTTACACATTCGCTCATACA | | | GCCAG | ATACTCG | ACA | T | - | -- | AA |
| | TGTATGACCGTTAACTACAG | | | | | | | | | |
| | AGTCTA | | | | | | | | | |

| | | | | | | | | | |
|-------|----------------------|----|------------|--------|--------|--------|--------|------|-------|
| GAM86 | TCGTAAGATACTCCTTCATG | 72 | TATGAAGTAA | 421 | A | C-- | GAAC | TCA | A |
| | AACATAATCAGTTACAAAAC | | AGTATCTACG | | TCGTA | GATACT | CTTCAT | ATAA | GTT C |
| | GTTTATATGAAGTAAAGTAT | | A | | | | | | |
| | CTACGA | | AGCAT | CTATGA | GAAGTA | TATT | CAA | A | |
| | | | - | AAT | ---- | TG- | A | | |

| | | | | | | | | |
|-------|----------------------|----|------------|-------|--------------|-------|--------------|-----------|
| GAM87 | TTCACCGTTTGCATGTTACC | 73 | CCGTTTGCAT | 422 | C | C | TTACCACTATCA | AA |
| | ACTATCAACCGCATAATACA | | GTTACCACTA | | TTCAC | GTTTG | ATG | ACCGCAT T |
| | ATGCGGTGTTTCCTTTGTCA | | TCAA | | | | | |
| | TCAAATTGTGAA | | | AAGTG | TAAAC | TAC | TGGCGTA | A |
| | | | T | - | TGTTTCCTTTG- | AC | | |

| | | | | | | | | | | | | |
|-------|-----------------------|----|-------------|--------|--------|-------|-----|-----|---------|---------|---------|---|
| GAM88 | TTTCAGGAGATGATCTCGCC | 74 | GCTACAGTTC | 423 | ----- | - | C | C | T | TACCA-- | A | T |
| | GTAGCTACCATGATAGTAGA | | CTTGTTTCGTC | | TTTCAG | GAGAT | GAT | TCG | CG | AGC | TG | |
| | TAGTAGA G | | | | | | | | | | | |
| | TGCCTCTGCTACAGTTCCTT | | GACA | | | | | | | | | |
| | GTTTCGTCGACATCTATCTTT | | | AAAGTC | TTCTA | CTA | AGC | GC | TTG | AC | ATCGTCT | C |
| | GCATTCTGAAA | | | TTACGT | T | C | T | - | TTCCTTG | - | C | |

GAM89 TGATGCATTAATTTTTGTAT 75 TGCATTAATT 424 C A A TTC CCTAAAA AAAA
AATAAG
TGATTCTCAATCCTAAAAAC TTTGTATTGA TGATG ATTA TTTTTGT TTGA TCAAT ACT
TATG T
TAAATATGAATAAGTATTA TTCT ||||| ||||| ||||| ||||| ||||| ||||| |||||
AACATAGCGGTGTACTAATT ATTGT TGAT AAAAATA AATT AGTTA TGG ATAC /
GATTTAACATAAAAAATAGT - A C T-- ATCATG- CG-- AAATTA
TGTTA

GAM90 GTTGTTTTGCGATAGCCATG 76 TGTTTTGCGA 425 TG T A CCAT---- A CAG
TATCTACTAATCAGATCTAT TAGCCATGTA GT T TTGCG TAG GTATCT CTAAT A
TAGAGATATTATTAATTCTG TCTA || ||||| ||||| ||||| |||||
GTGCAATATGAC CA A AACGT GTC TATAGA GATTA /
GT T G TTAATTAT - TCT

GAM91 ACTGATTCTGGACATAGCTT 77 TAAGTTTGGC 426 T GACA T C G----- AT
TCCGACTGGCGCATTTGGTG AGCTAGCAGA ACTGA TCTG TAGCT TC GACT GCGC T
TGATGGTTCCCATAAAGTTTG TTCA ||||| ||||| ||||| ||||| |||||
GCAGCTAGCAGATTCAGT TGACT AGAC ATCGA GG TTGA TGTG /
T G--- C T ATACCCTTGGTAG GT

GAM92 ATATGTGTATTATCAGATAT 78 TCCTCCTAGG 427 T T AAAATTTT ATG
CCAAAATTTTGTATGAAGAA ATATTTGTAA ATATG GTATTA CAGATATCC GT A
CTCCTCCTAGGATATTTGTA TATC ||||| ||||| ||||| ||||| |||||
ATATCTATGT TGTAT TATAAT GTTTATAGG CA /
C - ATCCTCCT AGA

GAM93 ATCATCATTTTTTTCACCATT 79 TGAGAATACT 428 A TTTTCACCATTAC TC - CA
ACTTCTTCCATGTCCAATAT AAAATTCCTA ATCATC TT TTCT CATG TC A
GATCATGTGAGAATACTAAA ACGA ||||| ||||| ||||| ||||| |||||
ATTCTAACGATGAT TAGTAG AA AAGA GTAC AG T
C TCCTTAAATCAT GT T TA

GAM94 GAAATTGTTGCTCCCATGGA 80 TAATAGTTAC 429 AA T TCC GAA CCAA T
ATGACCCAATAAGTAGATT CACGTGCTGT GA TTG TGC CATG TGAC TAAG A
AATAGTTACCACGTGCTGTA ACCA || ||||| ||||| ||||| |||||
CCAAAGTC CT AAC ATG GTGC ATTG ATTT G
GA C TC- ACC ATA- A

GAM95 TGGTTCTTTCCATAGTACAT 81 TCCATAGTAC 430 TCT GTACATAG GGTG
AGTTGTTGCGGTGCAGAAGC ATAGTTGTTG TGGT TTCCATA TTGTTGC C
AATAAATACAGAGTGTGGAA CGGT ||||| ||||| ||||| |||||
CACCA ACCA AAGGTGT AATAACG /

C-- GAGACATA AAGA

GAM96 TTAATAGTTTACACCTTTTA 82 TAGTAGGACT 431 TTTTA A C TA-- -- CAT CT
GAATTCCA
GTAGGACTAGTATCGTACAA AGTATCGTAC ACACC GT GGA TAG TCGT ACAATT AG
GTATTTT A
TTCATAGCTGTATTTTGAAT AATT ||||| ||||| ||| ||||| || |||||
TCCAATCACGCATAAAAATA TGTGG TA CCT ATC AGCA TGTAA TC TATAAAA
T
TCTTCCAATTGTTGACGAAG CCTAC - A CAGA GT CCT -- ATACGCAC
ACCTAATCCATCATCCGGTG
TAATATTAA

GAM97 TTCATCCGATAAACTCCAAT 83 TTTGTGGTAT 432 - AACT A G GATA
AAAAAGATGATATATCTAGT TGGATAGAA TTC ATCCGATA CCA TAAAAA AT T
GTTTTTGTGGTATTGGATAG ||| ||||| ||| ||||| ||
AA AAG TAGGTTAT GGT GTTTTT TG A
A ---- - G ATCT

GAM98 TTAGTGACAGACCAGACCTA 84 TGACAGACCA 433 T ----- GA --- TC
GGAGCTATTCTACCATAGCA GACCTAGGAG TTAG GACAGA CCA CCTAGGA GCTAT T
AATCTTAGGCATGGACATAC CTAT ||| ||||| ||| ||||| |||||
TAATATCTGTCTTAA AATT CTGTCT GGT GGATTCT CGATA A
- ATAATCATACA AC AAA CC

GAM99 AACAAAGAAATGGAAATCGT 85 TTGAAATTGT 434 AG T TAATACC T
AATACCAGTTATGTTTAACT TTTTATTTT AACAA AAATGGAAA CG AGTTA G
TTGAAATTGTTTTTTATTTT CTTG ||||| ||||| ||| |||||
CTTGTT TTGTT TTTATTTT GT TCAAT T
CT T TAAAGTT T

GAM100 TTCCACTGTCCAAAATGATG 86 TCCAAAATGA 435 ACT A G - C CCTTTTTA
CCTCTGCCTTTTTTATACATG TGCCTCTGCC TTCC GTCCAA AT ATG C TCTG T
TTCCAGATGTCATAATATTG TTTT ||||| ||||| ||| |||||
GATTGGGAA AAGG TAGGTT TA TAC G AGAC /
GT- A A T T CTTGTACA

GAM101 CTGTGACCAAGATAGAGAGC 87 GTGAATCCAT 436 ACCA GCTCC-- TGAAT T CTA
AGTTT
TCCTTTGGTGAATCCATCTC CTCTATGTTT CTGTG AGATAGAGA TTTGG CCA CT
TGTTTC A
TATGTTTCAGTTTAACCAAG CAGT ||||| ||||| ||||| ||| ||| |||||
AAACAGTCAGCTGGTCTAAA GACAT TCTATCTCT AAATC GGT GA ACAAAG /
ATTTCCATCTCTATCTAATA AA-- ACCTTTA T---- C CTG AACCA
CAG

GAM102 GTTCTTTTAGAAGTGATTC 88 GAAGTGATTC 437 T-- GAA TT- A G
 TTTGATGGTGTGACGATACG TTTGATGGTG GTTCT TTA GTGATTC TG TG T
 AATTACAATAATGCAGAAAC TCAG ||||| || ||||| |||
 CAAAGA AAT CATTAAG AC AC G
 CGT AA- CAT G T

GAM103 TTGATACGATATTTGTTGGA 89 TTTGTTGGAT 438 TACGA- - CCTG TT
 TTCCTGATTATTTACTATAA TCCTGATTAT TTGA TATTTGT TGGATT ATTAT A
 TATAATCTAGACAGATAGAT TTAC |||| ||||| ||||| ||||
 GATTCGA AGCT ATAGACA ATCTAA TAATA /
 TAGTAG G TA-- TC

GAM104 AATATCGGGCCAATAGTAGC 90 GGCCAATAGT 439 CG A AG - C
 TATTACCGTGCACACGTGTA AGCTATTACC AATAT GGCCA TAGT CTATTAC CGT G
 GTGGGAACATATGGCCAAATG GTCG |||| |||| |||| ||||
 TT TTGTA CCGGT ATCA GGTGATG GCA A
 AA - AG T C

GAM105 AGACTTCTGGCGGTTGCCAT 91 TTATCCCAAT 440 ---- CG CCAT- ATA
 AGAATATACGTCGTTCTTAT TACCAACTAG AGACTTCT GG GTTG AGAAT C
 CCCAATTACCAACTAGAAGT AAGT ||||| || |||| ||||
 CT TCTGAAGA CC TAAC TCTTG /
 TCAA AT CCTAT CTG

GAM106 GAAGTTTTTGGAGAATAATA 92 GGAATTGGAG 441 GAATAAT ----- TATT CA
 ACAA G
 TGAATCATGATCTATTTTCGT GCGATGATCT GA ATGACTCAT GATC TCGTC TAA
 TCTA A
 CCATAACAATCTAGACATA TAAT || ||||| |||| |||| ||||
 GGAATTGGAGGCGATGATCT CT TGCTGAGTA CTAG AGCGG GTT GGAT
 C
 TAATTTTGTGCAATGAGTCG AAC---- ACGTGTTTAAATT T--- AG AA-- A
 TCAATCCTATAACTTC

GAM107 TAATCCCTTTTTCAGATGCC 93 GCGCTCCCCT 442 - TTTTCA GCCTCTTTTA CA
 TCTTTTAGTTTATCAAAAAT AGTCGACTC TAATCC CT GAT GTTTAT A
 AAGCGCTCCCCTAGTCGTAC AGAG ||||| || ||||
 TCAGAGGATTA ATTAGG GA CTG CGAATA /
 A CTCATG ATCCCCTCG- AA

GAM108 TTAAATAGTTACGCAATATC 94 TTAGCTGTTT 443 TTAC T C----- T- T
 TCAATAGTTTCATAATTGTT TCATCAAGAT TTAAATAG GCAA ATCT AATAGTT CA A
 AGCTGTTTTTCATCAAGATTT TTGT ||||| |||| ||||| ||
 GTACCCTGTTTAA AATTTGTC TGTT TAGA TTGTCGA GT A
 CCA- - ACTACTT TT T

GAM109 TGCCGTTACTATTATTTATA 95 TATTATTTAT 444 C AT--- TAA TG A C
 ACTGATGTAACCCACGTAAC AACTGATGTA TGC GTTACTATT TTA C ATGT AC C
 ATTGGAATTAACATATCGATA ACCC ||| ||||| ||| | ||| ||
 GTAATGCA ACG TAATGATAG AAT G TACA TG A
 - CTATC TAA GT A C

GAM110 ACACGCGTGTCTAACTAGTG 96 ACGCGTGTCT 445 G - A TCGTCA T AGTT A
 GAGGTTCTGTCAGCTGCTCTA AACTAGTGGA ACAC CGTGTC TAACT GTGGAGGT GCTGC CT
 TGA T
 GTTTGAATCATCATCGGCGT GGTT |||| ||||| |||| ||||| |||| || |||
 AGTATTCCTACTTTTACAGT TGTG GCACAG ATTGA CATTTC A TGATG GG ACT C
 TAGGACACGGTGT - G - TCCTTA C CT-- A

GAM111 CAGCATCCGGCTTATCCGCC 97 CGAGGAGGAA 446 A T- - G C TCA
 TCCGTTGTCATAAACCAACG TATCGTCGGA CAGC TCCGGC TAT CC CCTC GTTG T
 AGGAGGAATATCGTCGGAGC GCTG |||| ||||| ||| || |||| ||||
 TG GTCG AGGCTG ATA GG GGAG CAAC A
 - CT A A - CAA

GAM112 CCATTAATATCTCTATTATA 98 TATACCAGAA 447 ATCTCTATTATAGCT AC TC
 GCTTCTGGACATAATTCATC TTAATGG CCATTAAT TCTGG ATAAT A
 TATTATACCAGAATTAATGG ||||| |||| ||||
 GGTAATTA AGACC TATTA T
 ----- A- TC

GAM113 CTTCAATTATGAATTGATTCT 99 TGAATTGATT 448 T T ---G TAT-- C-- CA TT TAG
 TT
 TGAGGTATAAACCTAACACA CTTGAGGTAT A GAAT GATTCT TAGG AAAC TAACA AA
 ATATTAT AC T
 AATTATATTATTAGACTTTT AAAC | ||| ||||| | ||| |||| ||| ||||| ||
 CGTATGTAATGTCTTTTCATG T TTTA CTAAGA G TCC TTTG ATTGT TT TGTAATG
 TG /
 TTATAAGTTTTTAATCCTGG - T TAA G TAATT AAT AC TC TA- CT
 AATAGAATCTATTTTAATGA
 GG

GAM114 GAAGAGATGTAACGGGAACA 100 ACGGGAACAG 449 -- ACG CAG TG
 GGGTTTGTTGATTTCGCAAAC GGTTTGTGTA GAAGAG ATGTA GGAA GGTTTGT A
 TATTCTAATACATAATTCTT TTCG ||||| ||||| |||| |||||
 C CTTCTT TACAT TCTT TCAAACG T
 AA AA- A-- CT

GAM115 GTTAATACGTCTTGACGTA 101 TGCACGTAAT 450 - C- CTAT CC
 ATCTATTATAGATGCCAAGA CTATTATAGA GTTAATA CGTCTTGCA GTAAT TATAGATG A

TATCTATATAATTATTTTGT TGCC ||||| ||||| ||||| |||||
AAGATGATGTTAAC CAATTGT GTAGAATGT TATTA ATATCTAT A
A TT AT-- AG

GAM116 GTTTTTGATATCGATCTGAT 102 TTCATATTTA 451 ATCG T CCTA A-
ATAACGTGCTC A TT
TGATCCTAGAACTAGATATA TTAGATACCG ATCTGAT GAT GAACT GATATATTA
ATTAGGC GT A
TTAATAACGTGCTCATTAGG CATT ||||| ||| ||||| ||||| ||
CAGTTTATGGCAGCTTGATA TAGATTA TTA CTTGA TTATATGAT TAGTTCG
CG /

ATTAGATATAGTATATTCCA CA-- T TA-- CC ATAGATTAA-- A GT
GTTTCATATTTATTAGATACC
GCATTGC

GAM117 TAATGGTGACAGGGTTAGCA 103 TATGATCCTC 452 T C GCA- CCAATCAATA TTT
TCTTTCCAATCAATAATTTT TCTCATTG TAATGG GA AGGGTTA TCTTT ATTTT A
TTTAGCCGGAATAACATCAT ||||| || ||||| ||||| |||||
CAAAAGACTTATGATCCTCT GTTACT CT TCCTAGT AGAAA TAAGG /
CTCATTG - C ATTC ACTACTACAA CCG

GAM118 TCGTTTAGATTTTCCATCTG 104 TAGGAGAGTT 453 TTA T TCCATCT TATCG A C CG-
A

CCTTATCGAATACTCTTCCG ACTAGGCCCA TCGT GA TT GCCT AAT CTCTT CGT
ATGTCT C
TCGATGTCTACACAGGCATA ACTG |||| ||| |||| ||| ||||| |||||
AAATGTAGGAGAGTTACTAG AGCA CT AG CGGA TTG GAGGA GTA TACGGA A
GCCCAACTGATTCAATACGA TAA T TCAACC- TCA-- A T AAA C

GAM119 TGATGTAGTACTTTGATGAT 105 TAAGTCTTCC 454 AGT T T TTCC CC
TTTTCCATGGCCCATTTCTAT AAGTTGGCAT TGATGT ACTT GA GATTT ATGG C
TAAGTCTTCCAAGTTGGCAT CA ||||| ||||| ||||| |||||
CA ACTACG TGAA CT CTGAA TATC A
GT- C T T--- TT

GAM120 TTGGTAACTCATTCTATATA 106 TAGAATATAC 455 A TC ----- G T GTT
TGCTTTTCTTGTTGATGAAG TCAATAGAAT TTGGTA C ATTCTA TATAT CT TCCTT G
GATAGAATATACTCAATAGA TTGT ||||| || ||||| ||||| |||||
ATTTGTACCAA AACCAT G TAAGAT ATATA GA AGGAA /
- TT AACTC A T GTA

GAM121 TTTCTAAGATATGGGATTTT 107 TAAGATATGG 456 A-- A G ACT T A TC
ACTTAATATAATATTATTTT GATTTTACTT TTTCT AGAT TGG ATTTT TAATA AAT TTATT C
CCGTAATAAATTTTATTAGA AATA ||||| ||||| ||||| ||||| |||||
AATGCCAAATCTATAAGAAA AAAGA TCTA ACC TAAAG ATTAT TTA AATAA C
ATA A G --- T - TG

GAM122 TCTAGTTATCAATAACAGTT 108 TCAATAACAG 457 GTTA C-- - TTAG- TA
 AGTAGTTTAGTTATACATTG TTAGTAGTTT TCTA TCAATAA AGTTAGTA GT TTA C
 AATCATACATATTAATTTT AGTT |||| ||||| ||||| || ||
 TTATTGAGATAGA AGAT AGTTATT TTAATTAT CA AGT /
 AG-- TTT A TACTA TA

GAM123 TCCGCACTATCGATTTGATA 109 TAAAGCTATC 458 CACT T- - - T
 CTTTCTTTTCAGAGTAAAGC GTCATTGATC TCCG ATCGAT TGATA CTTT CTT T
 TATCGTCATTGATCATCGGA ATCG |||| ||||| ||||| |||| ||
 AGGC TAGTTA GCTAT GAAA GAG C
 TAC- CT C T A

GAM124 TTCTAGAGTAGTAGTCCTAA 110 TCTTATTGTC 459 T CT CATTCTCT--- TTAT- TCCT
 TT ATGT GT
 TCATTCTCTTAAATTTTATG TGATTTATTT TAG AGTC AAT TAAATT GTA AGT CA
 CTC A
 TATCCTAGTTTCAATGTCTC CTTT ||||| || ||||| || ||| || ||
 GTAATGAGTTTGTGCTGCTC ATC TCGG TTA ATTTAG TAT TCG GT GAG /
 TTATTGTCTGATTTATTTCT - TT CCATTTTCTTT TCTGT TC-- TC GTTT TA
 TTTACCATTTTGGCTCTATT
 CTGAA

GAM125 GATCTATAGTCTTCGTATCT 111 TGTTACGAAA 460 - CTTC- CT T AA TAT TT
 GTTACGAAAATCAATATATT ATCAATATAT GATC TATAGT GTAT GTACGA ATCAA
 ATTCAGGA A
 CAGGATTATTTTCTGAATCA TCAG ||||| ||||| ||||| ||||| ||||| |||||
 CTTGATTCGTCACATAATATA CTAG ATATCA TATA CA TGCT TAGTT TAAGTCTT /
 CATAACTATATGATC T ATACA AT C -- CAC TT

GAM126 TGTACGATTGTATTGCGTTA 112 TTAGTCAATG 461 A TATT - AC TAA
 CTAACGATAAATAATTCTT CTTTAACGTA TGTACG TTG GCGTT ACTAA GA A
 AGTCAATGCTTTAACGTACA CA ||||| ||||| ||||| ||||| ||
 ACATGC AAT CGTAA TGATT CT T
 - TT-- C -- TAA

GAM127 GCGTATCTACTACTCCAAAT 113 TCCAAATTGC 462 CTA CTCCA A TTC TAT
 TGCAGTTTCTGGTATCCATC AGTTTCTGGT GCGTATCTA AATTGC GT TGG C
 CATACGCGTAATTATCAAAT ATCC ||||| ||||| ||||| ||||| ||
 AGATATGT TGTATAGAT TTAATG CG ACC /
 AA ACTA-- - CAT TAC

GAM128 TATATCCTACCGCTTTTTAT 114 TAATAAGATG 463 CG TTT C-- -- ATG TTTTATGTTAT
 TTA TTA
 CA ACTATGTAATGAGTTTTT CTAATACATC CT TAT AACT ATGTA AGT GTCTT
 GTTAGG A

ATGTTATGTCTTTTAGTTAG AGGT || ||| |||| |||| || |||| |||||
 GTTAATATTCTAATAAGATG GA ATG TTGG TACAT TCG TAGAA TAATCT /
 CTAATACATCAGGTTAAAGT A- TT- AAA AC AA- ----- --- TAT
 ATTAGAATGGGATTATA

GAM129 ATCAGACCATATACTGAGTT 115 TGAGTTGGCT 464 AC TAT TT - ---- - CGT
 GGCTACTATCTTGTACGTAT ACTATCTTGT ATCAG CA ACTGAG GGCTA CTA TCT TGTA A
 ATTGCATGGAATCATAGATG ACGT ||||| || ||||| ||||| ||| ||| |||||
 GCCTTTTCAGTTGAACTGGT TGGTC GT TGA CTT CCGGT GAT AGG ACGT /
 AA --- TT A ACTA T TAT

GAM130 TAGTCACGACTGAAATAACC 116 CGGCATGGTT 465 ACT AA-- C -- TTT
 GCGTGATTATTTTTTGGTAT TCTGTGACTA TAGTCACG GAAAT CCG GT GATTAT T
 AATTCTACACGGCATGGTTT ||||| |||| ||| || |||||
 CTGTGACTA ATCAGTGT CTTTG GGC CA TTAATA T
 --- GTAC A TC TGG

GAM131 TCATCCAATATTATTGAAAT 117 TGATGGACAG 466 CA TTGA- TT CAG TACAAATA
 A AC T C
 GACGTTGATGGACAGATGAT ATGATACAAA ATATTA AATGACG GATGGA ATGA AGA
 GGT GG AC T
 ACAATAAGAAGGTACGGTA TAAG ||||| ||||| ||||| ||| ||| ||| |||
 CCTTTGTCCACCATCTCCTC TGTAAT TTA CTTG TTATCT TACT TCT CCA CC
 TG T
 CAATTCATGCTCTATTTTGT -- TTCAA T- CG- TAACCTCC A -- - T
 CATTAACTTTAATGTATGA

GAM132 TCGTCGGTATTTTTTATGGC 118 CGGTATTTTT 467 CG A C TTTACTCT
 AAAC TTTACTCTTCCAGCAT TATGGCAAAC TCGT GTATTTTTT TGG AAAC T
 CCGTTTCTAAAAAATATTA TTTA ||| ||||| ||| |||||
 ACGA AGCA TATAAAAAA ATC TTTG C
 AT - - CCTACGAC

GAM133 ACCATTCCAAGTCACTGTGT 119 TATCATAAGC 468 TTCCA CTG- TA GAT
 GTAAGAAGATTATATTCTAT TTGACTACAT ACCA AGTCA TGTG AGAA T
 CATAAGCTTGACTACATTTG TTGG ||| ||||| ||| |||||
 GT TGGT TCAGT ATAC TCTT /
 TTACA TCGA TA ATA

GAM134 ATATCTTTAACTAAGTCAAT 120 TCAATGATTT 469 AACT ATTCATCAACCG-- TC
 GATTTTCATCAACCGTTAGAT CATCAACCGT ATATCTTT AAGTCAATG TTAGA T
 CTATTTTAAAGTTAATCATA TAGA ||||| ||||| ||||| |||||
 TAGGCATTGATTTTAAAAG TATGGAAA TTTAGTTAC AATTT /
 GTAT ATT- GGATATACTAATTGA TA

GAM135 CAGCCGAAACATATTCTACC 121 CATGGCTCCG 470 CC ATTCTACC GC A- T
 ATGGCTCCGTTTAATTTGTT TTTAATTTGT CAG GAAACAT ATG TCCGTTT ATT G
 GATGAAGATGGATTTCATCCT TGAT ||| ||||| ||| ||||| |||
 TAAATGTTTTCTCTG GTC TTTTGTA TAC AGGTAGA TAG T
 TC AATTCC-- TT AG T

GAM136 CCGTTTTTAGACCGAGACTC 122 TAACTCGGAT 471 TTT- - ACTCCA TAAA CA
 CATCCGTAAAAATGCATACT CTGCTATATG CCGT TAGACCGAG TCCG AATG T
 CGTTAGTTTGGAATAACTCG G |||| ||| ||||| |||| ||||
 GATCTGCTATATGG GGTA GTCT GGCTC AGGT TTGC A
 TATC A AATA-- TTGA TC

GAM137 CGCTTCTATCTTGTTTAGAT 123 TGA CTAGATA 472 ---- GTTT TT TAAA TCTC--
 ACATA
 TTATTTTTATAAAGTTTAGT AACTATCAGT TCTATCTT AGATTTATT TA GTTTAGTC
 CTGCCA A
 CTCTCCTTCCAACATAATAA AAGT ||||| ||||| || ||||| |||||
 AAGTGGAAGTCATTTGACTA AGATAGAG TTTGAATGA AT TAGATCAG GAAGGT
 T
 GATAAACTATCAGTAAGTTT AAGC ATAT CT CAAA TTTACT GAAAA
 TATAGAGATAGACGAACAAT
 TAGCG

GAM138 GACATACATACTATCTTTAA 124 ACTATCTTTA 473 C TT----- CTCT C--- AAT--
 T
 TAGAACTCTTTTCATCCAGT ATAGAACTCT CATA TATCT AATAGAA TTTCAT CAGTTG
 GGA T
 TGAATGGATTGTCCTTAAC TTTC ||| |||| ||||| ||||| ||||| |||
 CAACTGATTAATGAGATCTT GTAT GTAGA TTATCTT AGAGTA GTCAAC CCT
 C
 CTATTTTATCATTTTCCAGA A CCTTTTACTATT CT-- ATTA CAATT G
 TGATATGTATGTC

GAM139 TACAAAGGAGATGATTTATC 125 TATGGTATTA 474 ----- TTATCTAT TT - C TC
 A
 TATGGTATTAAGAATTCGTT AGAATTCGTT ACAAAGGA GATGAT GGTA AAG AATT
 GTTTT GAC T
 TTTCGACATCCGTCAAAACC TTTC ||||| ||||| ||| ||| ||||| |||
 AATTCCTTTTGCCTGTATC TGTTTCCT CTACTA CCGT TTC TTAA CAAAA
 CTG C
 ATCCAGTTTTCCATCCTTTG ACCTTTTGAC TGT----- TT C C -- C
 TA

GAM140 TGTCAC TTTGTTATTGGCCA 126 TTCCTCGGCC 475 --- T-- AACC-- TT
 ACCTTTGTTGTACAAATTCC ATTTAATAT TGTCAC TT TGTTA TGGCC TTTG G
 TCGGCCATTTTAATATTTAA TTAA ||||| ||||| ||||| ||||
 GTGATA ATAGTGAA ATAAT ACCGG AAAC /
 TTT TTT CTCCTT AT

GAM141 TTGCTAGACACCTTTTCAAT 127 TTTGATAAAG 476 T ACAC- - T A T
 GTTTAATTTTTTTGAAATAA CCTTCCTCGC TTGC AG CTTT TCAA GTTTA TTT T
 GCTTTGATAAAGCCTTCCTC AA |||| ||| |||| |||| |||
 GCAA AACG TC GAAA AGTT CGAAT AAG T
 C CTTCC T T A T

GAM142 CACCGCCTCTAGATATCGCC 128 CGCCTTTATT 477 CG ATCG-- TTTAT ACATT
 AAATCCA
 TTTATTTCCACATTAGATGG TCCACATTAG CAC CCTCTAGAT CC TTCC AGATGGT
 A
 TAAATCCAATAGTGAAACTA ATGG ||| ||||| || ||| |||||
 TCTTTTATAGGAATGTATGGA GTG GGAGATTG GG AAGG TCTATCA /
 CTCGCGTTTAGAGGAGTG A- CGCTCA TATGT ATTT AAGTGAT

GAM143 GACACTTTGCCGGCGGTTGT 129 ACATATCCGT 478 CT CC T-- ATTTATCA
 AGATTTATCATATTTCTCCA TACAATTTGT GACA TTG GGCGG TGTA T
 CTACATATCCGTTACAATTT T |||| ||| |||| ||||
 GTT TTGT AAC TTGCC ACATC A
 TT A- TAT ACCTCTT

GAM144 GAGACTTGATAGATATTAGT 130 TCACCACGTG 479 - - TAG TA- TTGAA
 GATGAATTGAAAATTATTT TGTTCAGGA GA GA CTTGA ATAT GTGATGAA A
 TATCACCACGTGTGTTTCAG TCAT || ||||| ||| |||||
 GATCATC CT CT GGA CT TGTG CACTATTT A
 A A TTG CAC TTATT

GAM145 GGCTATTCTGGCGGCTAGAA 131 TGCTATTTCG 480 C TA TAAT GA TGT
 TGGCATAATCCGGATGTTGT GCTGCCAGAG GG TATTCTGGCGGC GAATGGCA CCG TGT
 G
 GTAGTACAAGTGGCTGCTAT TGTC || ||||| ||||| ||| |||
 TTCGGCTGCCAGAGTGTCC CC GTGAGACCGTCG TTTATCGT GGT ACA T
 T GC C--- GA TGA

GAM146 TATATACGATAAGATATGTT 132 TAAGATATGT 481 C --- TTT A ----- -- AATT
 TATTCATAAACGCGTCAAAT TTATTCATAA TATATA GATAA GATATG ATTC TAAAC GCG
 TCA T
 TTTTCATGAATCGCTAAGGA ACGC ||||| |||| |||| ||| |||| ||| |||
 GTTTAAGAATCTCATGTCAA ATATAT CTGTT CTGTAC TAAG ATTTG CGC AGT /
 ATTGTCCTATATA C AAA TC- A AGGAAT TA ACTT

GAM147 TCTGGTTCTATGTTCTCGT 133 TCTATGTTCC 482 TC --- TT C TATT
 TTCCTGTATTCTTTTAAAGA TCGTTTCCTG TCTGGT TAT GTTCCTCG TC TG C
 TCGAGGAACGCCATAATATC TATT ||||| ||| ||||| || ||

AGACTA ATA CAAGGAGC AG AT /
TA CCG T- A TTTT

GAM149 TTCCTTTTCGTTGATCTCTC 135 TCGTTGATCT 484 CGTT TCT TA G
ATAGATTTAGAAATAAATTC CTCATAGATT TTCCTTTT GATC CA GATTTA A
TTGCGATCCTCCAAAAGGAG TAGA ||||| ||| || |||||
GAGGAAAA CTAG GT TTAAAT A
CCTC C-- TC A

GAM151 GTATATCATCAGCTGAAAAA 137 TTCCTTCGGC 486 CA----- AAAC TT
CTATGTTTTACACGTATTCC ATTTCTTTTT GTATATCAT GCTGAA TATGT T
TTCGGCATTCTTTTAAATG AATG ||||| ||||| ||||
ATATAT TATATAGTA CGGCTT ATGCA /
ATTTTTCTTTA CCTT CA

GAM153 GGATTTTAGAATTTCCAAAT 139 TGAAATCCAA 488 T AATT AAA--- --- T
TCACCAGCGATTTATCGGTT GGATTTATTA GGAT TTAG TCC TTCACCAG CGA T
TTGGTGAAATCCAAGGATTT ATGT |||| ||| ||||| ||
ATTAATGTCC CCTG AATT AGG AAGTGGTT GCT T
T ATT AACCTA TTG A

GAM154 ATGGTCGAAGTATAGCAGGA 140 TAGCAGGACA 489 ---- A CATT- GCTC CCG TA

CATTGATGCTCTAGACCGTG TTGATGCTCT ATGGT CGAAGTATAGC GGA GAT TAGA TG
 T
 TATAACAAAATCTACAAATT AGAC ||||| ||||||||| || || ||||| ||
 TTTCATCCGCTATATTTTGT TATCA GTTTTATATCG CCT TTA ATCT AC /
 TTCACTAT CTTT - ACTTT AAC- AAA AA

GAM155 GGTGTTAATCCACTATATGT 141 TCCACTATAT 490 T - ----- - A--- C ATAACA
 CAT
 TTCTGTAGCGGCTGATAACA GTTCTGTAG GGTGT AATC CACT ATATGT TTCTGT GCGG
 TG CAG C
 CAGCATCCAACTGAGCATCC CGGC ||||| ||||| ||||| ||||| ||||| ||||| || |||||
 GCGTCCGCAGAGCACATATT CTACA TTGG GTGA TATACA GAGACG CGCC AC
 GTC /
 TTTAACAGTGAGGTTACATC - A CAATTTT C CCTG T GA---- AAC

GAM156 GTTAGCAAGAAATTAACATT 142 TTCCGCATAT 491 C A-- CATTG ATTC A T TCCC
 GGCATTCCGAACACTCTGGAT TTTAATGACT GTTAG AAGA ATTAA GC GAAC CTC GGA A
 CCCAACATTCTCGAGGTTCC CTTC ||||| ||||| ||||| || ||||| |||||
 GCATATTTTAATGACTCTTC CAATC TTCT TAATT CG CTTG GAG TCT /
 TAAC - CAG TTATA C--- - C TACA

GAM157 TCAGTGGGTACTCCCGGAGG 143 GAGCTCAACA 492 TACTCCC-- A ----- GT
 CGGATCCCGTTTTAGGGAGCT CTTACTCCGC TCAGTGGG GG GGCGGA TCCC T
 CAACACTTACTCCGCCACCC CACC ||||| || ||||| ||||| |||||
 ATATTTATCTCATTGA AGTTACTC CC CCGCCT AGGG /
 TATTTATAC A CATTCACTCG AT

GAM158 ACACGACTGTGGTAGATTTG 144 TGTGGTAGAT 493 C TG-- A T AGA C T
 TTCTATAGAGCCGTTGCCG TTGTTCTATA ACA GAC TGGTAG TTTGT CTAT GC GG T
 CAAATAGATAGAACTACCAA GAGC ||||| ||||| ||||| ||||| |||||
 TATGTCTGT TGT CTG ACCATC AGATA GATA CG CC /
 - TATA A - AA- - G

GAM159 ACAGTTTGAAAAATAACAGT 145 AACAGTATCA 494 AATA TCATTTAAACAT TG
 ATCATTTAAACATTTAACCTT TTAAACATT ACAGTTTGAAA ACAGTA TTAAC T C
 GCGGGGTTAATTTCACTA TAAC ||||| ||||| ||||| |||||
 TTAAGCTGT TGTCGAATTTT TGTCAT AATTGG /
 ---- TTCAACACTTT- GG

GAM160 CCACCTGTTTTAACATATAA 146 TAATATTGAT 495 T- -- GA T TATCCGTCATTG- -----
 --- TT
 TAGGCAGGAGATAGATATCC AAAATCTCCA ATAATAG GCAG GA AGA CAATATT
 CCT T
 GTCATTGCAATATTCCTTTT TTCT ||||| ||||| ||||| ||||| |||||

CGTAGGCACACAATCTAATA TATTATT CGTC TT TCT GTTATAA GGA C
TTGATAAAATCTCCATTCTC TC TA TC C TACCTCTAAAATA TCTAACACAC TG
TTCTCTGCATTTATTATCTT
GTTTCGGTGG

GAM161 TACTTTTTCTTTACCTTGAG 147 TGAGAATATC 496 TTTACC -- T - CGT TGG
AATATCCATCGTTTGCTTGG CATCGTTTGC TACTTTTTTC TTGA GAA ATC CAT TTGCT T
TCAATAGCGATATGTGATT TTGG ||||| ||| ||| ||| |||
TTTATCAACCACTCGAAAAA ATGAAAAAG AACT TTT TAG GTA AGCGA C
GTA CTCACC AT T T T-- TAA

GAM162 TAGTACTAGACTGACTTCTA 148 TATTAAAGTC 497 TAC CT C-- A A CTCACCTG
ACAAACATCTCACCTGCCAT TTCTATTTCT TAG TAGA GACTT TA CAA CAT C
AAATAAATGCTTGATATTAA A ||| ||| ||| ||| |||
AGTCTTCTATTTCTA ATC ATCT CTGAA AT GTT GTA C
TTT T- ATT A C AATAAATA

GAM163 AAATTATTCTTATCATGCGT 149 ATTATTCTTA 498 T TATCAT TCC TCC T
CCATAGTCCCGTTCCGTATC TCATGCGTCC AAA TATTCT GCG ATAG CG T
TATTATCGTTAGAATATTT ATAG ||| ||| ||| ||| |||
TTTATAAGA TGC TATC GC/
T T----- TAT TAT C

GAM164 ACATCCATTTTTAAGTATTA 150 TTTTATAGATA 499 C TTA AAA- TC GTTTA
TATTAAAATTTAATCAATGT AAAAAATATAA ACATC ATTT AGTATTATATT ATTTAA AAT T
TTATTTTTAGTTTTTTAGAT TATT |||| ||| ||||| |||| |||
AAAAAATATAATATTATGAG TGTAG TGAG TTATAATATAA TAGATT TTG /
TCGATGT C TA- AAAA TT ATTTT

GAM165 ATTTTATTACCGTGTGGGAT 151 TACCGTGTGG 500 TT G G ATAAA C TCCAT-- A
G
ATAAAAGTCCTTGATCCATT GATATAAAAG ATTTTA ACC TGTGG AT AGTC TTGA TG
TCTG A
GATCTGGAAACGGGCATCTC TCCT |||| ||| |||| ||| ||| |||
CATTTAAGACTAGATGCCAC TAAAAT TGG GCACC TA TCAG AATT AC GGGC A
GGGGTTTAAAAT T- G G GA--- - TACCTCT - A

GAM166 CTATCGGTTTACTATTTATT 152 GTTTACTATT 501 C T TTAT G A
GATAACGCAGATGTTTGAGT TATTGATAAC CTAT GG TTACTAT TGATAAC CAG T
TGTCATCCATGGTAATCCAT GCAG |||| ||| |||| |||
AG GATA CC AATGGTA ACTGTTG GTT G
- T CCT- A T

GAM167 GTACATGTGAAAATAGTCAT 153 CATGTGAAAA 502 CA- T- TCA - GAT AA AAAGT
CT

ATTCCTGATTAGGATAATCA TAGTCATATT GTA TGTGAAAA AG TATT CCT TAGGAT TC
 TAACAA A
 AAGTTAACAACACTACTTTGTT CCTG ||| ||||| || ||||| ||||| |||||
 ACGGACGATCTTATTAAGGT CAT ATACTTTT TC ATGA GGA ATTCTA AG ATTGTT
 /
 AGTACATCTTTTTTTCATAA TTA TT TAC T ATT GC GC--- TC
 TTTAC

GAM168 TGAAGAACATATTTAATTCA 154 TGAATACAAC 503 AACATATTTA GA AAAAT
 GATCTAAAAAATACATATAT GAATACTTCA TGAAG ATTCA TCTAA A
 TAGAATGAATACAACGAATA |||| |||| ||||
 CTTCA ACTTC TAAGT AGATT C
 ATAAGCAACA A- ATATA

GAM169 CAGCTACTTCTACCCAATCA 155 TTAATTGGTT 504 TC CAA GTAT T TTT---- --
 TA
 CCAGGCAATAAATGTATTTT TAATCGTTTA CAA ACCAGG TAAAT TTTATTTT AATAAAC
 CC TTGGCG T
 ATTTTAAATAAACTTTCTT TTAA ||| ||||| |||| ||||| ||||| || |||||
 GCGTATTCTTGTTAATTGG GTT TGGTTC ATTTA AAATGAAA TTATTTG GG
 AATTGT T
 TTTAATCGTTTATTAAAGTA -- A-- ---- - CTAATTT TT TC
 AAATTTAACTTGGTTTGACG
 CTAATAGTTG

GAM170 TTGCAAGTTTCTGTTTCTGA 156 TTCCACAGAG 505 C TC T A- CG TCC
 GAGTAAACGAATCCCTGTTT CACTAATTTT TTG AAGTT TGTT CTG GAGTAAA AA C
 TATTTTATTCCACAGAGCAC CAA ||| ||||| |||| ||| ||||| ||
 TAATTTCCAA AAC TTAA ACGA GAC CTTATTT TT T
 C TC - AC TA TTG

GAM171 CCGCTTCTATTTACTCCCGC 157 CCGCAGCACA 506 C-- CTCCCG-- AC A AA
 AGCACAATGAACCAACACGG ATGAACCAAC CCGCTT TATTTA CAGC AATGA CC C
 GCTCGTTTCGTTGATCACAT ACGG ||||| ||||| ||| ||||| ||
 TTAGATAAAAAGGCGG GGCGGA ATAGAT GTTG TTGCT GG A
 AAA TTACACTA CT C GC

GAM172 GTTAGGCAATGTATATTTAT 158 CAATGTATAT 507 - CA TATTTAT
 AAATTTAAAACATATT CT
 CCATCGTCAAATTTAAAACA TTATCCATCG GTTA GG ATGTA CCATCGTC TGAA T
 TATTTGAACTTAACTTCAGA TCAA ||| || |||| ||||| ||||
 TGATGGTGCATCCATAGC CGAT CC TACGT GG TAGTAG ACTT A
 A -- ----- CA

GAM173 ACTTTTTATGAAGAGCCGCG 159 TGAAGAGCCG 508 TAT A CG A--- C
 TTTAACAATGCTTTATTGTC CGTTTAAACAA ACTTTT GA GAGC CGTTT ACAATG T
 TCCGAACGTAGCTCTCTTAA TGCT ||||| ||||| ||||| |||||

GAGT

TGAGAA CT CTCG GCAAG TGTTAT /

TT- - AT CCTC T

GAM174 TCGTCATATCCCGTATAGTC 160 TTGAATTTAC 509 TATCCC ---- CA---- A
AGAGATAGGAATCTTGAATT TAATCTTGCC TCGTCA GTA TAGT GAGAT G
TACTAATCTTGCCCTTGTTG CTTG ||||| ||| ||| |||||
GCGG GCGGGT CGT ATCA TTCTA G
TGTTCC TCTA TTAAAG A

GAM175 CGCCTAATAGCTTGCGGCAG 161 TCCAATCGCA 510 ---- - CA- TGT
ATATGTTTTCTTATCCAATC TAGCTATAAA CGCCTA ATAGCT TGCGG GATA T
GCATAGCTATAAAATAGGCG ATAG ||||| ||||| ||||| |||||
GCGGAT TATCGA ACGCT CTAT T
AAAA T AAC TCT

GAM176 GCGCACTAATTGCCAATATA 162 TTGATGTTTT 511 C TAATT T A AAGAA
ATAACAAAGAATATAAGTGT GGCTGCTTGT GCG AC GCCAA ATA TAACA T
TGATGTTTTGGCTGCTTGTA ACGC ||| || ||||| ||| |||||
CGC CGCTG CGGTT TGT GTTGT /
A TTCGT T A GAATA

GAM177 AATACGAGTTATATTTTCGT 163 AGTTATATTT 512 AG-- C-- TATCCAT TTCA
CTATCCATTGTTTCACATTT TCGTCTATCC AATACG TTATATTTT GTC TGT C
ACATATTTTCGACAAAAAGAT ATTG ||||| ||||| ||| |||
ATAAAATGCGTATT TTATGC AATATAGAA CAG ACA /
GTAA AAA CTTTAT- TTAA

GAM178 GCCGATCTCTGAATGGATAC 164 TCTCTGAATG 513 ATCTCT - ACTA TA T- TA
TAGTTTTCTAAGTTCTAATG GATACTAGTT GCCG GAAT GGAT GTTTTC AG TC A
TGATTCTCTGAAAATGTAAA TTCT ||| ||| ||| ||||| || |||
TCCAATTCCTCCGGC CGGC CTTA CCTA TAAAAG TC AG T
CTC--- A AATG TC TT TG

GAM179 GCGGTATAATTAGTTTTTTTT 165 TGTGATGGAA 514 GG T - C ATT T
CTCTCAATTTCTATTTTTAG AAATGACTAA GC TA AATTAGTT TTTTCT TCA TCTA T
ATGTGATGGAAAAATGACTA TTTT || || ||||| ||||| ||| |||||
ATTTTGTAGC CG GT TTAATCAG AAAAAGG AGT AGAT T
AT T T T GT- T

GAM180 GTGGAAACGATAACTGTATT 166 GATAACTGTA 515 ACG-- A TTAATCAC- CA
TTTAATCACGTCAGCGGCAT TTTTAAATCA GTGGAA ATA CTGTATTT GT G
CTAAATTAAATATAGGTATA CGTC ||||| ||| ||||| |||
TTTATTCCAC CACCTT TAT GATATAAA CG /

ATTTA G TTAATCTA GC

GAM181 AAATTCATGTGAAACTTTGT 167 TTCATGTGAA 516 T T CTTT TTCCTACAACT TAA
CCTTTCTACAAACTTGATA ACTTTGTCCT AAAT CATG GAAA GTCCT TGA C
ACTATTTTCATCGGGACTTAT TTCC ||||| ||||| ||||| ||||| |||||
TTCTATGTGTTT TTTG GTAT CTTT CAGGG ACT T
T - ATT- CT----- TTA

GAM182 AATTGTTTCGGCTATACTCGA 168 TACTCGATGC 517 TC ATA CG AG T A T AGA
TGCGTGAGTCTTGCAATTCAT GTGAGTCTTG AATTGT GGCT CTCGATG TG TCT GC TTCA
CTCC T
CTCCAGATATCGGAGTGAGG CATT ||||| ||||| ||||| || ||||| ||||| |||||
GTCAGATCCAAATATTGAGA TTAATA CCGA GAGTTAT AC AGA TG GAGT GAGG /
AGCCTTATAATT TT A-- AA CT C G - CTA

GAM183 ACCGTCGATACTGCAGAGAT 169 TCGATACTGC 518 T C C- TC T TA
TCTAGTAATAATTTTCTTAA AGAGATTCTA ACCG CGATA TG AGAGAT TAG AA A
GATCTTTAACGATATTGTCTG GTAA ||||| ||||| ||||| ||||| |||||
GT TGGC GTTAT GC TTTCTA ATT TT /
T A AA GA C TT

GAM184 AGGAGATGGAGAATTTTTTTT 170 TGGAGAATTT 519 A - TTTTTTTC TT T AT
CAGTTGTTTGATGATATTCC TTTTCAGTTG AGGAG TGGA GAA AGTTGT GAG A
TCTATAACTACTTCTTCTTC TTTG ||||| ||||| ||||| ||||| |||||
CACTTCCT TCCTT ACCT CTT TCAATA CT C /
C T CTTCA--- T- C TT

GAM185 GGAGAAAGAATTACATTCTC 171 TTAGTTCATC 520 A T T AG----- AATAT CG
TCGT
TGGAGAAGCCATAAATATAT ATATGGAAC ATT CAT C CTGGAGA CCATA ATGA
TGATAGAG C
GACGTGATAGAGTCGTCAAT TTTT ||||| ||||| ||||| ||||| ||||| |||||
TCCTTTATTAGTTCATCATA TAA GTG G GATCTCT GGTAT TACT ATTATTTC
A
TGGAAC TTTTTCATTGTCTC - T - GTTACTTTTCAA AC--- TG CTTA
TAGGTGTGAATTCTATTTC

GAM186 GGATAAGTTATTCATGACGG 172 TAAGTTATTC 521 T AT--- - - CATAA CGG GAA
TAGCATAATGTCTCGGATGA ATGACGGTAG GGA AAGTT TCAT GAC GGTAG TGTCT AT
A
AAAGAATAATGGATAGCAAA CATA ||||| ||||| ||||| ||||| ||||| |||||
CTGCCAGTCGATGATATTAA CCT TTCAA AGTA CTG CCGTC ATAGG TA /
ACTTTCC - ATTAT G A AAACG TAA AGA

GAM187 GTATTTCTTTGACTTGAATA 173 CACTAGTTTA 522 TTCT C GAAT TCC CAC
 CTATCCGATCACAAATATCC GATTCAACAT GTAT TTGA TT ACTA GAT A
 ACTAGTTTAGATTCAACATA AC |||| |||| || ||||
 C CATA AACT AG TGAT CTA /
 C--- T ATT- CAC TAA

GAM188 GTTATCTATAGCATCTACTA 174 TCTATAGCAT 523 TA-- CTA AC CAT
 ACTGTACATTTTTTACATCT CTACTAACTG GTTATCTA GCAT CTA TGTA T
 AGACCATGTACCTTAGATAA TACA |||||| |||| || ||||
 T TAATAGAT TGTA GAT ACAT /
 TCCA CCA CT TTT

GAM189 TCCTTTACCATTCTCTAAAAT 175 TGTAAGCTCT 524 TTTCTAA- T CCATG TCTTTTTG
 A ATGA
 AGTCGTTGCCATGTAAGCTC TTTTGAAATT ACCA AATAG CGTTG TAAGC AAATTG
 TGGAGT C
 TTTTGGAAATTGATGGAGTA GATG |||| |||| |||| |||| ||||
 TGACCTACCACTTCAGCAGT TGGT TTATC GCAAT GTTTG TTTGAC ACTTCA
 C
 TTGTTTGATAGTTAACGCTA TTTTCAA - TGATA ----- G CCAT
 TTAACCTTTTTTGGTGACGGA

GAM190 TAGTGGCTTCTAATCAGATG 176 ATATCATTGA 525 TCTAAT T TAATAAATATTTTAAA
 ATCT A
 TTCTAATAAATATTTTAAAA CCATTGTCT TAGTGGCT CAGATG TC AATGA
 TGATT A
 ATGAATCTTGATTA AAAATC GGCT |||||| |||| |||| ||||
 ATATCATTGACCATTGTCT GTCATCGG GTTTAC AG TTA CT ACTAA /
 GGCTACTG TCT--- C ----- AT-- A

GAM191 TTGATTTTCTTTCTAATACT 177 TGGAATAAAA 526 T TC A C ATAT TC A A TC
 ATATATTTCTCTCGAAGAAG ATACTACTGT TTGATTT CTT TA TA TAT TTCTC GA GA GT T
 TTCTTGACATCATCTGGGA TGAG |||||| || |||| |||| ||||
 ATAAAATACTACTGTTGAGT GACTAAA GAG GT AT ATA AAGGG CT CT CA T
 AAATCAG T TT C C AAAT T- A A CG

GAM192 AGGTATCGGTCTCTACTGAA 178 TAGCTTCTAC 527 TAT TCTCT AATCTA TC
 TCTACTAACATGTCTCGTAT AGTCTTTCGT AGG CGG ACTG CTAACATG T
 GTTAGCTTCTACAGTCTTTC TTCC || || |||| ||||
 GTTTCCT TCC GCT TGAC GATTGTAT /
 TTT TTC-- ATCTTC GC

GAM193 CGTCATTATTTTCAGCAGCC 179 TGAGAAAAGT 528 ATTATT CA- - - - T A
 TCTCTACCAGAAGGTTGAGA GTGTTCTGAA CGTC TTCAG GC C TCTC ACC G
 AAAGTGTGTTCTGAATCGCA TCGC |||| |||| || ||||

CGACG

GCAG AAGTC TG G AGAG TGG A
CACGCT TTG T AAA T A

GAM194 GGGTGTAGGATATAGTTTCA 180 TAGGATATAG 529 ----- TTTC AACAT AT---
CATTTC

TAATAGGAACATGATATTTT TTTCATAATA T GTAGGATATAG ATAATAGG GAT
TTTTTGTAC A
TTGTACCATTTCACCAACAA GGAA | ||||| ||||| || |||||
GTATAGAAATGCAAATCTAT A CATTTTATGTT TATTATCT CTA AAAGATATG
C
ATCTATTATTTTGTATTTTA ATCTAC T--- ATAT- AACGT AACAAC
CCATCTAACCC

GAM195 GAATAGTTACATTTGATTCA 181 TATTACACAC 530 CATT ATCTTCG TTT TC ACTAT
CC A AT

TCTTCGATGTTTAATGTTCC GGAACGTTTA GTTA TGATTG ATG AATGTTCC TG AT
CC ACGTG A
TCTGACTATATCCCCAACGT TAAC ||| |||| | ||||| || || |||||
GATAATACGCGTAGGTTATT CAAT ATTAAG TAT TTGCAAGG AC TA GG
TGCGC A
ACACACGGAACGTTTATAAC T--- ACATCAA --- C- ACAT- TT A AT
TACAGAATTATTA ACTATTT

GAM196 GCTACCAAGGCGAACAACAA 182 TAACACGCTT 531 C - C-- ACA A- CCTGATC
AGCGATTATTGTTTTACCTG CTGTTCTCAT GCTA CA AGG GAACA AAGCG TTATTGTTTA
C

ATCCCATAATATGGAACAAT CTAT ||| || |||| |||| |||||
AACACGCTTCTGTTCTCATC TGAT GT TCT CTTGT TTCGC AATAACAAGGT /
TATGATAGT A A ACT C-- AC ATAATAC

GAM197 TCAGGCATTTTCGTAATATGA 183 AGGCATTTTCG 532 G -- TATTCTTCC--- CA

TATTCTTCCTTTAAGCAAAT TAATATGATA TCAGGCATTTTC TAAT ATGA TTTAAG A
CCTTAAGTACATTCACACCT TTCT ||||| |||| ||||
CGTTCGTTAAGAAAGTGTCTG AGTCTGTGAAG ATTG TGCT GAATTC A
A A CT CCACACTTACAT CT

GAM198 AAGAATATAGAAATAATGAT 184 TATAGAAATA 533 AAATA TA TC TCATCG

AAGTCCATCATCGTGT TTTT ATGATAAGTC AAGAATATAG ATGA AG CA T
TTGCCTCTTCATAAGAACTA CATC ||||| |||| || ||
TATTTT TTTTATATC TACT TC GT G
AAGAA TC C- TTTT

GAM199 CTTGATAGTTGTTTCCTAGAT 185 TACTAGGTAG 534 T - - A AAAAT

ATGTAAAATAATCCAACGTA CAAATTGTCT CT GATAGTT GTT CCTAG TATGT A
CTAGGTAGCAAATTGTCTAG AG || ||||| || |||||
GA CTGTAA CGA GGATC ATGCA /

T A T - ACCTA

GAM200 TAATATACTTGCGTGTGCGTC 186 TTCAATTTAT 535 AT TGCG TC TATAC
TTTCTATAGTTCT TAT
GTTCAATTTATACGGATTTCT ACGGATTTCT TA ATACT TGTCGTGCGT AATT GGA
CTGT A
TATAGTTCTCTGTTATATAA ATAG || |||| |||||| ||| ||| |||
TACGGTTTTCCATCATGATT AT TGTGA ACAGCAGCA TTAG CCT GGCA T
AGACGACGACAATAGTGTTCT CT TA-- GA TACTA TTT----- TAA
TA

GAM201 GCGGACACGGATACTCGTTT 187 ACTCGTTTAT 536 ACAC - GT--- G - A GGT
ATGACACCATAGGCATTGGT GACACCATAG GCGG GGAT ACTC TTAT ACAC CAT GGCATT
T
TAACGAATGCCGTGAGTGTA GCAT ||| ||| ||| ||| ||| ||| ||| |||
ATAATTTGAGAGTCATCCTC CGCT CCTA TGAG AATA TGTG GTG CCGTAA A
GC ---- C AGTTT A A - GCA

GAM202 TTTCTGTTTGGACAAATAA 188 TTTCTAGTTC 537 - GGAC AATTC ATC CT
TTGGAATAATTCAGAAATAA TAATTATTTCT TTTC CTGTTT AAATAATTGGAAT AGAAATA
GTTT T
TCGTTTCTTTCTAAACATGT AGAA ||| |||| |||||| |||| |||
TTCTAGTTCTAATTATTTCA AAAG GATAAG TTTATTAATCTTG TCTTTGT CAAA T
GAATAGAGAAA A AC-- A--- A-- TC

GAM203 CGGGATTGTCCGGCATATCA 189 CATCGTATAC 538 - T C C C AGT
TGTAAGATAGTTACCGTCTAC TCGACCATCT CG GGAT GTC GG ATAT ATGTAGAT T
ATCGTATACTCGACCATCTA ACG || ||| || ||| ||||||
CG GC TCTA CAG TC TATG TACATCTG /
A C C A C CCA

GAM204 GCCATTATAAAGTGACGTT 190 TATAAAGTGC 539 ATAAAGTGCA AC TC GGAG
TACATATCTACGTTCTGGAG ACGTTTACAT GCCATT CGTTT ATA TACGTTCT G
GAGTAAGAACGTGACTATTG ATCT |||| |||| || ||||||
AGACGAATGGC CGGTAA GCAGA TAT GTGCAAGA /
----- GT CA ATGA

GAM205 GCTCTTGAAACCAAGGTTTT 191 TGAGAAGTCT 540 CT CC GT TC A --- TC
CCAACCGGACTCATTGTGCGA TTTTCATTAG GCT TGAAA AAG TT CA CCG GAC A
TCGGTGAGAAGTCTTTTTCA C ||| |||| || || ||| |||
TTAGC CGA ACTTT TTC AA GT GGC CTG /
TT -- TG GA - TAG TT

GAM206 AATTCAGTAAATAGAGAGAT 192 CCGCACTAGC 541 GT--- ATA AG--- C C CC C
T TT

ATCAGCCGCACTAGCATCCC ATCCCCTTTC AATTCA AAATAGAGAG TC CCGCA TAG AT
CCTTT AA AG C
CTTTCAATAGTTCTCCCTTT AATA ||||| ||||| || ||||| ||||| ||||| |||||
TTAAAGGTATCTAATGCGGA TTAAGT TTTATCTCTC AG GCGGT ATC TA GGAAA
TT TC T
TTTAGAAAACCTCTCTATTTT AATTC AAA ATTTA A - T- T T CC
TTAATGAATT

GAM207 GAACGTAAACGTAGTAGCCA 193 TGATATACCT 542 C CG - GC- A CTC A
TACGTCTCAGAATTCTAAAT GTTTTTATTT GAA GTAAA TAG TA CAT CGT AG A
GATGATATACCTGTTTTTAT C ||||| ||||| ||||| ||||| |||||
TTC CTT TATTT GTC AT GTA GTA TC T
- TT C ATA - AA- T

GAM208 TATTAACGTATCGCATTAA 194 TAACGTATCG 543 T TATCGCATTAACT TAGCGA-
C C
ACTGTTTTCTTAGCGAATGA CATTAATACT TA TAACG GTTTTCT ATGATG AGA C
TGCAGACCCTTCTACGTCAT GTTT ||||| ||||| ||||| ||||| |||||
CAAAAATAGAAAACCTCGTTA AT ATTGC CAAAAGA TACTGC TCT C
TTA T T----- TAAAAAC A T

GAM209 TCAAAGACTAGACATTTACC 195 ACTAGACATT 544 GAC- CATTTACCA TGCT
ATGGGATGCTAATATTCCCA TACCATGGGA TCAAA TAGA TGGGA A
AACATACATCTATAAATTTG TGCT ||||| ||||| |||||
A AGTTT ATCT ACCCT /
AAAT ACATACAA- TATA

GAM210 ATGTATAGATTGTTTTCAGT 196 TAGATTGTTT 545 - TCA- ---- A G
GAGATGATTATTAGATTTAA TCAGTGAGAT ATGTA TAGATTGTTT GTGA GATG TTATTA A
TAGCATCTCGTTCACGTTTG GATT ||||| ||||| ||||| ||||| |||||
AACAGTTTATTGCGT TCGGT ATTTGACAAG CACT CTAC GATAAT T
T TTTG TGCT - T

GAM211 TAATGACGCATATTCTACTC 197 ACGCATATTC 546 G C AT TACTC- T TAG ATA
TTGGAATTAATAGTTTTGAT TACTCTTGGA TAAT ACG AT TC TTGGAA TAA TTTTG T
ATTAGTAAAAAATTTATTTT ATTA ||||| ||||| ||||| ||||| |||||
TAAATTTTGTATCATCGTAA ATTA TGC TA AG AATCTT ATT AAAAT /
TTA A - CT TTTTAA T TAA GAT

GAM212 TAATGGCGGAAAACCTTTTTTA 198 TTCGTGTTCC 547 GC- A TTTTT GTTATAT
GAAATGTTATATATAAAAGA AAACATTA TAATG GGAA AC AGAAAT A
ATTTTTTCGTGTTCCAAACA ||||| ||||| ||||| ||||| |||||
TTA ATTAC CCTT TG TTTTAA /
AAA G CT--- AGAAAAT

GAM220 AGGATGAGTACATTTTCACAG 206 TGAAATAGCT 555 TG ACATTTTCAC ACT ATTG ATGT
A
AAACACTAGCATTGTTCAAT CGTTTCTATT AGGA AGT AGAAAC AGC TTCA
GCTCTTTAC T
GTGCTCTTTACATGGGTAAG TGTT |||| ||| ||||| ||| ||| |||||
GAGTTGAAATAGCTCGTTTC TCTT TTA TCTTTG TCG AAGT TGAGGAATG G
TATTTGTTCT GT ----- C-- ATA- ---- G

GAM221 GATGGCGGCGTCGTCGTTTT 207 AGATAATATC 556 G - TC C TTTG---- TTA
TTGATCTTTATTAAATTTAG CTGAACAGCA GATG CG GCG GT GTTT ATCTTTA A
AGATAATATCCTGAACAGCA TTGC |||| |||| || |||| |||||
TTGCTCGGCGTC CTGC GC CGT CG CAAG TAGAGAT /
G T TA A TCCTATAA TTA

GAM222 GTTATAGCTTTCTGCTATTA 208 TAGTATAGCG 557 GCTT A T C- TTCAAA TT
TACCCGCTATTTCAAATAGA TCGTTTAAGA GTTATA TCTGCT TTA AC CGCTAT TAGAC A
CTTATACGTCTAGTATAGCG GCAG |||| |||| ||| ||| ||||| |||||
TCGTTTAAGAGCAGATATAT TAGTAT AGACGA AAT TG GCGATA ATCTG T
GAT AT-- G T CT TG---- CA

GAM223 GTTTTTGAAGTTTCCAAATT 209 TTGAAGTTTC 558 T AA TTCCAA T- A TG
TTGATAATATAGTCTAGATG CAAATTTTGA GTT TTG GT ATTTTGATAA AT GTCTAGA G
GAATTTTAGACCATCTTTGT TAAT |||| || ||||| || |||||
CAAATCGTTTACCGACAAC CAA AGC CA TAAACTGTT TA CAGATTT A
C -- TTTGC- TC C TA

GAM224 AGGATCTAGATAATTAATAA 210 TTCTTTGTAT 559 --- --- TT T T
TGATGGGTTTTCTATTCTTA TTTGGCATAT AGGAT CTAG ATAA AATAA GATGGG T
TTCTTTGTATTTTGGCATAT CCT |||| |||| ||| ||||| |||||
CCT TCCTA GGTT TGTT TTATT TTATCT /
TAC TTA TC C T

GAM225 CAGAGTTGGGATAGTATTTT 211 TAGTATTTT 560 - - T T T- C TATTATAT G TC
T
TCTAACGTCGGTATTATATT CTAACGTCGG CAGA GTTGG GATAG ATTT TC AACGT GG
TATTA GA TACGT C
ATTAGGATCTACGTTTCATAT TATT |||| |||| |||| ||| ||||| ||| |||||
GTATCATAATATTAATCATC GTCT CGATT CTATC TAAA AG TTGCA CC ATAAT CT
ATGTA A
CACGTTTTGATAAATCTATC T T - T TT - TACTAATT A -- T
TTTAGCTTCTG

GAM226 CGTATAAATTTTAGAAATAA 212 AATTTTAGAA 561 AAA -- TA -- AAT
CATTAGCGAATTGTTGTGCA ATAACATTAG CGTAT TTTTAGAA A ACATTA GCG T

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|----------------------|-------|----------|----|----|-----|-------|
| TTGATGTCGTTATTCTGAAA | CGAA | | | | | |
| CAGTATG | GTATG | AAAGTCTT | T | TG | AGT | CGT G |
| | AC- | AT | GC | TA | GTT | |

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|--------|----------------------|-----|------------|-----|--------|-----------|-----------|------|--------|
| GAM227 | TAGAGTTAAGAGAGATTAGA | 213 | TGGCTACAAA | 562 | GTAA-- | ATT | ACATTA | A | GTC |
| | GTTTGTACATTAAGCAACAT | | CTTTTCCTTT | | TAGA | GAGAG | AGAGTTTGT | AGC | ACAT T |
| | GTCTCTAAATGTGGCTACAA | | TCCA | | | | | | |
| | ACTTTTCCTTTTCCACATCA | | ATCT | | CTTTT | TTTCAAACA | TCG | TGTA | C |
| | TCTA | | ACTACAC | | CCT | ----- | G | AAT | |

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|--------|-----------------------|-----|------------|------|----------|------|--------|------|------|
| GAM228 | GAGTCATTCTGAAGCGTCAAT | 214 | TTTCCGGCTG | 563 | CG | GCGT | ----- | T | CT |
| | AGAATATGTCTCTTAACTAT | | TTGTATATTT | | GAGTCATT | AA | CAATAG | AATA | GT C |
| | TTCCGGCTGTTGTATATTTA | | AAAT | | | | | | |
| | AATGACTT | | TTCAGTAA | TT | GTTGTC | TTAT | CA | T | |
| | | | AT | ATAT | GGCCT | - | AT | | |

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|--------|----------------------|-----|------------|-----|--------|-------|------|------|------|------|----------|
| GAM229 | GACTTGACTAGATCGTCAGT | 215 | TAGCATCGCT | 564 | --- | ---- | G | T | TA - | CGTC | T |
| | ATCC | | | | | | | | | | |
| | AGTAATTTGTGCATCGTCTA | | TTGAGATTCT | | ACTTGA | CTA | GATC | TCAG | AG | AT | TTGTGCAT |
| | TATTC GC G | | | | | | | | | | |
| | TTCTGCATCCGCTTCGTCGA | | CCAT | | | | | | | | |
| | ATAATGTATAGCATCGCTTT | | | | TGAACT | GAT | TTAG | AGTT | TC | TA | GATATGTA |
| | TG / | | | | | | | | | | |
| | GAGATTCTCCATAGCTATCA | | | | ATC | ACCTC | - | - | GC | C | ---- |
| | AGTC | | | | | | | | | | C CTTC |

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|--------|----------------------|-----|------------|-----|-------|----|------|----|-------|-----|---------|---------|
| GAM230 | ATAATAGTGGCCGGAGAATC | 216 | TTCCTCTGGA | 565 | A | G | G | AA | A | --- | GA | TA |
| | ATCATCTGGAAATAGATCTT | | GATGACACTA | | ATAAT | GT | GCCG | AG | TCATC | TCT | GGAAATA | |
| | TCTTCAT A | | | | | | | | | | | |
| | CATTAAGTTGTGAGGATATT | | CGGC | | | | | | | | | |
| | TCCTCTGGAGATGACACTAC | | | | TATTA | CG | CGGC | TC | AGTAG | AGG | CCTTTAT | AGGAGTG |
| | G | | | | | | | | | | | |
| | GGCGGCATTAT | | | | - | G | A | AC | - | TCT | -- | TT |

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|--------|-----------------------|-----|------------|-----|------|----------|---------|-------|------|---------|
| GAM231 | GATAATGTTTATGACAATAA | 217 | TATTGTTTAA | 566 | AT | C----- | A | TT | ---- | TAA |
| | TAATCACGTTAGTGACGATA | | TCGTTTTATA | | GATA | GTTTATGA | AATAATA | TCACG | AGT | |
| | GACGA T | | | | | | | | | |
| | ATTTTTCGTTTTCTACTTTC | | GATT | | | | | | | |
| | GTGATATTGTTTAAATCGTTT | | | | CTAT | TAGATATT | TTGTTAT | AGTGC | TCA | TTGCT / |
| | TATAGATTCTATC | | | | CT | TTGCTAAT | - | TT | TCTT | TTT |

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|--------|----------------------|-----|------------|--------|------------|------------|-----|---------|
| GAM232 | GTTGTTGACGTTGTTCCGAT | 218 | GGAGGTGGAG | 567 | T | GATATCAATA | CT | A |
| | ATCAATAACTCTCTACGAAA | | TATCGTCAAT | | GTTGTTGACG | TGTTCC | ACT | CTACG A |
| | CGTAGGAGGTGGAGTATCGT | | AAT | | | | | |
| | CAATAAT | | TAATAACTGC | ATGAGG | TGG | GATGC / | | |

T ----- AG A

GAM233 TAGTATTCTGGTAAAATTAT 219 TATCAGATGA 568 A C AT TCTAAATTA
ATTTTGTATTAGATC TC
CTAAATTATCAGATGATTTT TTTTGTATTA AGT TT TGGTAAA TA TCAGATG
GTTGATT T
GTATTAGATCGTTGATTTCT GATC ||| || ||||| || ||||| |||||
AAGATTAACCACTTCATCCT TCA AA ACTATTT AT AGTCTAC CAATTAG /
CCAACATCTGAATTCTTTTA - T CT TTTCTTA-- AACCTCCTACTTCAC AA
TCTTTATCATAAACTA

GAM234 ATAAAGTCTTGGTATGACTC 220 ACTACCTTTG 569 CT TA ----- TTT A
CTTTCTAATATAGTACGGAC TCACCCAACT ATAAAGT TGG TGAC TCC CTA T
TACCTTTGTCACCCAACTTT TTAT ||||| ||| ||| ||| |||
AT TATTTCA ACC ACTG AGG GAT /
-- C- TTTCCATC CAT A

GAM235 GCTGAAGTAATTAATTTTTTC 221 TGAAGTAATT 570 TG - TTTTTC C TTT ACTAGTT
TGCCTCGTTTTTACTACAAC AATTTTTCTG GC A AGTAATTAA TGC TCGTT ACTACA T
TAGTTTTTCATCAATGTAGTG CCTC || | ||||| ||| ||||| |||||
ACGATGTATTGTTTAGTTAC TG T TCATTGATT ATG AGCAG TGATGT /
TCTTGGT GT C TGTT-- T --- AACTACT

GAM236 GGGTATTAATAATATCTATA 222 ATTCACGTGA 571 AATATCTATATTT G A TAAC C
TTTCCAGCGTTAAGTGTAAC CGTGGTATCA GGGTATTAAT CCA CGTTA GTG ATTAAA
A
ATTAAACAGTTTTTAATTCAC ATTA ||||| ||| ||||| ||| |||||
GTGACGTGGTATCAATTAAA CCCGTAATTA GGT GCAGT CAC TAATTT G
TAATTAATGCC ATAAATTA ACTAT - G T--- T

GAM237 GTTCTAGTACAATTAGACGT 223 TACAATTAGA 572 TAGTAC C TC C AATTTT- C
A
AAGTTCTGCTTGGAATTTT CGTAAGTTCT GTTC AATTAGA GTAAGT TG TTGGG
TTAACG TAA G
TTAACGCTAAAGAGTTAACG GCTT ||| ||||| ||||| ||| ||||| ||||| |||
TTAATCGTGCACCCAACGTA CAAG TTGATCT CATTTA GC AACCC AATTGC ATT A
TTTACATCTAGTTCTTTGAA TTTC-- A T- - ACGTGCT A G
C

GAM238 TGATTTTGGTTTACATGTAA 224 TACATGTAAT 573 - TTA A TT-TG C
TACATTTTGAACCTTTGAT ACATTTTGAA TGATT TTGGT CATGT ATACA T AA T
TTTGTATCACATGCGCCGGC CTCT ||||| ||||| ||||| ||| |||
AGTCA ACTGA GGCCG GTACA TATGT A TT /
C C-- C TTT GT C

GAM239 ACTACTATTTAATTTTACCA 225 TCGAAAACAA 574 CCAT T -- ---- GAT TTTT--
CA
TATCTTCGAAAACAAAAATA AAATAGATAT AATTTTA ATCTCGAA AACAAA AATA ATTAT
GCAGTA A
GATATTATTTTGCAGTACA TATT ||||| ||||| ||||| ||| ||||| |||||
AACTATTGTTTTATATGGT TTAAAAT TAG GGCTT TTGTTT TTAT TGGTA
TGTTAT /
TTATATTCCACTTTGTTCAT T--- C AC CACC ATT TATTTT CA
TCGGCGATTATAAAATTTTA
TTAGT

GAM240 GAAGAGTAATGTATAGAGGA 226 TGTATAGAGG 575 - AAT-- A CGTTT T
CGTTTTGATTGATCATTTT ACGTTTTGAT GAAG AGT GTAT GAGGA TGAT C
CCTCATATTAGAACTACTT TCGA ||||| ||||| ||||| |||||
C CTTC TCA TATA CTCCT ACTA /
A AAGAT - TTT-- G

GAM241 TCCTAGTTTATCTACAGACA 227 TTTATCTACA 576 T CAGA CT TTCGT AATT
GACTAATAATTCGTTGCATG GACAGACTAA TCCTAGT TATCTA CAGA AATAA TGCATGA
T
AAATTCCTATCATGTACTT TAAT ||||| ||||| ||||| ||||| |||||
TATTTCTTTGATGGATGTGC AGGATCG GTAGGT GTTT TTATT ATGTACT /
TAGGA T A--- CT TC--- ATCC

GAM242 AAAGAATTATACTTTTCTAT 228 TTTGTACAGA 577 TA T- ATAGCC TC- AA
AGCCGCAGAAATCTGAAAATC CTAAGTAATT AAAGAAT TACTT TCT GCAGAA TGA A
TCAAACCTTTGTACAGACTA CTTT ||||| ||||| ||||| ||||| |||||
AGTAATTCTTT TTTCTTA ATGAA AGA TGTTTT ACT /
-- TC CA---- CAA CT

GAM243 AAGTAAAGATATTGACTTGG 229 AACATCTTTG 578 A TG CTT GTA TG
ATGGTATTTTCTGACAGAAA AAATCTTTAC AAGTAAAGAT T A GGATG TTTTC A
ACATCTTTGAAATCTTTACT TT ||||| ||||| ||||| ||||| |||||
T TTCATTTCTA A T TCTAC AAAAG /
AGT --- --- AC

GAM244 CCGTTATAAATGTCTTTGTC 230 TATCCAGAGA 579 - TCGAT TCAA TTC
GATGATATATTCAACGCTTC TATCTTGTA CCGTTATAA ATGTCTTTG GATATAT CGC C
CAATTGTGATATATCCAGAG TGG ||||| ||||| ||||| ||||| |||||
ATATCTTGTAATGG GGTAATGTT TATAGAGAC CTATATA GTG A
C ---- --- TTA

GAM245 TCATCTAATGCCGTAGCCGT 231 TACTTCTTTA 580 T C- GCCGT TAC TACA
AAGTACGTGGTTTACAACAT AAGTACTCGT TCATCTAA GC GTA AAG GTGGTT A
TAGCTACTTCTTTAAAGTAC TTTG ||||| ||||| ||||| ||||| |||||
TCGTTTTTGATGA AGTAGGTT TG CAT TTC CATCGA /

T CT GAAAT TT- TTAC

GAM246 TGTGATTGATTCCCACTAAT 232 TCTAAATTCG 581 GA CA - GA-- CCAC
GAAGATGCCACATATCCATC GCAGGAAAGT TGTGATT TTCC CT AAT AGATG A
TCTAAATTCGGCAGGAAAGT CACA ||||| ||| || ||| ||||
CACA ACACTGA AAGG GG TTA TCTAC /
-- AC C AATC CTAT

GAM247 AATGCTCGCAACATTAACAT 233 ATAAATTTAT 582 CT C ACATCT CCGT T AA
CTTGAACCGTTGGTACAATT AATGTTTCGCC AATG CG AACATTA TGAA TGG AC T
CCGTTCCATAAATTTATAAT ATT |||| || ||||| ||| ||| ||
GTTTCGCCATT TTAC GC TTGTAAT ATTT ACC TG T
C- - ----- AAAT T CC

GAM248 ATGGAGATTTTCTATTCTCG 234 TCCCTAATAA 583 TTTC T TCCATT ATAT C
TCCATTTTAGGATATGCTTT CTTCGTGAAT ATGGAGAT TATTC CG TTAGG GCTTT A
CATAAAGTCCCTAATAACTT AATG ||||| ||||| ||| ||||
CGTGAATAATGTTTCTAT TATCTTTG ATAAG GC AATCC TGAAA /
TA-- T TTCAAT C--- T

GAM249 TCTTTTATGCCAGAGATATC 235 GTTTCAGCGT 584 T CCA- T A C--- T
ATAGCCGCTCTTAGAGTTTC GATTTTCCAA TCT TTTAG GAGA ATCAT GC GCTC T
AGCGTGATTTTCCAACCTAA CCTA ||| |||| ||| ||||| || |||
ATAGA AGA AAATC CTTT TAGTG CG TGAG /
T CAAC - - ACTT A

GAM250 TTGCTTCGCGTTTAGCCTCT 236 TAGCCTCTGG 585 TTCGCG CT GC A A C
GGCTTTTATCAGCCTTTGT CTTTTATCA TTGC TTTAGC CTG TTTT TC GC T
AGAAAAAATTTCAGTTGCTG GCCT |||| ||||| ||| ||||| |||
GAATTGCAA AACG AGGTCG GAC AAAAA AG TG T
TTA--- TT TT A A T

GAM251 ACACCAGAAAAGACGGCTTG 237 TGAGATCAAC 586 A AAAGAC T - CT TCTAAT
ATAA A
AGATCAACTTTATCTAATGG TTTATCTAAT AC CCAGA GGC TGAGA TCAA TTA GGTTT
AACGAAGG G
TTTATAAACGAAGGAGGCC GGTT || |||| ||| ||||| ||| |||| |||||
TTCGTTTCGAAATCTAATTTG TG GGTCT CCG ATTTT AGTT AAT CTAAA
TTGCTTCC /
ACTTTTACGCCTCTGGCGT C ----- C C T- ----- GC-- G

GAM252 TGTGAGAAGTTTGCCTCGTT 238 TGGAATAGTT 587 GA-- GC C T T -- TTA----- TT
T

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|-----------------------|------------|------|--------|-------|----------|-------|------|
| AAGGTCTTCCATTAAATAT | TTTTACTAGT | TGA | AGTTT | CT GT | AAGG CT | TCCAT | AATA |
| ATATAACA T | | | | | | | |
| TATATAAACATTTGTGTTTG | AAAG | | | | | | |
| TATCTTATTCGTCTTTTATG | | ATT | TCGAA | GA CA | TTTT GA | AGGTA | TTAT |
| TATGTTTGT T | | | | | | | |
| GAATAGTTTTTTTACTAGTAA | | AACG | AT T T | T TA | TTTTCTGC | TC | G |
| AGCTGCAATTACA | | | | | | | |

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|--------------------------------|----------------|------------|---------|-----|-------|
| GAM253 ATAGATGCCATGTAAAAAT 239 | GATGCCATGT 588 | T | AAAAAT- | CG- | TCGA |
| GTCCGCCGTCGACTTTTTGG | TAAAAATGTC | ATAGATGCCA | GTT | GTC | CCG C |
| AACGATTGATAAAAGCTGGT | CGCC | | | | |
| GTTTAT | TATTTGTGGT CGA | TAG | GGT | / | |
| | - AAATAGT CAA | TTTT | | | |

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|---------------------------------|----------------|--------|--------|---------|--------|
| GAM254 ATAGCATCATCTTTAGATCA 240 | AGCATCATCT 589 | GC | CTTTA | C AA- | TACCTT |
| TTAATTGTTACCTTCCCAA | TTAGATCATT | ATA | ATCAT | GAT ATT | TTGT C |
| TACAACCAAATCATCATGAT | AATT | | | | |
| ATAT | TAT TAGTA | CTATAA | AACA | / | |
| | A- ---- | C ACC | TAACCC | | |

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|---------------------------------|----------------|-------------------|--------|-------|------|------------|
| GAM255 CTTTGGCTTATAAAATACAA 241 | TAAAATACAA 590 | AAT----- | CCC | TT-- | C-- | CT |
| TC | | | | | | |
| ATGACATTCCCTTATGTTTA | ATGACATTCC | ATACA | GACATT | TTATG | TAAT | TTAAT |
| TT T | | | | | | |
| ATCTTAATCTTTTCTTTAGT | CTTA | | | | | |
| TATTGAATCGTTACAATTAT | | TATGT | TTGTAG | AATAT | ATTG | AGTTA GA / |
| AAAATGATGTTTTTTCCAAA | | GAATCCAAAAACCTTTT | TAA | TAAC | CTA | TT TT |
| AACCTAAGTGTATTTAAAAT | | | | | | |
| AGATGCCATG | | | | | | |

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|---------------------------------|----------------|-------|------------|---------|-----------|
| GAM256 TACGACACTGATAAACCGCA 242 | ACACTGATAA 591 | C T | CGCA | ---- | G T |
| TTATCTGTGGACATTTTAAT | ACCGCATTAT | TACGA | AC GATAAAC | TTATCTG | T GACAT T |
| GTTGGTATCTAGATAACAAT | CTGT | | | | |
| GTTTATCGTATTGTA | | ATGTT | TG CTATTTG | AATAGAT | G TTGTA T |
| | A - | TAAC | CTAT G | A | |

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|---------------------------------|----------------|-------|-------------|----------|---------|
| GAM257 TGTATCCTCAACATAATCAA 243 | TTTATTGGGT 592 | --- C | AA- | - AG- | AAT |
| TGAGCCAGGTAATCAAGACA | AGTGTTGATG | TGT | ATC TCAACAT | TCAATGAG | CC GT C |
| TCGGATTTATTGGGTAGTGT | ATTC | | | | |
| TGATGATTCCGCA | | ACG | TAG AGTTGTG | GGTTATTT | GG CA / |
| | CCT T | ATG | A CTA | GAA | |

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|---------------------------------|-----------------|----|------|-------------|----------------|
| GAM258 GATTTGGCCAAATGTATCCA 244 | TAAC TAGTGT 593 | CC | G | CATCATAA--- | GG ATAA G |
| GTAAC T | | | | | |
| TCATAATCTGGGTATAAAC | AGAAAACAGA | GG | AAAT | TATC | TCTG TT AC GGT |
| AAGAATATA G | | | | | |
| GGGTGTAAACAAGAATATAT | GATA | | | | |

GTTTATATTTTTTAACTAGT
GTAGAAAACAGAGATAGTAA
ATAGATAGTTTTTCCAGATC

CC TTTG ATAG AGAC AA TG TCA TTTTATAT T
TT - ATAAATGATAG AA GATG A AT---- T

GAM259 AGCGAAGCTATCATCGTCCA 245 ATATTATCTA 594 TATCAT CC-- C ATT
ATATCTCATTCCCTAGAAATA CGTCATTGTT AGCGAAGC CGT AATAT TC C
TTATCTACGTCATTGTTTTG TTGT ||||| || |||||
TT TTGTTTTG GCA TTATA AG /
 TTA CT- TCTA A ATC

GAM260 GTGGTATTATACTCATGCCT 246 TATTATACTC 595 A AT- TCAT-- A AA---- - G T
AGTAATAGTCTCTTTGCGTT ATGCCTAGTA GTGGT TT AC GCCT GT TAGTCT CTTT CG
T
GACGGAAAGCAGACTAGAAA ATAG ||||| || ||||| ||||| |||||
TAACAGGCTAAAATGTTTCAG TACCA AG TG CGGA CA ATCAGA GAAA GC G
ACACCAT C ACT TAAAT - ATAAAG C G A

GAM261 GGCAAATAATTAATCAGTGA 247 AACGATGTTA 596 TA AATCA AG T AGT
TAGATTGTTTACATACAGTA CCAATCGTTT GGCAAA ATT GTGAT ATTGTTTACA AC A
TGTCGTTTGTAACGATGTT GCT ||||| || ||||| |||||
ACCAATCGTTTGCT TCGTTT TAA CATTG TAGCAAATGT TG T
GC C---- -- T CTG

GAM262 GGAATTTTGACAATTCTCTT 248 AGTGAAAAGA 597 A - TTC----- GA C A
TGAGCCGATAGTATCAGTGA ATGTAACTT GG ATTT TGACAA TCTTT GC GAT G
AAAGAATGTAACTTTGTCA TGTC ||||| ||||| ||||| |||||
TAAGTACC CC TGAA ACTGTT AGAAA TG CTA /
A T TCAAATGTA AG A T

GAM263 ATATTACGCAGCAAGCATAA 249 TTAGGTTTGT 598 A --- T A--- TA
CCAGCATAATCTGTCTTAGG TCATTGTCGT ATATTACGC GCAA GCA AACC GCA A
TTTGTTTCATTGTCGTGTGGT GTGG ||||| ||||| ||||| |||||
GT TGTGGTGTG TGT TGT TTGG TGT /
C ACT - ATTC CT

GAM264 GATAAAAATGTAGTGTAATT 250 TATAGTGTA 599 - GTAATT TAT AA ATGC TT
TCG TG
GTTATATAGTGTAACACGAA CACGAATGCA ATGTAGT GTTA AGTGT CACGA AG
TGGGAGTAT TTG C
TGCAGTTTGGGAGTATTCGT GTTT ||||| ||||| ||||| |||||
TGTGCTACAAATATATTTCC TATATTA CGAT TTACG GTGCT TC ACCTTTATA
AAC /
ATTCTTCGTGGCATTTTTAG G AAATAT TT- -- ---- TT TA- AT
CTATAAAATTATATGGGGTT
GTC

GAM272 ATTCGCGAAGCGACGTCATT 258 ACGTCATTTA 607 G CGTC AATAAA TTT
 TAATAAAAAAAGTATTTTTT ATAAAAAAG ATTCGCGAA CGA ATTT AAAAGTATT T
 TTTAATATTTTTTCACAAATA TATT ||||| ||| ||| |||||
 TCGTTCGCGGAT TAGGCGCTT GCT TAAA TTTTATAA /
 - A--- CAC--- TTT

GAM273 TATCTTGGCAATAACTAATT 259 TGGCAATAAC 608 CT AACT G A -- A T
 GAGATATTGATGCGAGTTCTG TAATTGAGAT TAT TGGCAAT AATT AG TATT GATGCG
 GTTCGGTA G
 GTATGCATATCGGACACGTA ATTG ||| ||||| |||| || ||||| |||||
 TCCGAGTACTGATTCCAAGT ATG ACCGTTG TTAG TC ATGA CTATGC CAGGCTAT C
 TGCCAGAGTA AG AACC - - GC A A

GAM274 ATAGATATGATAACAGGAAT 260 GATATGATAA 609 - A ATAA A TA- T AAATA
 AACATCTTTAGGTTTAAAAT CAGGAATAAC ATAGAT ATGAT ACAGGA C TCTT GGT TA A
 AATTATATACACCAGTAGGA ATCT ||||| ||||| ||||| ||||| |||||
 GTCTTGTATCGTCATCTAT TATCTA TGCTA TGTCT G AGGA CCA AT /
 C C ---- TGA C ATATT

GAM275 GAGTCGTCCATATTTTATTC 261 CGTCCATATT 610 TC CATATT - CC ----- A
 TGAGGCCTAATAGACCTCTG TTATTCTGAG GAG GTC TTATTCT GAGG TA ATAG C
 TACATAAAATATTCCTCTAG GCCT ||| ||| ||||| ||||| ||| |||||
 AATAGTAGACATCTC CTC CAG GATAAGA CTCC AT TGTC C
 TA AT---- T TT AAAATACA T

GAM276 GGATATTCTTGATACATTCT 262 TATGGCAAAT 611 T T T TTCTTTTT A TACAT- -----
 - CA
 TTTTATACAGTGAATTGCAT CTGCAATCAC ATA TCT GA ACA ATACAGTGA TTGCA CC
 GATA G
 ACATCCGATACAGCATTATC TGTA ||| ||| ||||| ||||| ||| |||||
 CATATATGGCAAATCTGCAA TGT AGA TT TGT TATGTCACT AACGT GG CTAT
 C
 TCACTGTATTGTTTTTAGAT T T T ----- - CTAAAC TATATAC TA
 TGTCC

GAM277 GTAGTCACCGTAAATTTATC 263 CACCGTAAAT 612 A AA T TCACC A A
 ACCAGAAATACTAATATCTA TTATCACCAG GT GTCACCGT AT TA AGA AT C
 TCTTTATGTCCATGGTGATC AAAT ||| ||||| ||||| ||||| |||||
 AC CATAGTGGTA TG AT TCT TA T
 C CC T TTCTA A A

GAM278 TATCTATCAGATTATTATGT 264 TAAGGTA CTT 613 ----- AT AT-- GG - - ATAAA
 GTTATAAGGTACTTTTTCTC TTTCTCATAA TATCTATCA GATT TATGTGTT AA TACT TTTT
 CTCATA C

ATAATAAACTAGAGTATGAG TAAA ||||| ||| ||||| || ||| ||| |||||
 TAAGATAGTGTTTTTCAAAA GTAGGTAGT CTAA ATATACAA TT GTGA AGAA
 GAGTAT /
 CATATAAATCTAAAATTGAT TAAAAT -- AACT TT T T GAGAT
 GGATG

GAM279 AAAGTATTGGTAATCGTGTC 265 TTTGTTCTAT 614 - TAATCGT CA TA TAAAAAG
 TTATTTTT TA
 ATATTAGTATAAAAAGTGAT CAACTACCTA AAAGTATT GG GT TAT GTA TGAT
 ACAAAAT T
 TTATTTTTACAAAATTATGT TAAA ||||| || ||| || ||| |||||
 ATTTTGTTCTATCAACTACC TTTCATAA CC CA ATA CAT ACTA TGTTTTA /
 TATAAACTTTCCAAATACT A TTT---- AA TC CA---- TCT---- TG
 TT

GAM280 ATGGCAGATCCAATTTGTAA 266 ATCCAATTTG 615 CA - AA TAAAA C ---- GAA
 AAAATCAGCGGTTGAAAGAA TAAAAAATCA ATGG GAT CC TTTG AAT AGCGGT TGAA T
 TATATTTACGTTATCGTTA GCGG ||| ||| ||| ||| ||||| |||||
 GTTAGGCTCAAAGGTATCCC TACC CTA GG AAAC TTG TTGCTA ACTTT /
 AT -- T -- TCGGA A TTGC ATA

GAM281 CGTGAAGATATCATTTCCCA 267 TCATTTCCCA 616 AA TC CA---- - TT TT
 TGTATTTTTTTTATGATTGT TGTATTTTTT CGTG GATA ATTTCC TGT AT TT T
 AGCAGTTTATGAAATTTTA TTAT ||| ||| ||||| ||| |||
 TCACGCG GCGC CTAT TAAAGG ACG TG AG /
 A- TT TATTTG A TT TA

GAM282 CTTGGTATAATTATCAAAAT 268 TGGAATTGGG 617 TTATCAAAATA GA- CG-- C
 ACAAGACGTCGCTTTTAGCA CTCCTTATAC CTTGGTATAA CAA CGT CTTTAG A
 GCTAAAAGAATAATGGAATT CAAG ||||| ||| ||| |||||
 GGGCTCCTTATACCAAG GAACCATATT GTT GTA GAAAATC /
 CCTCGG---- AAG ATAA G

GAM283 TACCTTATCAAATGATCCTG 269 TATCAAATGA 618 TT- A- G C T CA T TA
 TTGGGCATTTTCTACATTGA TCCTGTTGGG TACC ATC AAT AT CTG TGGG TT TC C
 TGACATCCATTAGAATAATT CATT ||| ||| ||| ||| ||| |||
 GGGATTGTGGTA ATGG TAG TTA TA GAT ACCT AG AG A
 TGT GG A A T AC T TT

GAM284 TCGCTACTTGGTTAGTGTAT 270 TTAATAATTA 619 CTACTT T T C TGA
 TATTCAGTATGAAGACCTAT CTTATCTTTT TCG GGT AGTG ATTATT AGTA A
 TAATAACTTATCTTTTG GACG ||| ||| ||| ||||| |||||
 ACGA AGC CTA TCAT TAATAA TTAT G
 AGTTTT T - - CCA

GAM285 TTTTGGTAATCTATTATTAT 271 TATTATTATT 620 CT TATT CTCT- ACCG
 TGGCTCTGATCACCGCATCT GGCTCTGATC TTTTGGTAAT AT ATTGG GATC C
 AGATCTACACCTAATCTATT ACCG ||||| || |||| ||
 AATTACCAAGA AGAACCATTA TA TAATC CTAG A
 AT TC-- CACAT ATCT

GAM286 TTTGGTCGATGTAAAATTTT 272 TGTAATAATT 621 CGA AAATTTTT - AAA
 TGTCGATAAAAATTAAAAA TTGTCGATAA TTTGGT TGTA GTCGATAA AAATTAA A
 TAACCTAATTTATTATTGAT AAAT |||| || ||||| |||||
 CTCGTGTGTACAACCGAA AAGCCA ACAT TAGTTATT TTAAATT T
 --- GTGTGCTC A CAA

GAM287 GATTCTCGTCGTACCCACCG 273 TCGTACCCAC 622 T C- CC G T TAA
 AGAGCGTGTGCGTAAAACAT CGAGAGCGTG GAT CTCGT GTAC ACCGAGA CGTG GCG A
 CGCCATGATTTGCGTTGTAC TGCG ||| |||| ||| ||||| |||||
 ACACGAGATC CTA GAGCA CATG TGGCTTT GTAC CGC A
 - CA T- A - TAC

GAM288 CGTATTATACGCATTATAAC 274 TTCGTTGTAT 623 CGCAT T C GTA
 TGACAGCGTCGTAAATAGAT ATAGTACG CGTATTATA TATAAC GA AGCGTC A
 GTTTCGTTGTATATAGTACG ||||| ||||| |||||
 GCATGATAT ATGTTG CT TTGTAG /
 ---- - - ATA

GAM289 GGTAGCAATTTATGGAACCT 275 TAACGGAGAT 624 --- T AAC GGTCATT CAC
 GAACAA
 ATATTGGTCATTATTTTGT TAAAAATATG GGT AGCAATTATGG TTATATT ATTTTGT
 AG A
 CACAGGAACAACTAATACT ACGC ||| ||||| ||||| ||||| ||||| ||
 ATAACGGAGATTAAAAATAT CCG TTGTAA TACC AGTATAA TAGAGGCA TC /
 GACGCCATAATTGTTAACG CAA - CGC AAAT--- ATA ATAATC
 CC

GAM290 GTATCATAATTTTCAAAGAT 276 GTTGTTGTTT 625 T AAT A- A TTA- TACTTCC
 GGTCGTTTAGACAATAGTAC GCGACTGCTT GTA CAT TTTC AAG TGGTCGT GACAATAG
 A
 TTCCATTATTATTTGTTGT CCGA ||| ||| ||| ||||| |||||
 TGTTTGCGACTGCTTCCGAA CAT GTA AAAG TTC GTCAGCG TTGTTGTT T
 ATACATGTAC - CAT CC - TTG TTATTAT

GAM291 TGTTCTCTATAGTTACATTA 277 TGTGACACCC 626 TA----- - TTA
 ATTAAAATTTTATATGTGAC ATTCATCTGG TGTTCTCTA GTTACAT TAA A
 ACCCATTCTCTGGAGAATA AGAA ||||| ||||| |||
 ATAAGAGGT CAGTGTA ATT A
 CTACTTACCCA T TTA

GAM292 CATCTTTTACCAACACAAAG 278 TCTTTTACCA 627 CT ACACAAA ATATTT TT -
 GATAAT ACA
 GGTGGATATTTGTTTCATTGG ACACAAAGGG AT TTTACCA GGGTGG G CATTG GAGTT
 AATAC C
 AGTTGATAATAATACACACA TGGA || ||||| ||||| | |||| |||| ||||
 AAGTATTTGGATTCACGGTG TA AGATGGT TCCATC T GTGGC CTTAG TTATG
 /
 GGTTACGACTACCTCAGACT AG CAGAC-- AGCAT- GG A GT---- AAA
 GGTAAGAATG

GAM293 GTACGCGTGTTCGATTCATCA 279 TGAGGCTACC 628 -- ----- A-- AT
 AGGTATATAAACCTGGGGAT TCGACATACG GTACGCGT GTCGA TTCATC AGGT A
 GAGGCTACCTCGACATACGT TGTG ||||| |||| ||||| ||||
 GTGC CGTGTGCA CAGCT GAGTAG TCCA T
 TA CCATCG GGG AA

GAM294 TAATTTTTTATAAACTAACA 280 TAACATGTTA 629 TT AAAC T A-- G
 TTGTTAATTGAAAAGGGATA CAGAATATAA TAATTT TAT TAACAT GTTA TT A
 ACATGTTACAGAATATAAAT ATTA ||||| || ||||| |||| ||
 TA ATTAAA ATA ATTGTA CAAT GA A
 T- AGAC - AGG A

GAM295 AACACGGCAGAATATCGCCC 281 TGAGATATTC 630 ----- GC----- TACT
 ATATACTTTATTTATGGATT TGAGCGCTAA AACACGG CAGAATATC CCATA T
 TGAATGAGATATTCTGAGCG CCTT ||||| ||||| ||||
 CTAACCTTATCCGTGTT TTGTGCC GTCTTATAG GGTAT /
 TATTCCAATCGCGA AGTAAGTTTA TTAT

GAM296 AGTAGCATACGGATGCTCGA 282 TGTACAAATT 631 GCA ---- - T C ATAT GT GT
 TATT--- GT
 TGTACAAATTGATATGGTCG GATATGGTCG GTA TACGG ATGC TCGA GTA AAATTG G C
 CG CA C
 TCGTATTCAGTCAATGTTAC TCGT ||| |||| |||| |||| ||||| || || ||
 AGTCGGTGGTCCAATTTTAA CAT ATGCC TACG AGCT CAT TTAAAC C G GC GT
 /
 CTTGACGCATAGTCCCGTA AAC CTGA C T T ---- TG TG TGACATT AA
 CAATACT

GAM297 CCCTATTTTCAATCCCCATG 283 CATGGAGTAG 632 AT TCAA CCA - TCA T A C
 TA
 TTTCCTCTTCAGTCTTCTCA ATGATAGAGG CCCT TT TCC TGTTTCC TCT GTCT CTC CAT
 GTC A
 CATCGTCTAATAGACATGGA GGAA |||| || ||| ||||| || |||| |||| ||||
 GTAGATGATAGAGGGGAACA GGGA AA AGG ACAAGGG AGA TAGA GAG GTA CAG
 /

GAAGGACTATAATCAGGG

CT TATC AAG G TAG T - - AT

GAM298 GAAAAGACGTGGGTACTAAA 284 AAGTTGGCTG 633 - C AA T C CA- A T
GTTGGCTGTCATCTTACCAA TCATCTTACC GAAAAGACGTG GGTA TA GT GG TGT TCTT
CCAAT G
TTGCAATTGGAAGAACAACG AATT ||||| ||| || || ||| ||| ||||
ACCTGCACTAATACCACATG CTTTTTGTAC CCAT AT CG CC GCA AGAA GGTTA C
TTTTTTC A A CA T A ACA - A

GAM299 GTCGTTAAAAGCGCTTCTAT 285 AATTATAGAT 634 C A CT TC CAT
ATCTCTCATTAGCTAGAATT ACGCTATTAA GT GTTAA AGCG TCTATA TCT T
ATAGATACGCTATTAATTAT TTAT || |||| ||| ||||| |||
TA TAATT TCGC AGATAT AGA A
T A AT TA TCG

GAM300 TGGTCGTGTAGCGCGATAGA 286 TTAGATATCC 635 C A C AGAGATA T
GATAGTCTAATATTAATATT GTAACACTAC TGGT GTGT GCG GAT GTCTAATA T
AGATATCCGTAACACTACCA CA ||| ||| ||| ||| |||||
ACCA CACA TGC CTA TAGATTAT A
T A - ----- A

GAM301 GACATGGTAAGATTACTGGC 287 TGGTAAGATT 636 T-- G ACTG - TCTAA
TCGTTTTCTAACTCCATGAA ACTGGCTCGT GACA GGTAATT GC TCGTTT C
TGATGCAAAATATTACCCTT TTTC ||| |||| ||| || |||||
TGTC CTGT CCATT TAA CG AGTAAG /
TTC A AA-- T TACCT

GAM302 AAGGGTGAATGCGATACAT 288 AAGAATTTAT 637 GAATG ACAT C --- ACACA
TGATCTATGTAGTTTTAAAA ATAAATCATT AAGGGTG CGAT TGAT TATGTAG TTTTAAA
C
CACACGCAAACCTTTGAAGAA CCAT ||||| ||| ||| ||||| |||||
TTTATATAAATCATTCCATC TTCCTAC GCTA ACTA ATATATT GAAGTTT G
GATACATCCTT ATA-- CCTT A TAA CAAAC

GAM303 ACTGTATGCTCCTAGCGGAG 289 TGTATGCTCC 638 A - A AATCCTTCG T
TTAATCCTTCGTTGTTTCTA TAGCGGAGTT ACTGT TGCTC CT GCGGAGTT TTGT T
CAAAGTCTCTCGACTCCGCG AATC |||| |||| || ||||| |||
AGAGAGTAACAGT TGACA ATGAG GA CGCCTCAG AACAC
- A G CTCTCTGA- T

GAM304 ATAATTCAGTAATAATAATT 290 TCAGTAATAA 639 - A ATAATTC T AAA
CAGTAATGTATATAAAAATG TAATTCAGTA ATAATT CAGTA TA AGTAA GTATATAA T
CATTGTATATTTACTCCAAT ATGT ||||| |||| || |||| |||||

ACTACTGTAGTTGT TGTGTA GTCAT AT TCATT TATATGTT /
T C AACC--- - ACG

GAM305 ATAGAGTCTACATTTATATG 291 TCTACATTTA 640 CTACATTT TCT -- AGAT
TTCTCTATCGGTGAGATACA TATGTTCTCT ATAGAGT ATATGT CTATC GGTG A
AATACCTAGATAGTCGCGTA ATCG ||||| ||||| |||| ||||
TCTTCATCCATTCTAT TATCTTA TATGCG GATAG CCAT /
 CCTACTTC CT- AT AAAC

GAM306 ATATCTTCAGTACATCGTTT 292 TACAAATAGC 641 T T G C--- A A
GTAAAGTAATTATTATACAA AGTGTAGTGC ATA CT CA TACAT GTTTGTA AGT A
ATAGCAGTGTAGTGCAGTAT AGTA ||| || ||||| ||||| |||
 TAT GA GT ATGTG TAAACAT TTA T
 - C G ACGA A T

GAM307 ATTGCACGAAGTTCTTCGGC 293 ATTGTCCCAC 642 C C TTTCAT-- G A AA
TTTAATG TC CG
 GGTTCATGGAGTCATTTT GGAAGTGAAT GTTCTT GG GGT GGA TCATTTCTG TG ACA
ATC CA C
 TGATGAAACATTTAATGATC CCTT ||||| || ||| || ||||| || ||| ||| ||
 TCCACGCAATTGTCGATATT CGAGAA CC CCA CCT AGTGAAGGC AC TGT TAG
GT A
 GTCCCACGGAAGTGAATCCT A A CTCAACTT A - CC TA----- CT TA
 TCAACTCACCACCAAAGAGC
 TCCGTTGCAT

GAM308 CCACATCCTTTATTAATAAT 294 TGAGAAAGAC 643 A TT ATAATAA AA TCTAT
AATTTAACAATCTCTATATC CAGTAGTATT CC CATCC TATTA TTT CAATC A
TATGGTTGAGAAAGACCAGT GGAT || ||||| ||||| || |||||
AGTATTGGATGGG GG GTAGG ATGAT AAA GTTGG /
 - TT GACCAG- GA TATCT

GAM309 GAAGGTAGTAATGTTAGTAG 295 TAGTTTATCA 644 GTA TTA A TAT G
ACAATTTTTATCTGTGAAAA TATACCTTT GAAGGTA ATG GTAGAC ATTTT CTGT A
CAGGAAATAGTTTATCATAT ||||| ||| ||||| ||||| |||||
ACCTTT TTTCCAT TAC TATTTG TAAAG GACA A
 A-- --- A --- A

GAM310 GCAATACTTCTGGTCTCGGA 296 TTCTGGTCTC 645 ACTTC A ----- C
TTAGGCGTCGTACGTATAT GGATTAGGCG GCAAT TGGTCTCGGATT GG CGT G
ATCCACCAATCCGAGACCAT TCGT ||||| ||||| ||||| ||| |||
TGATTGC CGTTA ACCAGAGCCTAA CC GCA T
 GTT-- - ACCTATATAT T

GAM311 GGCCTTTTTTATCGTTATCG 297 CCTTTTTTAT 646 C TT- CG CG - - TCACCTGG

GTTTTCTACACTCACCTGGT CGTTATCGGT GGC TT TTAT TTAT GT TTTC TACAC T
 TTATAAACGTGTGCGAGACA TTTC ||| ||| ||| ||| ||| ||| |||
 CAAATAATAATAATGTAACG TCG AA AATA AATA CA AGAG GTGTG /
 CT C TGT AT AA C C CAAATATT

GAM312 TCATAATATTAGAATATATT 298 TAGAATATAT 647 ATT TATATTTTAAAGGA TTA TAT
 TTAAAGGACTTATCGTTATT TTAAAGGAC TCATAAT AGAA CTTATCG TTA T
 ATATTTTTTTAACTCGGTGA TTAT ||||| ||| ||||| |||
 GGTATCTTCTTAACTTTCTC AGTATTA TCTT GAGTGGC AAT T
 GAATTATGA AGC TCAATTCTTCTATG TC- TTT

GAM313 TTCTGAAAGAGATGAGAAGC 299 TCTATGGGTC 648 GAAAG A AA CCC
 CTGTAGAGAGACCCTGCGCT CATCTATGAG TTCT AGATG G GCCTGTAGAGAGA T
 TTCTCTATGGGTCCATCTAT AA ||| ||||| ||||| |||||
 GAGAA AAGA TCTAC C TGGGTATCTCTTT G
 GTA-- --- CGC

GAM314 TTTCTTTTCACGATGCATCT 300 ATAAGTGGAC 649 TC- GA- ----- GA CGT
 TATTGAATGACGTTTTCTCA ATATAGATGC TTTCTTT AC TGCATCT TATT ATGA T
 TAAGTGGACATATAGATGCA AGAA ||||| || ||||| ||| |||
 GAAGTAATGAAGAAA AAAGAAG TG ACGTAGA GTGA TACT /
 TAA AAG TATACAG A- CTT

GAM315 TTTTATAAACATGAAACCA 301 TGTCTAAATG 650 --- AAACCACT- AAA TAATTA G
 T CTGTCTAAATGTAATTATGA TAATTATGAT TTTTATA AACATG GTCT TG TGATCTT
 ATT A TCTTGATTTATAGATGAAGA CTTG ||||| ||||| ||| || ||||| |||
 TCAGCCTTTAGAGGATTTTA AAAAGTAT TTGTAT TAGG AT ACTAGAA TAG T
 ACCAGTATGTTTAATATGAA AAT GACCAATTT AG- TTCCG- G A
 AA

GAM316 ATGTAGTAATCGTTGTCGTG 302 ATGGTTCTTT 651 C TG GTGTTCC- TCC TTCTCC -
 T TTCT TTCCTGTTTCCTACTTCTCC CCGTACAACA AT GT TC TGTT TAC AATCAT
 ATAGATATT TCT A TACT ||| || ||| ||| ||||| ||||| |||
 AATCATATAGATATTTTCTT TATA AG ACAA ATG TTGGTA TGTTTATAA AGG /
 TCTATCATGGATAATATTTG - GT ATTTGTCAT C- CTTTC A T TACT
 TAATGGTTCTTTCCGTACAA CATACTGTTTAGATGATATT
 GCGCAT

GAM317 GAATGACTCGTCCCTTAATA 303 TGAATCGTCC 652 GA G TAATA AGTAG - TCT
 GGCAGTAGGCTAGTATCTTT CTTAATAGGC GAAT CTC TCCCT GGC GCTA GTA T
 TTTACGTAGTAATCGTCGTA AGTA ||| ||| ||| ||| ||| |||
 GGGAGAGAATTC CTTA GAG AGGGA CTG TGAT CAT /
 A- - TG--- CTAA- G TTT

GAM318 GAGATTGTATCAGTTTCGTA 304 GATTGTATCA 653 -- - T TA TGA G T
 GTCTTGAGTATTGGTATTAC GTTTCGTAGT GAGATTGTA TC AGT TCG GTCT GTATTG TAT A
 TATATAGTATATAGATGTCG CTTG ||||| || ||| ||| ||||| |||
 ACGCTAGATATACAGTCTC CTCTGACAT AG TCG AGC TAGA TATGAT ATA C
 AT A C TG TA- - T

GAM319 GGCAAATCTTATCATTGGTC 305 TAACATCGAT 654 CTT - --- TG- TTGCTTT
 GGTGTTTGGTCTTGCTTTGT TCCCATATGA GGCAAAT ATCAT TGG TCGGTGTT GTC G
 GACTTTGATAATAACATCGA TGTT ||||| ||||| ||||| |||
 TTCCCATATGATGTTTGT TTGTTTG TAGTA ACC AGCTACAA TAG /
 --- T CTT TAA TTTCAGT

GAM320 ACCTCTTTCTGATGGAGTCG 306 TGATGGAGTC 655 TTTCT- T TC AAG CT TC
 TCTTC T CTCACAA
 TAAAAAAGTTTTATCTCTTT GTAAAAAAGT C GA GGAG GTAAAA TTTTAT CTT TC GA
 GGT A
 CTCTCTTCGATGGTCTCACA TTTA | ||||| ||||| ||||| ||| || |||||
 AAAATATTAAACCTCTTTCT G CT TCTC TATTTT AAAATG GAG AG CT CCA A
 GATGGAGTCGTAAAAAAGTT CTTCT T -- GAA CT GT TCTTT - AATTATA
 TTATCTCTTTCTCCTTCGAT
 GGT

GAM321 ACCTCTTTCTGATGGAGTCG 307 TGATGGAGTC 656 TTTCT TG TC AAG CT TC
 TCTTC T CTCACAA
 TAAAAAAGTTTTATCTCTTT GTAAAAAAGT TC GA GAG GTAAAA TTTTAT CTT TC GA
 GGT A
 CTCTCTTCGATGGTCTCACA TTTA || || ||| ||||| ||||| ||| || |||||
 AAAATATTAAACCTCTTTCT AG CT TTC TATTTT AAAATG GAG AG CT CCA A
 GATGGAGTCGTAAAAAAGTT CTTCT CT TC GAA CT GT TCTTT - AATTATA
 TTATCTCTTTCTCTCTTCGA
 TGGT

GAM322 ACCTCTTTCTGATGGAGTCG 308 TGATGGAGTC 657 TTTCT TG TC AAG CT TC
 TCTTC T CTCACAA
 TAAAAAAGTTTTATCTCTTT GTAAAAAAGT TC GA GAG GTAAAA TTTTAT CTT TC GA
 GGT A
 CTCTCTTCGATGGTCTCACA TTTA || || ||| ||||| ||||| ||| || |||||
 AAAATATTAAACCTCTTTCT AG CT TTC TATTTT AAAATG GAG AG CT CCA A
 GATGGAGTCGTAAAAAAGTT CTTCT CT TC GAA CT GT TCTTT - AATTATA
 TTATCTCTTTCTCTCTTCGA
 TGGT

GAM323 ACCTCTTTCTGATGGAGTCG 309 TGATGGAGTC 658 TTTCT TG TC AAG CT TC
 TCTTC T CTCACAA
 TAAAAAAGTTTTATCTCTTT GTAAAAAAGT TC GA GAG GTAAAA TTTTAT CTT TC GA
 GGT A
 CTCTCTTCGATGGTCTCACA TTTA || || ||| ||||| ||||| ||| || |||||
 AAAATATTAAACCTCTTTCT AG CT TTC TATTTT AAAATG GAG AG CT CCA A
 GATGGAGTCGTAAAAAAGTT CTTCT CT TC GAA CT GT TCTTT - AATTATA

TTATCTCTTTCTCTCTTCGA
TGGT

GAM324 ACCTCTTTCTGATGGAGTCG 310 TGATGGAGTC 659 TTTCT TG TC AAG CT TC
TCTTC T CTCACAA
TAAAAAAGTTTTATCTCTTT GTAAAAAAGT TC GA GAG GTAAAA TTTTAT CTT TC GA
GGT A
CTCTCTTCGATGGTCTCACA TTTA || || ||| ||||| ||||| ||| || |||||
AAAATATTAAACCTCTTTCT AG CT TTC TATTTT AAAATG GAG AG CT CCA A
GATGGAGTCGTAAAAAAGTT CTTCT CT TC GAA CT GT TCTTT - AATTATA
TTATCTCTTTCTCTCTTCGA
TGGT

GAM325 ACCTCTTTCTGATGGAGTCG 311 TGATGGAGTC 660 TTTCT TG TC AAG CT TC
TCTTC T CTCACAA
TAAAAAAGTTTTATCTCTTT GTAAAAAAGT TC GA GAG GTAAAA TTTTAT CTT TC GA
GGT A
CTCTCTTCGATGGTCTCACA TTTA || || ||| ||||| ||||| ||| || |||||
AAAATATTAAACCTCTTTCT AG CT TTC TATTTT AAAATG GAG AG CT CCA A
GATGGAGTCGTAAAAAAGTT CTTCT CT TC GAA CT GT TCTTT - AATTATA
TTATCTCTTTCTCTCTTCGA
TGGT

GAM326 ACCTCTTTCTGATGGAGTCG 312 TGATGGAGTC 661 TTTCT TG TC AAG CT TC
TCTTC T CTCACAA
TAAAAAAGTTTTATCTCTTT GTAAAAAAGT TC GA GAG GTAAAA TTTTAT CTT TC GA
GGT A
CTCTCTTCGATGGTCTCACA TTTA || || ||| ||||| ||||| ||| || |||||
AAAATATTAAACCTCTTTCT AG CT TTC TATTTT AAAATG GAG AG CT CCA A
GATGGAGTCGTAAAAAAGTT CTTCT CT TC GAA CT GT TCTTT - AATTATA
TTATCTCTTTCTCTCTTCGA
TGGT

GAM327 ACCTCTTTCTGATGGAGTCG 313 TGATGGAGTC 662 TTTCT TG TC AAG CT TC
TCTTC T CTCACAA
TAAAAAAGTTTTATCTCTTT GTAAAAAAGT TC GA GAG GTAAAA TTTTAT CTT TC GA
GGT A
CTCTCTTCGATGGTCTCACA TTTA || || ||| ||||| ||||| ||| || |||||
AAAATATTAAACCTCTTTCT AG CT TTC TATTTT AAAATG GAG AG CT CCA A
GATGGAGTCGTAAAAAAGTT CTTCT CT TC GAA CT GT TCTTT - AATTATA
TTATCTCTTTCTCTCTTCGA
TGGT

GAM328 ACCTCTTTCTGATGGAGTCG 314 TGATGGAGTC 663 TTTCT TG TC AAG CT TC
TCTTC T CTCACAA
TAAAAAAGTTTTATCTCTTT GTAAAAAAGT TC GA GAG GTAAAA TTTTAT CTT TC GA
GGT A
CTCTCTTCGATGGTCTCACA TTTA || || ||| ||||| ||||| ||| || |||||
AAAATATTAAACCTCTTTCT AG CT TTC TATTTT AAAATG GAG AG CT CCA A
GATGGAGTCGTAAAAAAGTT CTTCT CT TC GAA CT GT TCTTT - AATTATA
TTATCTCTTTCTCTCTTCGA
TGGT

GAM329 ACCTCTTTCTGATGGAGTCG 315 TGATGGAGTC 664 TTTCT TG TC AAG CT TC
TCTTC T CTCACAA
TAAAAAAGTTTTATCTCTTT GTAAAAAAGT TC GA GAG GTAAAA TTTTAT CTT TC GA
GGT A

CTCTCTTCGATGGTCTCACA TTTA || || ||| ||||| ||||| ||| || |||||
 AAAATATTAAACCTCTTTCT AG CT TTC TATTTT AAAATG GAG AG CT CCA A
 GATGGAGTCGTAAAAAAGTT CTTCT CT TC GAA CT GT TCTTT - AATTATA
 TTATCTCTTTCTCTCTTCGA
 TGGT

GAM330 ACCTCTTTCTGATGGAGTCG 316 TGATGGAGTC 665 TTTCT TG TC AAG CT TC
 TCTTC T CTCACAA
 TAAAAAAGTTTTATCTCTTT GTAAAAAAGT TC GA GAG GTAAAA TTTTAT CTT TC GA
 GGT A
 CTCTCTTCGATGGTCTCACA TTTA || || ||| ||||| ||||| ||| || |||||
 AAAATATTAAACCTCTTTCT AG CT TTC TATTTT AAAATG GAG AG CT CCA A
 GATGGAGTCGTAAAAAAGTT CTTCT CT TC GAA CT GT TCTTT - AATTATA
 TTATCTCTTTCTCTCTTCGA
 TGGT

GAM331 ACCTCTTTCTGATGGAGTCG 317 CGTAAAAAAG 666 TTTCT TG TC AAG CT C TTC--
 T CTCACAA
 TAAAAAAGTTTTATCTTTCT TTTTATCTTT TC GA GAG GTAAAA TTTTAT TTCT TC GA
 GGT A
 CTCTTCGATGGTCTCACAAA CTCT || || ||| ||||| ||||| ||| || |||||
 AATATTAAACCTCTTTCTGA AG CT TTC TATTTT AAAATG GAGG AG CT CCA
 A
 TGGAGTCGTAAAAAAGTTTT CTTCT CT TC GAA CT T TCTTT - AATTATA
 ATCTCTTTCTCTCTTCGATG
 GT

GAM332 ATTAATTATAAAATTATGTA 318 TAAGTTAGTA 667 TA-- - A-- - T
 TATGATTTACTAACTTTAGT ATACATAAAT ATTAAT TAAAATT ATGTAT TGATTTA CTAAC T
 TAGATAAGTTAGTAATACAT TTTA ||||| ||||| ||||| ||||| |||||
 AAATTTTAGTATATTAAT TAATTA ATTTTAA TACATA ATTGAAT GATTG T
 TATG A ATG A A

GAM333 GATGGAGTCGTAAAAAAGTT 319 TGATGGAGTC 668 T TC AAG -- T TCCTTC T
 CTCACAA
 TTATCTCTTTCTCCTTCGAT GTAAAAAAGT GA GGAG GTAAAA TTTTAT CTCT TC GA GGT
 A
 GGTCTCACAAAAATATTAAA TTTA ||||| ||||| ||||| ||||| || |||||
 CCTCTTTCTGATGGAGTCGT CT TCTC TATTTT AAAATG GAGG AG CT CCA A
 AAAAAAGTTTTATCTCTTTC T -- GAA CT T TCTTT- - AATTATA

GAM334 GATGGAGTCGTAAAAAAGTT 320 TGATGGAGTC 669 T TC AAG -- T TCCTTC T
 CTCACAA
 TTATCTCTTTCTCCTTCGAT GTAAAAAAGT GA GGAG GTAAAA TTTTAT CTCT TC GA GGT
 A
 GGTCTCACAAAAATATTAAA TTTA ||||| ||||| ||||| ||||| || |||||
 CCTCTTTCTGATGGAGTCGT CT TCTC TATTTT AAAATG GAGG AG CT CCA A
 AAAAAAGTTTTATCTCTTTC T -- GAA CT T TCTTT- - AATTATA

GAM335 GATGGAGTCGTAAAAAAGTT 321 TGATGGAGTC 670 T TC AAG -- T TCCTTC T
 CTCACAA

| | | | |
|----------------------|------------|--------------------------------|----------|
| TTATCTCTTTCTCCTTCGAT | GTAAAAAAGT | GA GGAG GTAAAA TTTTAT CTCT TC | GA GGT |
| A | | | |
| GGTCTCACAAAAATATTA | TTTA | | |
| CCTCTTTCTGATGGAGTCGT | | CT TCTC TATTTT AAAATG GAGG AG | CT CCA A |
| AAAAAAGTTTTATCTCTTC | | T -- GAA CT T TCTTT- - AATTATA | |

GAM336 GATGGAGTCGTAAAAAAGTT 322 TGATGGAGTC 671 T TC AAG CT TC TCTTC T CTCACAA

| | | | |
|----------------------|------------|--------------------------------|----------|
| TTATCTCTTTCTCTCTTCGA | GTAAAAAAGT | GA GGAG GTAAAA TTTTAT CTT TC | GA GGT |
| A | | | |
| TGGTCTCACAAAAATATTA | TTTA | | |
| ACCTCTTTCTGATGGAGTCG | | CT TCTC TATTTT AAAATG GAG AG | CT CCA A |
| TAAAAAAGTTTTATCTCTTT | | T -- GAA CT GT TCTTT - AATTATA | |
| C | | | |

GAM337 GATGGTCTCATAAAAAAGT 323 ATAAAAAAG 672 G TCATAAAA TTTTAC ATTCT-CTCTCTT TG

| | | | | | |
|----------------------|------------|-------------------------|--------|--------------|------|
| TTTACAAAAATATTTTTATT | TTTTACAAAA | AT GTC | AAAG | AAAAATATTTTT | CTTT |
| TGA G | | | | | |
| CTCTTTCTCTCTTTGATGGT | ATAT | | | | |
| CTCATAAAAAAGTTTTACA | | TG TAG TTTC TTTTATAAAAA | GAAA | ACT / | |
| AAAATATTTTTATTCTCTTT | | G TTTCTCTC TCTTA- | CATTTT | AAAAT-- | CT |
| CTCTCTTTGATGGTC | | | | | |

GAM338 GGAGTCATAAAATATTTTTTA 324 TAAAATATTT 673 TC A T- T TCTCTTC T CTCACAA

| | | | |
|----------------------|------------|-----------------------------|----------|
| TTCTCTTTCTCTCTTCGATG | TTATTCTCTT | GGAG ATAAAAT TTTTAT CTCT TC | GA GGT |
| A | | | |
| GTCTCACAAAAATATTAAC | TCTC | | |
| CTCTTTCTGATGGAGTCGTA | | TCTC TATTTTG AAAATG GAGG AG | CT CCA A |
| AAAAAGTTTTATCTCT | | -- A CT T TCTTT-- - AATTATA | |

GAM339 TTAAACCTCTTTCTGATGGA 325 TGATGGAGTC 674 CTTTCT TG TC AAG -- T TCCTTC T CTCACAA

| | | | |
|----------------------|------------|--|----------|
| GTCGTAAAAAAGTTTTATCT | GTAAAAAAGT | GA GAG GTAAAA TTTTAT CTCT TC | GA |
| GGT A | | | |
| CTTTCTCCTTCGATGGTCTC | TTTA | | |
| ACAAAAATATTAACCTCTT | | CT TTC TATTTT AAAATG GAGG AG | CT CCA A |
| TCTGATGGAGTCGTAAAAAA | | TCTTTC CT TC GAA CT T TCTTT- - AATTATA | |
| GTTTTATCTCTTTCTCCTTT | | | |
| CTCACAAAAA | | | |

GAM340 TTTTCTTTGGTACAAAATT 326 TCTTTGGTAC 675 T TT CACAA --- CA A TCACACAAGTTTTTATACAG AAAATTTTAC TTTTCTT GGTACAAAA TCA GTTTT TATA GACAA T

| | | | |
|---------------------|------|------------------------|--------------------|
| ACAAATTCTTGTCATATAT | ACAA | | |
| TTTAAACATTGACTTTTGT | | AAAAAGAA TCATGTTTT AGT | CAAAA ATAT CTGTT T |
| ACTAAGAAAAA | | - C- TA--- TTTT AC C | |

GAM341 AGAGATAAACTTTTTTACG 327 TGAGACCATC 676 -- AC ----- A A AAGA A T
 ACTCCATCAGAAAGAGGTTT GAAGGAGACT AGAGATA AACTTTTTT GA CTCC TC GA
 GGTTT ATA T
 AATATTTTTGTGAGACCATC CCAT ||||| ||||| || ||| || ||||| ||
 GAAGGAGACTCCATCAGAAA TTTTAT TTTGGAGAAA CT GAGG AG CT CCAGA
 TGT T
 GAGGTTTAATATTTTT AA GA ACCTCA A - A--- G T

GAM342 ATAAAAATATTTTTGTAAAA 328 AATATTTTTG 677 AAAA A-- GA
 CTTTTTTATGAGACCATCA TAAACTTTT ATAAAAATATTTTTGT CTTTTTT TGA C
 AAGAGAGAAAGAGAATAAAA TTTA ||||| ||||| ||
 ATATTTTTGT TGTTTTATAAAAATA GAAAGAGA ACT /
 AGA- GAA AC

GAM343 ATAAAAATATTTTTGTAAAA 329 AATATTTTTG 678 AAAA A-- GA
 CTTTTTTATGAGACCATCA TAAACTTTT ATAAAAATATTTTTGT CTTTTTT TGA C
 AAGAGAGAAAGAGAATAAAA TTTA ||||| ||||| ||
 ATATTTTTGT TGTTTTATAAAAATA GAAAGAGA ACT /
 AGA- GAA AC

GAM344 ATGGATTTTACTAGATCATT 330 TTATACGATC 679 - TTT - ATTT- ACC
 TATATACCAAAAATATTAT TACGTTTTAT ATG GAT AC TAGATC ATAT A
 ACGATCTACGTTTTATTATA TATA ||| || ||||| ||
 T TAT TTA TG ATCTAG TATA A
 A TTT C CATAT AAA

GAM345 CTTTTTTACGACTCCATCAG 331 CATCAGAAAG 680 A CTCCA G G T A G GACCA -
 AAAGA
 AAAGAGGTTTAATATTTTTG AGGTTTAATA T CGA TCA AAAGA GTT AAT TTTTT TGA TCG
 AAGAGAG G
 TGAGACCATCGAAGAGAGAA TTTT | ||| ||| ||||| ||| ||||| ||| |||||
 AGAGATAAACTTTTTTACG A GCT AGT TTTTT TAA TTG AGAAA ACT AGC TTTTTTC
 A
 ACTCCATCAGAAAGAGGTTT - ACCAG G A T G G ACCTC A AAAAT
 AATATTTTTGTGAGACCATC
 GAAGAGAG

GAM346 CTTTTTTACGACTCCATCAG 332 CATCAGAAAG 681 A CTCCA G G T A G GACCA -
 AAAGA
 AAAGAGGTTTAATATTTTTG AGGTTTAATA T CGA TCA AAAGA GTT AAT TTTTT TGA TCG
 AAGAGAG G
 TGAGACCATCGAAGAGAGAA TTTT | ||| ||| ||||| ||| ||||| ||| |||||
 AGAGATAAACTTTTTTACG A GCT AGT TTTTT TAA TTG AGAAA ACT AGC TTTTTTC
 A
 ACTCCATCAGAAAGAGGTTT - ACCAG G A T G G ACCTC A AAAAT
 AATATTTTTGTGAGACCATC

GAAGAGAG

GAM347 CTTTTTTACGACTCCATCAG 333 CATCAGAAAG 682 A CTCCA G G T A G GACCA -
AAAGA
AAAGAGGTTTAATATTTTTG AGGTTTAATA T CGA TCA AAAGA GTT AAT TTTTT TGA TCG
AAGAGAG G
TGAGACCATCGAAGAGAGAA TTTT | ||| ||| ||||| ||| ||||| ||| |||||
AGAGATAAACTTTTTTACG A GCT AGT TTTTT TAA TTG AGAAA ACT AGC TTTTTTC
A
ACTCCATCAGAAAGAGGTTT - ACCAG G A T G G ACCTC A AAAAT
AATATTTTTGTGAGACCATC
GAAGAGAG

GAM348 CTTTTTTACGACTCCATCAG 334 CATCAGAAAG 683 A CTCCA G G T A G GACCA -
AAAGA
AAAGAGGTTTAATATTTTTG AGGTTTAATA T CGA TCA AAAGA GTT AAT TTTTT TGA TCG
AAGAGAG G
TGAGACCATCGAAGAGAGAA TTTT | ||| ||| ||||| ||| ||||| ||| |||||
AGAGATAAACTTTTTTACG A GCT AGT TTTTT TAA TTG AGAAA ACT AGC TTTTTTC
A
ACTCCATCAGAAAGAGGTTT - ACCAG G A T G G ACCTC A AAAAT
AATATTTTTGTGAGACCATC
GAAGAGAG

GAM349 CTTTTTTACGACTCCATCAG 335 CATCAGAAAG 684 A CTCCA G G T A G GACCA -
AAAGA
AAAGAGGTTTAATATTTTTG AGGTTTAATA T CGA TCA AAAGA GTT AAT TTTTT TGA TCG
AAGAGAG G
TGAGACCATCGAAGAGAGAA TTTT | ||| ||| ||||| ||| ||||| ||| |||||
AGAGATAAACTTTTTTACG A GCT AGT TTTTT TAA TTG AGAAA ACT AGC TTTTTTC
A
ACTCCATCAGAAAGAGGTTT - ACCAG G A T G G ACCTC A AAAAT
AATATTTTTGTGAGACCATC
GAAGAGAG

GAM350 CTTTTTTACGACTCCATCAG 336 CATCAGAAAG 685 A CTCCA G G T A G GACCA -
AAAGA
AAAGAGGTTTAATATTTTTG AGGTTTAATA T CGA TCA AAAGA GTT AAT TTTTT TGA TCG
AAGAGAG G
TGAGACCATCGAAGAGAGAA TTTT | ||| ||| ||||| ||| ||||| ||| |||||
AGAGATAAACTTTTTTACG A GCT AGT TTTTT TAA TTG AGAAA ACT AGC TTTTTTC
A
ACTCCATCAGAAAGAGGTTT - ACCAG G A T G G ACCTC A AAAAT
AATATTTTTGTGAGACCATC
GAAGAGAG

GAM351 CTTTTTTACGACTCCATCAG 337 CATCAGAAAG 686 A CTCCA G G T A G GACCA -
AAAGA
AAAGAGGTTTAATATTTTTG AGGTTTAATA T CGA TCA AAAGA GTT AAT TTTTT TGA TCG
AAGAGAG G
TGAGACCATCGAAGAGAGAA TTTT | ||| ||| ||||| ||| ||||| ||| |||||
AGAGATAAACTTTTTTACG A GCT AGT TTTTT TAA TTG AGAAA ACT AGC TTTTTTC
A
ACTCCATCAGAAAGAGGTTT - ACCAG G A T G G ACCTC A AAAAT
AATATTTTTGTGAGACCATC

GAAGAGAG

GAM352 CTTTTTTACGACTCCATCAG 338 CATCAGAAAAG 687 A CTCCA G G T A G GACCA -
AAAG
AAAGAGGTTTAATATTTTTG AGGTTTAATA TT CGA TCA AAAGA GTT AAT TTTTT TGA TCG
AAGAGAG A
TGAGACCATCGAAGAGAGAA TTTT || ||| ||| ||||| ||| ||||| ||| |||||
AGATAAACTTTTTTACGAC AA GCT AGT TTTTT TAA TTG AGAAA ACT AGC
TTTTTTC T
TCCATCAGAAAGAGGTTTAA - ACCAG G A T G G ACCTC A AAAA
TATTTTTGTGAGACCATCGA
AGAGAG

GAM353 GTGTGCCTGAATCGTTCGAT 339 TGAATAGAGT 688 C TTCGAT C C CAA
TAACCCTACTCATCCAATTT TATCGATTCA GTGTG CTGAATCG TAAC CTA TCATC T
CAGATGAATAGAGTTATCGA GACA ||||| ||||| ||||| |||||
TTCAGACACAC CACAC GACTTAGC ATTG GAT AGTAG T
A T----- A A ACT

GAM354 TCAGAAAGAGGTTTAATATT 340 AGAGGTTTAA 689 AAA GTTT-- GAGACCA- GA
TTTGTGAGACCATCGAAGAG TATTTTTGTG TCAG GAG AATATTTTTGT TC A
AGAAAGAGAATAAAAAATATT AGAC ||| ||| ||||| |||
TTATGACTCCATTGA AGTT CTC TTATAAAAATA AG /
AC- AGTATT AGAGAAAG AG

GAM355 TGAGACCATCAAAGAGAGAA 341 AGAGAGAAAAG 690 ACCA AAG AGA- AAAA
A-- GA
AGAGAATAAAAAATATTTTTG AGAATAAAAA TCA AGAGAAAG ATAAAAATATTTTTGT
CTTTTTTT TGA C
TAAACTTTTTTTATGAGAC TATT ||| ||||| ||||| ||||| ||||| |||
CATCAAAGAGAGAAAGAGAA AGT TTTTTTC TGTTTTTATAAAAAATA GAAAGAGA
ACT /
TAAAAATATTTTTGTAAAC CCAG A-- AAAA AGA- GAA AC
TTTTTTTATGAGACCATCA

GAM356 TTTTATGAGACCATCAAAGA 342 GAAGAGAGAA 691 ACCA AAG AGA- AAAA---
- A
GAGAAAGAGAATAAAAAATAT AGAGAATAAA TCA AGAGAAAG ATAAAAATATTTTTGT
CTTTTTTTG TG G
TTTTGTAAACTTTTTTTGT AATA ||| ||||| ||||| ||||| ||||| |||
GAGACCATCGAAGAGAGAAA AGT TTTTTTC TGTTTTTATAAAAAATA
GAGAGAAGC AC A
GAGAATAAAAAATATTTTTGT CCAG A-- AAAA AGAGAAA T C
AAAACTTTTTTTATGAGACC
ATCAAAGAGAG

GAM357 TTTTCTTAGTACAAAAGTC 343 TCAATGTTTT 692 A- G- AT--- AAAA G
AATGTTTTTAAATATATGGA AAAATATATG TTTTCTT GTACAAAA TCA GTTTT
TATATGGACAA A
CAAGAATTTGTCTGTATAAA GACA ||||| ||||| ||| ||| |||||
AACTTGTGTGAAATTTTGTA AAAAGAA CATGTTTT AGT CAAAA ATATGTCTGTT A

CCAAAGAAAAA

AC AA GTGTT ---- T

GAM358 TCACCTTATCAAAGTCGTTT 344 TTGGTTGTGG 693 CCTT A TT CACAT TATA T-
TT

ATATCACATTGTATATAGTT ATCTTCTACA TCA ATCA AGTCGT ATAT TGTA
GTTTATAACC TAACT C
TATAACCTTAACTTTTCGAGG ATAT ||| ||| ||||| ||| ||| ||||| |||||
TTATTGGTTGTGGATCTTCT AGT TAGT TCAGTA TATA ACAT TAGGTGTTGG
ATTGG /
ACAATATCTATGACTCTGAT TCTT C TC ---- CTTC TT AG
TTCTTGA

GAM359 TCGGCCATACGTTTACTTTT 345 TATCATAAAG 694 AC T C- - GT
TGCGTATACATGTCCTGGTG GGTATGCTCA TCGGCCAT GT TACTTTTTG GTATA CAT C
ATATATCATAAAGGGTATGC TGGC ||||| || ||||| ||||| |||
TCATGGCCGA AGCCGGTA CG ATGGGAAAT TATAT GTG C
CT T AC A GT

GAM360 TCGATGATACATGTATTA 346 TGATACATGT 695 A--- TGTA T TCC
ATACTTTCCGAATAAGTCTT ATTAAAATAC TCG TGATACA TAAAA ACTT G
TTAAATATTGTATTAATTAT TTTC ||| ||||| ||||| |||
GA AGT ATTATGT AATTTT TGAA /
ATTA TATA C TAA

GAM361 AAAATCGATTCCGTCCAAGA 347 TCGATTCCGT 696 C CCAAG AAAAACA
TGATAAAAACATTTACCGGC CCAAGATGAT AAAAT GATTCCGT ATGAT T
ATCATAAACACGGAGTTTAT AAAA ||||| ||||| |||||
TTT TTTTA TTGAGGCA TACTA T
T CAAA- CGGCCAT

GAM362 CATGGAGATACTTTATTACT 348 TAATGTCCTG 697 ----- T TAAATA
CCATTAAATAATTTATCATG TTTCATTTGT CATGGAGAT AC TTATTACTCCAT A
GAGTGATAATGTCCTGTTTC TTCC ||||| || ||||| |||||
ATTTGTTTCCATG GTACCTTTG TG AATAGTGAGGTA /
TTTACTTTGTCC T CTATT

GAM363 AGTATGTTGTACGGAAAGAA 349 TGATTGGAGA 698 -- A GAAAGAACCA-- AAATATTA
TG--- AAGA
CCATTACAAATATTATCCAT AGTAGGAAAC AGTA TGTTGT CG TTAC TCCA
ATAGA A
GATAGAAAGAAAATATCTAT AGGA ||| ||||| || ||| ||| |||||
ATGATTGGAGAAGTAGGAAA TCAT GCAACA GC GATG AGGT TATCT /
CAGGAACACGACAACGATTA TA - ACAAGGACAAAG AAG----- TAGTA ATAA
CT

| GENE | TARGET | UTR SEQUENCE | SEQID | BINDING-SITE |
|-------|-----------|---------------------------|-------|--------------|
| GAM15 | CAPN2 | 3' AAAACTTTATGAACTTCACCA | 855 | A _ AAA |
| | | TG TGGAGT CGTAA AGTTTT | | |
| | | | | |
| | | AC ACTTCA GTATT TCAAAA | | |
| | | C A _ | | |
| GAM15 | DAAM2 | 3' AAAATTTTTCTAAACTCCATC | 3559 | CG A |
| | A | TGATGGAGT TA AAAAGTTTT | | |
| | | | | |
| | | ACTACCTCA AT TTTTAAAA | | |
| | | AA C | | |
| GAM15 | SELE | 3' AAAACTCTCCTACACTTCCATT | 747 | _ C AAAA |
| | A | TGATGGA GT GTA AGTTTT | | |
| | | | | |
| | | ATTACCT CA CAT TCAAAA | | |
| | | T _ CCTC | | |
| GAM15 | KIAA0475 | 3' AAAACCTTGCATTCCATCA | 1570 | C AAAA |
| | | TGATGGAGT GTAA GTTTT | | |
| | | | | |
| | | ACTACCTTA CGTT CAAAA | | |
| | | _ C _ | | |
| GAM15 | LOC222671 | 5' GCTTCTACGACTCCGCCA | 3582 | A AAA |
| | | TG TGGAGTCGTA AAGT | | |
| | | | | |
| | | AC GCCTCAGCAT TTCG | | |
| | | C C _ | | |
| GAM15 | LOC254901 | 5' AATTTCTTCACTGACTCCACCA | 3699 | A _ A A |
| | | TG TGGAGTC GT AA AAGTT | | |
| | | | | |
| | | AC ACCTCAG CA TT TTTAA | | |
| | | C T C C | | |
| GAM15 | LOC257615 | 5' GCTTCTACGACTCCGCCA | 3749 | A AAA |
| | | TG TGGAGTCGTA AAGT | | |
| | | | | |
| | | AC GCCTCAGCAT TTCG | | |
| | | C C _ | | |
| GAM16 | CAPN2 | 3' AAAACTTTATGAACTTCACCA | 855 | A _ AAA |
| | | TG TGGAGT CGTAA AGTTTT | | |
| | | | | |
| | | AC ACTTCA GTATT TCAAAA | | |
| | | C A _ | | |
| GAM16 | DAAM2 | 3' AAAATTTTTCTAAACTCCATC | 3559 | CG A |
| | A | TGATGGAGT TA AAAAGTTTT | | |
| | | | | |
| | | ACTACCTCA AT TTTTAAAA | | |
| | | AA C | | |
| GAM16 | SELE | 3' AAAACTCTCCTACACTTCCATT | 747 | _ C AAAA |
| | A | TGATGGA GT GTA AGTTTT | | |
| | | | | |

| | | | | | |
|-------|-----------|----|-------------------------|------|----------|
| | | | ATTACCT CA CAT TCAAAA | | |
| | | | T _ CCTC | | |
| GAM16 | KIAA0475 | 3' | AAAACCTTGCATTCCATCA | 1570 | C AAAA |
| | | | TGATGGAGT GTAA GTTTT | | |
| | | | | | |
| | | | ACTACCTTA CGTT CAAAA | | |
| | | | _ C__ | | |
| GAM16 | LOC222671 | 5' | GCTTCTACGACTCCGCCA | 3582 | A AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C__ | | |
| GAM16 | LOC254901 | 5' | AATTTCTTCACTGACTCCACCA | 3699 | A _ A A |
| | | | TG TGGAGTC GT AA AAGTT | | |
| | | | | | |
| | | | AC ACCTCAG CA TT TTTAA | | |
| | | | C T C C | | |
| GAM16 | LOC257615 | 5' | GCTTCTACGACTCCGCCA | 3749 | A AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C__ | | |
| GAM17 | CAPN2 | 3' | AAAACCTTTATGAACTTCACCA | 855 | A _ AAA |
| | | | TG TGGAGT CGTAA AGTTTT | | |
| | | | | | |
| | | | AC ACTTCA GTATT TCAAAA | | |
| | | | C A _ | | |
| GAM17 | DAAM2 | 3' | AAAATTTTCTAAAACCTCCATC | 3559 | CG A |
| | A | | TGATGGAGT TA AAAAGTTTT | | |
| | | | | | |
| | | | ACTACCTCA AT TTTTAAAA | | |
| | | | AA C | | |
| GAM17 | SELE | 3' | AAAACCTCTCCTACACTTCCATT | 747 | _ C AAAA |
| | A | | TGATGGA GT GTA AGTTTT | | |
| | | | | | |
| | | | ATTACCT CA CAT TCAAAA | | |
| | | | T _ CCTC | | |
| GAM17 | KIAA0475 | 3' | AAAACCTTGCATTCCATCA | 1570 | C AAAA |
| | | | TGATGGAGT GTAA GTTTT | | |
| | | | | | |
| | | | ACTACCTTA CGTT CAAAA | | |
| | | | _ C__ | | |
| GAM17 | LOC222671 | 5' | GCTTCTACGACTCCGCCA | 3582 | A AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C__ | | |
| GAM17 | LOC254901 | 5' | AATTTCTTCACTGACTCCACCA | 3699 | A _ A A |
| | | | TG TGGAGTC GT AA AAGTT | | |
| | | | | | |

| | | | | | |
|-------|-----------|----|-----------------------------|---|----------|
| | | | AC ACCTCAG CA TT TTTAA | | |
| | | | C T C C | | |
| GAM17 | LOC257615 | 5' | GCTTCTACGACTCCGCCA 3749 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C__ | | |
| GAM18 | CAPN2 | 3' | AAAACCTTTATGAACTTCACCA 855 | A | _ AAA |
| | | | TG TGGAGT CGTAA AGTTTT | | |
| | | | | | |
| | | | AC ACTTCA GTATT TCAAAA | | |
| | | | C A ____ | | |
| GAM18 | DAAM2 | 3' | AAAATTTTTCTAAACTCCATC 3559 | | CG A |
| | A | | TGATGGAGT TA AAAAGTTTT | | |
| | | | | | |
| | | | ACTACCTCA AT TTTTAAAA | | |
| | | | AA C | | |
| GAM18 | SELE | 3' | AAAACCTCTCCTACACTTCCATT 747 | | _ C AAAA |
| | A | | TGATGGA GT GTA AGTTTT | | |
| | | | | | |
| | | | ATTACCT CA CAT TCAAAA | | |
| | | | T _ CCTC | | |
| GAM18 | KIAA0475 | 3' | AAAACCTTGCATTCCATCA 1570 | | C AAAA |
| | | | TGATGGAGT GTAA GTTTT | | |
| | | | | | |
| | | | ACTACCTTA CGTT CAAAA | | |
| | | | _ C__ | | |
| GAM18 | LOC222671 | 5' | GCTTCTACGACTCCGCCA 3582 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C__ | | |
| GAM18 | LOC254901 | 5' | AATTTCTTCACTGACTCCACCA 3699 | A | _ A A |
| | | | TG TGGAGTC GT AA AAGTT | | |
| | | | | | |
| | | | AC ACCTCAG CA TT TTTAA | | |
| | | | C T C C | | |
| GAM18 | LOC257615 | 5' | GCTTCTACGACTCCGCCA 3749 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C__ | | |
| GAM19 | CAPN2 | 3' | AAAACCTTTATGAACTTCACCA 855 | A | _ AAA |
| | | | TG TGGAGT CGTAA AGTTTT | | |
| | | | | | |
| | | | AC ACTTCA GTATT TCAAAA | | |
| | | | C A ____ | | |
| GAM19 | DAAM2 | 3' | AAAATTTTTCTAAACTCCATC 3559 | | CG A |
| | A | | TGATGGAGT TA AAAAGTTTT | | |
| | | | | | |

| | | | | | |
|-------|-----------|----|------------------------------|------|-------|
| | | | ACTACCTCA AT TTTTAAAA | | |
| | | | AA C | | |
| GAM19 | SELE | 3' | AAAACCTCTCCTACACTTCCATT 747 | _ C | AAAA |
| | A | | TGATGGA GT GTA AGTTTT | | |
| | | | | | |
| | | | ATTACCT CA CAT TCAAAA | | |
| | | | T _ CCTC | | |
| GAM19 | KIAA0475 | 3' | AAAACCTTGCATTCCATCA 1570 | C | AAAA |
| | | | TGATGGAGT GTAA GTTTT | | |
| | | | | | |
| | | | ACTACCTTA CGTT CAAAA | | |
| | | | _ C__ | | |
| GAM19 | LOC222671 | 5' | GCTTCTACGACTCCGCCA 3582 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C__ | | |
| GAM19 | LOC254901 | 5' | AATTTCTTCACTGACTCCACCA 3699 | A | _ A A |
| | | | TG TGGAGTC GT AA AAGTT | | |
| | | | | | |
| | | | AC ACCTCAG CA TT TTAA | | |
| | | | C T C C | | |
| GAM19 | LOC257615 | 5' | GCTTCTACGACTCCGCCA 3749 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C__ | | |
| GAM20 | CAPN2 | 3' | AAAACCTTTATGAACCTTCACCA 855 | A | _ AAA |
| | | | TG TGGAGT CGTAA AGTTTT | | |
| | | | | | |
| | | | AC ACTTCA GTATT TCAAAA | | |
| | | | C A _ | | |
| GAM20 | DAAM2 | 3' | AAAATTTTTCTAAAACCTCCATC 3559 | CG A | |
| | A | | TGATGGAGT TA AAAAGTTTT | | |
| | | | | | |
| | | | ACTACCTCA AT TTTTAAAA | | |
| | | | AA C | | |
| GAM20 | SELE | 3' | AAAACCTCTCCTACACTTCCATT 747 | _ C | AAAA |
| | A | | TGATGGA GT GTA AGTTTT | | |
| | | | | | |
| | | | ATTACCT CA CAT TCAAAA | | |
| | | | T _ CCTC | | |
| GAM20 | KIAA0475 | 3' | AAAACCTTGCATTCCATCA 1570 | C | AAAA |
| | | | TGATGGAGT GTAA GTTTT | | |
| | | | | | |
| | | | ACTACCTTA CGTT CAAAA | | |
| | | | _ C__ | | |
| GAM20 | LOC222671 | 5' | GCTTCTACGACTCCGCCA 3582 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |

| | | | | | | |
|-------|-----------|----|-------------------------|-------|---|----------|
| | | | AC GCCTCAGCAT | TTCG | | |
| | | | C | C__ | | |
| GAM20 | LOC254901 | 5' | AATTTCTTCACTGACTCCACCA | 3699 | A | _ A A |
| | | | TG TGGAGTC GT AA AAGTT | | | |
| | | | | | | |
| | | | AC ACCTCAG CA TT TTAA | | | |
| | | | C | T C C | | |
| GAM20 | LOC257615 | 5' | GCTTCTACGACTCCGCCA | 3749 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | | |
| | | | | | | |
| | | | AC GCCTCAGCAT | TTCG | | |
| | | | C | C__ | | |
| GAM21 | CAPN2 | 3' | AAAACCTTTATGAACTTCACCA | 855 | A | _ AAA |
| | | | TG TGGAGT CGTAA AGTTTT | | | |
| | | | | | | |
| | | | AC ACTTCA GTATT TCAAAA | | | |
| | | | C | A _ | | |
| GAM21 | DAAM2 | 3' | AAAATTTTTCTAAACTCCATC | 3559 | | CG A |
| | A | | TGATGGAGT TA AAAAGTTTT | | | |
| | | | | | | |
| | | | ACTACCTCA AT TTTTAAAA | | | |
| | | | AA C | | | |
| GAM21 | SELE | 3' | AAAACCTCTCCTACACTTCCATT | 747 | | _ C AAAA |
| | A | | TGATGGA GT GTA AGTTTT | | | |
| | | | | | | |
| | | | ATTACCT CA CAT TCAAAA | | | |
| | | | T _ CCTC | | | |
| GAM21 | KIAA0475 | 3' | AAAACCTTGCATTCCATCA | 1570 | | C AAAA |
| | | | TGATGGAGT GTAA GTTTT | | | |
| | | | | | | |
| | | | ACTACCTTA CGTT CAAAA | | | |
| | | | _ C__ | | | |
| GAM21 | LOC222671 | 5' | GCTTCTACGACTCCGCCA | 3582 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | | |
| | | | | | | |
| | | | AC GCCTCAGCAT | TTCG | | |
| | | | C | C__ | | |
| GAM21 | LOC254901 | 5' | AATTTCTTCACTGACTCCACCA | 3699 | A | _ A A |
| | | | TG TGGAGTC GT AA AAGTT | | | |
| | | | | | | |
| | | | AC ACCTCAG CA TT TTAA | | | |
| | | | C | T C C | | |
| GAM21 | LOC257615 | 5' | GCTTCTACGACTCCGCCA | 3749 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | | |
| | | | | | | |
| | | | AC GCCTCAGCAT | TTCG | | |
| | | | C | C__ | | |
| GAM22 | CAPN2 | 3' | AAAACCTTTATGAACTTCACCA | 855 | A | _ AAA |
| | | | TG TGGAGT CGTAA AGTTTT | | | |
| | | | | | | |

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|-------|-----------|----|-----------------------------|-----|-------|
| | | | AC ACTTCA GTATT TCAAAA | | |
| | | | C A ____ | | |
| GAM22 | DAAM2 | 3' | AAAATTTTCTAAACTCCATC 3559 | CG | A |
| | A | | TGATGGAGT TA AAAAGTTTT | | |
| | | | | | |
| | | | ACTACCTCA AT TTTTAAAA | | |
| | | | AA C | | |
| GAM22 | SELE | 3' | AAACTCTCCTACACTTCCATT 747 | _ C | AAAA |
| | A | | TGATGGA GT GTA AGTTTT | | |
| | | | | | |
| | | | ATTACCT CA CAT TCAAAA | | |
| | | | T _ CCTC | | |
| GAM22 | KIAA0475 | 3' | AAAACCTTGCATTCCATCA 1570 | C | AAAA |
| | | | TGATGGAGT GTAA GTTTT | | |
| | | | | | |
| | | | ACTACCTTA CGTT CAAAA | | |
| | | | _ C ____ | | |
| GAM22 | LOC222671 | 5' | GCTTCTACGACTCCGCCA 3582 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C ____ | | |
| GAM22 | LOC254901 | 5' | AATTTCTTCACTGACTCCACCA 3699 | A | _ A A |
| | | | TG TGGAGTC GT AA AAGTT | | |
| | | | | | |
| | | | AC ACCTCAG CA TT TTAA | | |
| | | | C T C C | | |
| GAM22 | LOC257615 | 5' | GCTTCTACGACTCCGCCA 3749 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C ____ | | |
| GAM23 | CAPN2 | 3' | AAACTTTTATGAAGTTCACCA 855 | A | _ AAA |
| | | | TG TGGAGT CGTAA AGTTTT | | |
| | | | | | |
| | | | AC ACTTCA GTATT TCAAAA | | |
| | | | C A ____ | | |
| GAM23 | DAAM2 | 3' | AAAATTTTCTAAACTCCATC 3559 | CG | A |
| | A | | TGATGGAGT TA AAAAGTTTT | | |
| | | | | | |
| | | | ACTACCTCA AT TTTTAAAA | | |
| | | | AA C | | |
| GAM23 | SELE | 3' | AAACTCTCCTACACTTCCATT 747 | _ C | AAAA |
| | A | | TGATGGA GT GTA AGTTTT | | |
| | | | | | |
| | | | ATTACCT CA CAT TCAAAA | | |
| | | | T _ CCTC | | |
| GAM23 | KIAA0475 | 3' | AAAACCTTGCATTCCATCA 1570 | C | AAAA |
| | | | TGATGGAGT GTAA GTTTT | | |
| | | | | | |

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|-------|-----------|----|-----------------------------|---|----------|
| | | | ACTACCTTA CGTT CAAAA | | |
| | | | — C— | | |
| GAM23 | LOC222671 | 5' | GCTTCTACGACTCCGCCA 3582 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C— | | |
| GAM23 | LOC254901 | 5' | AATTTCTTCACTGACTCCACCA 3699 | A | — A A |
| | | | TG TGGAGTC GT AA AAGTT | | |
| | | | | | |
| | | | AC ACCTCAG CA TT TTTAA | | |
| | | | C T C C | | |
| GAM23 | LOC257615 | 5' | GCTTCTACGACTCCGCCA 3749 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C— | | |
| GAM24 | CAPN2 | 3' | AAACTTTTATGAACTTCACCA 855 | A | — AAA |
| | | | TG TGGAGT CGTAA AGTTTT | | |
| | | | | | |
| | | | AC ACTTCA GTATT TCAAAA | | |
| | | | C A — | | |
| GAM24 | DAAM2 | 3' | AAAATTTTCTAAACTCCATC 3559 | | CG A |
| | A | | TGATGGAGT TA AAAAGTTTT | | |
| | | | | | |
| | | | ACTACCTCA AT TTTTAAAA | | |
| | | | AA C | | |
| GAM24 | SELE | 3' | AAACTCTCCTACACTTCCATT 747 | | — C AAAA |
| | A | | TGATGGA GT GTA AGTTTT | | |
| | | | | | |
| | | | ATTACCT CA CAT TCAAAA | | |
| | | | T — CCTC | | |
| GAM24 | KIAA0475 | 3' | AAAACCTTGCATTCCATCA 1570 | C | AAAA |
| | | | TGATGGAGT GTAA GTTTT | | |
| | | | | | |
| | | | ACTACCTTA CGTT CAAAA | | |
| | | | — C— | | |
| GAM24 | LOC222671 | 5' | GCTTCTACGACTCCGCCA 3582 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C— | | |
| GAM24 | LOC254901 | 5' | AATTTCTTCACTGACTCCACCA 3699 | A | — A A |
| | | | TG TGGAGTC GT AA AAGTT | | |
| | | | | | |
| | | | AC ACCTCAG CA TT TTTAA | | |
| | | | C T C C | | |
| GAM24 | LOC257615 | 5' | GCTTCTACGACTCCGCCA 3749 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |

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|-------|-----------|----|-------------------------|--------------|-----|------------|
| | | | AC GCCTCAGCAT | TTCG | | |
| | | | C | C__ | | |
| GAM25 | CAPN2 | 3' | AAAACCTTTATGAACTTCACCA | 855 | A | _ AAA |
| | | | TG TGGAGT CGTAA | AGTTTT | | |
| | | | | | | |
| | | | AC ACTTCA GTATT | TCAAAA | | |
| | | | C | A | | |
| GAM25 | DAAM2 | 3' | AAAATTTTTCTAAACTCCATC | 3559 | | CG A |
| | A | | TGATGGAGT | TA AAAAGTTTT | | |
| | | | | | | |
| | | | ACTACCTCA | AT TTTTAAAA | | |
| | | | AA | C | | |
| GAM25 | SELE | 3' | AAAACCTCTCCTACACTTCCATT | 747 | | _ C AAAA |
| | A | | TGATGGA GT GTA | AGTTTT | | |
| | | | | | | |
| | | | ATTACCT CA CAT | TCAAAA | | |
| | | | T | _ CCTC | | |
| GAM25 | KIAA0475 | 3' | AAAACCTTGCATTCCATCA | 1570 | | C AAAA |
| | | | TGATGGAGT GTAA | GTTTT | | |
| | | | | | | |
| | | | ACTACCTTA CGTT | CAAAA | | |
| | | | | C__ | | |
| GAM25 | LOC222671 | 5' | GCTTCTACGACTCCGCCA | 3582 | A | AAA |
| | | | TG TGGAGTCGTA | AAGT | | |
| | | | | | | |
| | | | AC GCCTCAGCAT | TTCG | | |
| | | | C | C__ | | |
| GAM25 | LOC254901 | 5' | AATTTCTTCACTGACTCCACCA | 3699 | A | _ A A |
| | | | TG TGGAGTC GT AA | AAGTT | | |
| | | | | | | |
| | | | AC ACCTCAG CA TT | TTTAA | | |
| | | | C | T C C | | |
| GAM25 | LOC257615 | 5' | GCTTCTACGACTCCGCCA | 3749 | A | AAA |
| | | | TG TGGAGTCGTA | AAGT | | |
| | | | | | | |
| | | | AC GCCTCAGCAT | TTCG | | |
| | | | C | C__ | | |
| GAM26 | ITGB7 | 5' | AGAGAAAGTCTGACTTGCCCCA | 783 | | AAAA_ TTAT |
| | C | | GT AAGTT | CTTTCTCT | | |
| | | | | | | |
| | | | CA TTCAG | GAAAGAGA | | |
| | | | CCCCG | TCT_ | | |
| GAM26 | RPP30 | 3' | AGAGAAAGACAACCTGTTCTGCG | 1297 | A A | TTA |
| | | | CGTA AA AGTT | TCTTTCTCT | | |
| | | | | | | |
| | | | GCGT TT TCAA | AGAAAGAGA | | |
| | | | C G | C__ | | |
| GAM26 | FLJ13263 | 3' | AGAGAAAGATTTTAGCTTTT | 2139 | | TT_ |
| | | | AAAAGTT | ATCTTTCTCT | | |
| | | | | | | |

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|-------|-----------|----|------------------------------|---------|-----|
| | | | TTTTCGA TAGAAAGAGA | | |
| | | | TTT | | |
| GAM26 | FLJ23074 | 5' | AGAGAAAGACAAGGGTTT 2133 | G A | |
| | | | AAA TTTT TCTTTCTCT | | |
| | | | | | |
| | | | TTT GGAA AGAAAGAGA | | |
| | | | G C | | |
| GAM26 | GTF2A2 | 3' | AGAAAAAATATGACTTTTTTTAC 1119 | T C_ | |
| | | | GTAAAAAAGTT TAT TTTCT | | |
| | | | | | |
| | | | CATTTTTTCAG ATA AAAGA | | |
| | | | T AA | | |
| GAM26 | IMP-2 | 3' | AGAGAAAGCAGGCTTTTCTA 1308 | A TAT | |
| | | | TA AAAAGTTT CTTTCTCT | | |
| | | | | | |
| | | | AT TTTTCGGA GAAAGAGA | | |
| | | | C C_ | | |
| GAM26 | KIAA0212 | 3' | AGAAAGGTAAATCTTTTTTAC 1518 | A T | |
| | | | GTAAAAA G TTTATCTTTCT | | |
| | | | | | |
| | | | CATTTTT C AAATGGAAAGA | | |
| | | | _T | | |
| GAM26 | OSBPL2 | 5' | AGAGAAAGTTTGTAATAATTCCT 1566 | AAA | ___ |
| | TAC | | GTAA AGTTTTAT CTTTCTCT | | |
| | | | | | |
| | | | CATT TTAAATG GAAAGAGA | | |
| | | | CC_ TTT | | |
| GAM26 | OSBPL2 | 5' | AGAGAAAGTTTGTAATAATTCCT 2482 | AAA | ___ |
| | TAC | | GTAA AGTTTTAT CTTTCTCT | | |
| | | | | | |
| | | | CATT TTAAATG GAAAGAGA | | |
| | | | CC_ TTT | | |
| GAM26 | RBM9 | 3' | AGAAAGAATACTTTTTTAT 1489 | TTTA | |
| | | | GTAAAAAAGT TCTTTCT | | |
| | | | | | |
| | | | TATTTTTTCA AGAAAGA | | |
| | | | TA_ | | |
| GAM26 | LOC254826 | 3' | AGAGAAAGTCTTGCTTTTT 3732 | TTTAT | |
| | | | AAAAAGT CTTTCTCT | | |
| | | | | | |
| | | | TTTTTCG GAAAGAGA | | |
| | | | TTCT_ | | |
| GAM27 | CAPN2 | 3' | AAACTTTTATGAACCTCACCA 855 | A _ AAA | |
| | | | TG TGGAGT CGTAA AGTTTT | | |
| | | | | | |
| | | | AC ACTTCA GTATT TCAAAA | | |
| | | | C A _ | | |
| GAM27 | DAAM2 | 3' | AAAATTTTTCTAAACTCCATC 3559 | CG A | |
| | A | | TGATGGAGT TA AAAAGTTTT | | |
| | | | | | |

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|-------|-----------|----|-----------------------------|------|-------|
| | | | ACTACCTCA AT TTTTAAAA | | |
| | | | AA C | | |
| GAM27 | SELE | 3' | AAACTCTCCTACACTTCCATT 747 | _ C | AAAA |
| | A | | TGATGGA GT GTA AGTTTT | | |
| | | | | | |
| | | | ATTACCT CA CAT TCAAAA | | |
| | | | T _ CCTC | | |
| GAM27 | KIAA0475 | 3' | AAAACCTTGCATTCCATCA 1570 | C | AAAA |
| | | | TGATGGAGT GTAA GTTTT | | |
| | | | | | |
| | | | ACTACCTTA CGTT CAAAA | | |
| | | | _ C__ | | |
| GAM27 | LOC222671 | 5' | GCTTCTACGACTCCGCCA 3582 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C__ | | |
| GAM27 | LOC254901 | 5' | AATTTCTTCACTGACTCCACCA 3699 | A | _ A A |
| | | | TG TGGAGTC GT AA AAGTT | | |
| | | | | | |
| | | | AC ACCTCAG CA TT TTAA | | |
| | | | C T C C | | |
| GAM27 | LOC257615 | 5' | GCTTCTACGACTCCGCCA 3749 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C__ | | |
| GAM28 | CAPN2 | 3' | AAACTTTATGAAGTTCACCA 855 | A | _ AAA |
| | | | TG TGGAGT CGTAA AGTTTT | | |
| | | | | | |
| | | | AC ACTTCA GTATT TCAAAA | | |
| | | | C A _ | | |
| GAM28 | DAAM2 | 3' | AAAATTTTCTAAAAGTCCATC 3559 | CG A | |
| | A | | TGATGGAGT TA AAAAGTTTT | | |
| | | | | | |
| | | | ACTACCTCA AT TTTTAAAA | | |
| | | | AA C | | |
| GAM28 | SELE | 3' | AAACTCTCCTACACTTCCATT 747 | _ C | AAAA |
| | A | | TGATGGA GT GTA AGTTTT | | |
| | | | | | |
| | | | ATTACCT CA CAT TCAAAA | | |
| | | | T _ CCTC | | |
| GAM28 | KIAA0475 | 3' | AAAACCTTGCATTCCATCA 1570 | C | AAAA |
| | | | TGATGGAGT GTAA GTTTT | | |
| | | | | | |
| | | | ACTACCTTA CGTT CAAAA | | |
| | | | _ C__ | | |
| GAM28 | LOC222671 | 5' | GCTTCTACGACTCCGCCA 3582 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |

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|-------|-----------|----|-----------------------------|---|----------|
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C__ | | |
| GAM28 | LOC254901 | 5' | AATTTCTTCACTGACTCCACCA 3699 | A | _ A A |
| | | | TG TGGAGTC GT AA AAGTT | | |
| | | | | | |
| | | | AC ACCTCAG CA TT TTTAA | | |
| | | | C T C C | | |
| GAM28 | LOC257615 | 5' | GCTTCTACGACTCCGCCA 3749 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C__ | | |
| GAM29 | CAPN2 | 3' | AAAACCTTTATGAACTTCACCA 855 | A | _ AAA |
| | | | TG TGGAGT CGTAA AGTTTT | | |
| | | | | | |
| | | | AC ACTTCA GTATT TCAAAA | | |
| | | | C A _ | | |
| GAM29 | DAAM2 | 3' | AAAATTTTTCTAAACTCCATC 3559 | | CG A |
| | A | | TGATGGAGT TA AAAAGTTTT | | |
| | | | | | |
| | | | ACTACCTCA AT TTTTAAAA | | |
| | | | AA C | | |
| GAM29 | SELE | 3' | AAAACCTCTCCTACACTTCCATT 747 | | _ C AAAA |
| | A | | TGATGGA GT GTA AGTTTT | | |
| | | | | | |
| | | | ATTACCT CA CAT TCAAAA | | |
| | | | T _ CCTC | | |
| GAM29 | KIAA0475 | 3' | AAAACCTTGCATTCCATCA 1570 | | C AAAA |
| | | | TGATGGAGT GTAA GTTTT | | |
| | | | | | |
| | | | ACTACCTTA CGTT CAAAA | | |
| | | | _ C__ | | |
| GAM29 | LOC222671 | 5' | GCTTCTACGACTCCGCCA 3582 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C__ | | |
| GAM29 | LOC254901 | 5' | AATTTCTTCACTGACTCCACCA 3699 | A | _ A A |
| | | | TG TGGAGTC GT AA AAGTT | | |
| | | | | | |
| | | | AC ACCTCAG CA TT TTTAA | | |
| | | | C T C C | | |
| GAM29 | LOC257615 | 5' | GCTTCTACGACTCCGCCA 3749 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C__ | | |
| GAM30 | FGF2 | 3' | ATATTTTTGTGGCTGCTTTTT 884 | | T_ |
| | | | AAAAAGT TTACAAAAATAT | | |
| | | | | | |

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|-------|-----------|----|-----------------------------|--------|---|
| | | | TTTTTCG GGTGTTTTTATA | | |
| | | | TC | | |
| GAM30 | MPHOSPH1 | 3' | ATATTTTATAAGGCTTTTTT 1670 | C | |
| | | | AAAAAAGTTTTA AAAAATAT | | |
| | | | | | |
| | | | TTTTTTCGGAAT TTTTATA | | |
| | | | A | | |
| GAM30 | FLJ11274 | 3' | ATATCTTTGTAGTAGCTTTTTT 1820 | _ | A |
| | TA | | TAAAAAAGTT TTACAAA ATAT | | |
| | | | | | |
| | | | ATTTTTTTCGA GATGTTT TATA | | |
| | | | T C | | |
| GAM30 | FLJ31101 | 3' | ATATTTTTGTAAAATGTATTTG 1771 | AAAA | |
| | T | | ATAAA GTTTTACAAAAATAT | | |
| | | | | | |
| | | | TGTTT TAAAATGTTTTTATA | | |
| | | | ATG_ | | |
| GAM30 | GPT2 | 3' | ATATTTTTGTAACAATTGCTTT 2417 | T_____ | |
| | TTT | | AAAAAAGT TTACAAAAATAT | | |
| | | | | | |
| | | | TTTTTTCG AATGTTTTTATA | | |
| | | | TTAAC | | |
| GAM30 | RMP | 3' | TTTGTAAAACTTTTTTTTC 2430 | T | |
| | | | A AAAAAAAGTTTACAAAA | | |
| | | | | | |
| | | | C TTTTTTTCAAAATGTTTT | | |
| | | | T | | |
| GAM30 | RMP | 3' | TTTGTAAAACTTTTTTTTC 1059 | T | |
| | | | A AAAAAAAGTTTACAAAA | | |
| | | | | | |
| | | | C TTTTTTTCAAAATGTTTT | | |
| | | | T | | |
| GAM30 | SOX6 | 3' | ATATTTTGTCTTACTTTTTTTT 2328 | TTT | |
| | | | AAAAAAAGT ACAAAAATAT | | |
| | | | | | |
| | | | TTTTTTTCA TGTTTTTATA | | |
| | | | TTC | | |
| GAM30 | LOC136288 | 3' | ATATTTCTGAGGCTTTTTTTGT 3018 | CAA | |
| | | | ATAAAAAAAGTTTTA AAATAT | | |
| | | | | | |
| | | | TGTTTTTTTCGGAGT TTTATA | | |
| | | | C_ | | |
| GAM31 | AICDA | 3' | AGAAAGAGAACAATATTT 1922 | TTTA | |
| | | | AAATATT TTCTCTTTCT | | |
| | | | | | |
| | | | TTTATAA AAGAGAAAGA | | |
| | | | C_ | | |
| GAM31 | AS3 | 3' | AGAAAGATTTAAAGTATTTTA 1652 | TATTC | |
| | | | TAAAATATTTT TCTTTCT | | |
| | | | | | |

| | | | | | |
|-------|--------------|----|-------------------------|--------------|---------|
| | | | ATTTTATGAAA | AGAAAGA | |
| | | | TTT__ | | |
| GAM31 | EPM2A | 3' | AGAAAGAGAAGTGT | TTT 1234 | TTT |
| | | | AAAATAT | TTCTCTTCT | |
| | | | | | |
| | | | TTTTGTG | AAGAGAAAGA | |
| | | | _____ | | |
| GAM31 | HRH1 | 3' | AGAAAGAGAAAATGAAATATTTT | 780 | TA |
| | | | AAAATATTTT | TTCTCTTCT | |
| | | | | | |
| | | | TTTTATAAAG | AAGAGAAAGA | |
| | | | TA | | |
| GAM31 | MAPK14 | 3' | GAGAAAGGGCAAATTATTTTA | 818 | T TATT |
| | | | TAAAATA TTT | CTCTTTCTC | |
| | | | | | |
| | | | ATTTTAT AAA | GGGAAAGAG | |
| | | | T C__ | | |
| GAM31 | MAPK14 | 3' | GAGAAAGGGCAAATTATTTTA | 2465 | T TATT |
| | | | TAAAATA TTT | CTCTTTCTC | |
| | | | | | |
| | | | ATTTTAT AAA | GGGAAAGAG | |
| | | | T C__ | | |
| GAM31 | MAPK14 | 3' | GAGAAAGGGCAAATTATTTTA | 2466 | T TATT |
| | | | TAAAATA TTT | CTCTTTCTC | |
| | | | | | |
| | | | ATTTTAT AAA | GGGAAAGAG | |
| | | | T C__ | | |
| GAM31 | NOTCH2 | 3' | GAGAATTAATAATATTTTA | 2058 | T |
| | | | TAAAATATTTT | ATTCTC | |
| | | | | | |
| | | | ATTTTATAAAA | TAAGAG | |
| | | | T | | |
| GAM31 | SIM1 | 3' | GAGAAAGAGAGAGATA | 1181 | TAT |
| | | | TATTTT | TCTCTTCTC | |
| | | | | | |
| | | | ATAGAG | AGAGAAAGAG | |
| | | | _____ | | |
| GAM31 | C11orf25 | 3' | AAAGAGAAAAATATTTTA | 2193 | TAT |
| | | | TAAAATATTTT | TCTCTT | |
| | | | | | |
| | | | ATTTTATAAAA | AGAGAAA | |
| | | | _____ | | |
| GAM31 | DKFZP564D116 | 3' | GAAAAGCAATAAAAAATATTTTA | 2938 | _ C |
| | | | TAAAATATTTT | TATT CT TTTC | |
| | | | | | |
| | | | ATTTTATAAAAATAA | GA AAAG | |
| | | | C _ | | |
| GAM31 | DSCR6 | 3' | GAGAAAGAGAAGGTCTATGTCA | 1866 | A TTTTA |
| | | | A ATAT | TTCTCTTCTC | |
| | | | | | |

| | | | | | |
|-------|-----------|----|-----------------------------|---------|--|
| | | | A TGTA AAGAGAAAGAG | | |
| | | | C TCTGG | | |
| GAM31 | FLJ10006 | 3' | GAGAAAGAAGATATTTTA 3152 | A | |
| | | | TAAAATATTTTT TTCTC | | |
| | | | | | |
| | | | ATTTTATAGAAG AAGAG | | |
| | | | A | | |
| GAM31 | HTPAP | 3' | GAGAATAAAAAAGATTTTA 2255 | A | |
| | | | TAAAAT TTTTATTCTC | | |
| | | | | | |
| | | | ATTTTA AAAAATAAGAG | | |
| | | | G | | |
| GAM31 | KIAA0979 | 3' | AGAAAGATTTAAAGTATTTTA 1601 | TATTC | |
| | | | TAAAATATTTT TCTTCT | | |
| | | | | | |
| | | | ATTTTATGAAA AGAAAGA | | |
| | | | TTT__ | | |
| GAM31 | KIAA1634 | 3' | GAGAATAAAACTATTTTA 2657 | T | |
| | | | TAAAATA TTTTATTCTC | | |
| | | | | | |
| | | | ATTTTAT AAAATAAGAG | | |
| | | | C | | |
| GAM31 | PTD012 | 3' | GAGATTGGGAACAAAAATAT 1465 | A TT | |
| | | | ATATTTTT TTCTC TCTC | | |
| | | | | | |
| | | | TATAAAAA AAGGG AGAG | | |
| | | | C TT | | |
| GAM31 | SAMHD1 | 3' | AGAAAGAGAAAGAAATAT 2593 | A | |
| | | | ATATTTTT TTCTCTTCT | | |
| | | | | | |
| | | | TATAAAGA AAGAGAAAGA | | |
| | | | - | | |
| GAM31 | LOC196758 | 3' | GAGAAAGAGCAGGTGAAATATT 3410 | TATT_ | |
| | TT | | AAAATATTTT CTCTTCTC | | |
| | | | | | |
| | | | TTTTATAAAG GAGAAAGAG | | |
| | | | TGGAC | | |
| GAM31 | LOC219790 | 3' | GAGAATAAAAAATAATTTA 3520 | A | |
| | | | TAAA TATTTTTATTCTC | | |
| | | | | | |
| | | | ATTT ATAAAAATAAGAG | | |
| | | | A | | |
| GAM32 | CAPN2 | 3' | AAACTTTTATGAACTTCACCA 855 | A _ AAA | |
| | | | TG TGGAGT CGTAA AGTTTT | | |
| | | | | | |
| | | | AC ACTTCA GTATT TCAAAA | | |
| | | | C A ____ | | |
| GAM32 | DAAM2 | 3' | AAAATTTTTCTAAACTCCATC 3559 | CG A | |
| | A | | TGATGGAGT TA AAAAGTTTT | | |
| | | | | | |

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|-------|-----------|----|-----------------------------|------|-------|
| | | | ACTACCTCA AT TTTTAAAA | | |
| | | | AA C | | |
| GAM32 | SELE | 3' | AAACTCTCCTACACTTCCATT 747 | _ C | AAAA |
| | A | | TGATGGA GT GTA AGTTTT | | |
| | | | | | |
| | | | ATTACCT CA CAT TCAAAA | | |
| | | | T _ CCTC | | |
| GAM32 | KIAA0475 | 3' | AAAACCTTGCATTCCATCA 1570 | C | AAAA |
| | | | TGATGGAGT GTAA GTTTT | | |
| | | | | | |
| | | | ACTACCTTA CGTT CAAAA | | |
| | | | _ C__ | | |
| GAM32 | LOC222671 | 5' | GCTTCTACGACTCCGCCA 3582 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C__ | | |
| GAM32 | LOC254901 | 5' | AATTTCTTCACTGACTCCACCA 3699 | A | _ A A |
| | | | TG TGGAGTC GT AA AAGTT | | |
| | | | | | |
| | | | AC ACCTCAG CA TT TTAA | | |
| | | | C T C C | | |
| GAM32 | LOC257615 | 5' | GCTTCTACGACTCCGCCA 3749 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C__ | | |
| GAM33 | CAPN2 | 3' | AAACTTTATGAAGTTCACCA 855 | A | _ AAA |
| | | | TG TGGAGT CGTAA AGTTTT | | |
| | | | | | |
| | | | AC ACTTCA GTATT TCAAAA | | |
| | | | C A _ | | |
| GAM33 | DAAM2 | 3' | AAAATTTTCTAAAAGTCCATC 3559 | CG A | |
| | A | | TGATGGAGT TA AAAAGTTTT | | |
| | | | | | |
| | | | ACTACCTCA AT TTTTAAAA | | |
| | | | AA C | | |
| GAM33 | SELE | 3' | AAACTCTCCTACACTTCCATT 747 | _ C | AAAA |
| | A | | TGATGGA GT GTA AGTTTT | | |
| | | | | | |
| | | | ATTACCT CA CAT TCAAAA | | |
| | | | T _ CCTC | | |
| GAM33 | KIAA0475 | 3' | AAAACCTTGCATTCCATCA 1570 | C | AAAA |
| | | | TGATGGAGT GTAA GTTTT | | |
| | | | | | |
| | | | ACTACCTTA CGTT CAAAA | | |
| | | | _ C__ | | |
| GAM33 | LOC222671 | 5' | GCTTCTACGACTCCGCCA 3582 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |

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|-------|-----------|----|-----------------------------|----|--------|
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C_ | | |
| GAM33 | LOC254901 | 5' | AATTTCTTCACTGACTCCACCA 3699 | A | _ A A |
| | | | TG TGGAGTC GT AA AAGTT | | |
| | | | | | |
| | | | AC ACCTCAG CA TT TTAA | | |
| | | | C T C C | | |
| GAM33 | LOC257615 | 5' | GCTTCTACGACTCCGCCA 3749 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C_ | | |
| GAM34 | ADCY6 | 3' | TTGTACAATATTTTGTACAAAG 1617 | G | TTCAC |
| | A | | TCTTTG TACAAAAT ACAA | | |
| | | | | | |
| | | | AGAAAC ATGTTTTA TGTT | | |
| | | | _ TAACA | | |
| GAM34 | ADCY6 | 3' | TTGTACAATATTTTGTACAAAG 1933 | G | TTCAC |
| | A | | TCTTTG TACAAAAT ACAA | | |
| | | | | | |
| | | | AGAAAC ATGTTTTA TGTT | | |
| | | | _ TAACA | | |
| GAM34 | APBB2 | 5' | TGAGCTTTGTACCAAAGA 2946 | | AT |
| | | | TCTTTGGTACAAA TTCA | | |
| | | | | | |
| | | | AGAAACCATGTTT GAGT | | |
| | | | C_ | | |
| GAM34 | ATP8B2 | 3' | TGATTTTTATACCAAAGA 2716 | C | TT |
| | | | TCTTTGGTA AAAA TCA | | |
| | | | | | |
| | | | AGAAACCAT TTTT AGT | | |
| | | | A T_ | | |
| GAM34 | CEACAM1 | 3' | TGTGTGAAGTAGCAAAGA 848 | G | CAAAAT |
| | | | TCTTTG TA TTCACACA | | |
| | | | | | |
| | | | AGAAAC AT AAGTGTGT | | |
| | | | G C_ | | |
| GAM34 | CHST1 | 3' | TGTGATATTTCTTTGTGCCAAA 1046 | | _ T |
| | | | TTTGGTACAAA AT TCACA | | |
| | | | | | |
| | | | AAACCGTGTTT TA AGTGT | | |
| | | | CTT T | | |
| GAM34 | FBXL7 | 3' | TGCGTGTTTTCCACCAAAGA 1425 | AC | TTT A |
| | | | TCTTTGGT AAAA CAC CA | | |
| | | | | | |
| | | | AGAAACCA TTTT GTG GT | | |
| | | | CC _ C | | |
| GAM34 | HOXC9 | 3' | TGCGTGCGAGATTTTGTAC 2592 | _ | A |
| | | | GTACAAAATTT CAC CA | | |
| | | | | | |

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|-------|----------|----|----------------------------|----------|--|
| | | | CATGTTTTAGA GTG GT | | |
| | | | C C | | |
| GAM34 | IGF1 | 3' | TGTGGCATTGTACCAA 763 | ATT | |
| | | | TTTGGTACAAA TCACA | | |
| | | | | | |
| | | | AAACCATGTTT GGTGT | | |
| | | | AC_ | | |
| GAM34 | ITGAL | 3' | TGTGAAATTCTGTCCAAA 907 | T A | |
| | | | TTTGG ACA AATTTCACA | | |
| | | | | | |
| | | | AAACC TGT TTAAAGTGT | | |
| | | | _ C | | |
| GAM34 | LBR | 3' | TGTACTGGATTGCACCAAGGA 2522 | A AAT C_ | |
| | | | TCTTTGGT CAA TTCA ACA | | |
| | | | | | |
| | | | AGGAACCA GTT AGGT TGT | | |
| | | | C _ CA | | |
| GAM34 | MIP | 3' | TGTGTGAAATCTTTCAAG 1399 | TACAAA | |
| | | | TTTGG ATTTCACACA | | |
| | | | | | |
| | | | GAACT TAAAGTGTGT | | |
| | | | TTC_ | | |
| GAM34 | RLN2 | 3' | TGTTGGTTGTACCAA 1175 | AATT C | |
| | | | TTTGGTACAA TCA ACA | | |
| | | | | | |
| | | | AAACCATGTT GGT TGT | | |
| | | | _ _ | | |
| GAM34 | SART2 | 3' | TGATTTTCATACCAAAGA 1444 | CA TT | |
| | | | TCTTTGGTA AAA TCA | | |
| | | | | | |
| | | | AGAAACCAT TTT AGT | | |
| | | | AC T_ | | |
| GAM34 | TPK1 | 3' | AAATTTTGCTACCAAAGA 1987 | _ | |
| | | | TCTTTGGTA CAAAATT | | |
| | | | | | |
| | | | AGAAACCAT GTTTTAAA | | |
| | | | C | | |
| GAM34 | TRIP12 | 3' | TGTGTGAAATTAAAAAAGG 1094 | GGTACA | |
| | | | TCTTT AAATTCACACA | | |
| | | | | | |
| | | | GGAAA TTAAAGTGTGT | | |
| | | | AAA_ | | |
| GAM34 | BRD3 | 3' | GTGTGAGATTCGTACCGAAGA 1398 | AA | |
| | | | TCTTTGGTAC AATTCACAC | | |
| | | | | | |
| | | | AGAAGCCATG TTAGAGTGTG | | |
| | | | C_ | | |
| GAM34 | FLJ13397 | 3' | GTGTGAAATTTACTAGCAA 2116 | G CA | |
| | | | TTTG TA AAATTCACAC | | |
| | | | | | |

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|-------|----------|----|-----------------------------|------------|--|
| | | | AAAC AT TTTAAAGTGTG | | |
| | | | G CA | | |
| GAM34 | FLJ22202 | 3' | TGTATCATTTTGTACCAA 2103 | TTC | |
| | | | TTTGGTACAAAAT ACA | | |
| | | | | | |
| | | | AAACCATGTTTTA TGT | | |
| | | | CTA | | |
| GAM34 | GROS1 | 3' | TGTGTAGACAACCAAAGA 1986 | ACAAAATT _ | |
| | | | TCTTTGGT TC ACACA | | |
| | | | | | |
| | | | AGAAACCA AG TGTGT | | |
| | | | AC_____ A | | |
| GAM34 | KIAA0981 | 3' | TGTGTAAAACTGCCAAGGA 2598 | CAAAA C | |
| | | | TCTTTGGTA TTT ACACA | | |
| | | | | | |
| | | | AGGAACCGT AAA TGTGT | | |
| | | | C_____ A | | |
| GAM34 | KIAA1243 | 3' | TGTGACATGACCAAAGA 2978 | A AAATT | |
| | | | TCTTTGGT CA TCACA | | |
| | | | | | |
| | | | AGAAACCA GT AGTGT | | |
| | | | _ AC_____ | | |
| GAM34 | KIAA1462 | 3' | TTGTGTGAGAGGAACCCAAAGA 3524 | TACAAAA | |
| | | | TCTTTGG TTTACACAA | | |
| | | | | | |
| | | | AGAAACC AGAGTGTGTT | | |
| | | | CAAGG_____ | | |
| GAM34 | MGC1136 | 3' | TTGTGTGAAACCCCTAGCATAG 2041 | T G CAAAA | |
| | A | | TCT TG TA TTTACACAA | | |
| | | | | | |
| | | | AGA AC AT AAAGTGTGTT | | |
| | | | T G CCCC_____ | | |
| GAM34 | MSTP043 | 3' | TGTCTTTATTTTACCAAAGA 2223 | C TTC_ | |
| | | | TCTTTGGTA AAAAT ACA | | |
| | | | | | |
| | | | AGAAACCAT TTTTA TGT | | |
| | | | _ TTTC | | |
| GAM34 | Nup43 | 3' | TGTGCAAATTTTAGTATCAGA 2075 | _ CA | |
| | | | TTTGGTAC AAAATTT CACA | | |
| | | | | | |
| | | | AGACTATG TTTTAAA GTGT | | |
| | | | A AC | | |
| GAM34 | RPS6KA4 | 3' | TGTGCAATTACGTCCACCAAAG 1072 | __ AA T | |
| | A | | TCTTTGGT AC AATT CACA | | |
| | | | | | |
| | | | AGAAACCA TG TTAA GTGT | | |
| | | | CC CA C | | |
| GAM34 | SLC17A6 | 3' | TGAAACTTGTGCCACAGA 1911 | T AA | |
| | | | TCT TGGTACAA TTTCA | | |
| | | | | | |

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|-------|-----------|----|-----------------------------|----------|--|
| | | | AGA ACCGTGTT AAAGT | | |
| | | | C C_ | | |
| GAM34 | TERA | 3' | TGTATGAATAGTACCAAAG 1949 | AAAAT C | |
| | | | CTTTGGTAC TTCA ACA | | |
| | | | | | |
| | | | GAAACCATG AAGT TGT | | |
| | | | AT__ A | | |
| GAM34 | VAV3 | 3' | TTGTGTAGAGTTCTAATACCAA 1273 | CAA_ TC | |
| | AGA | | TCTTTGGTA AATT ACACAA | | |
| | | | | | |
| | | | AGAAACCAT TTGA TGTGTT | | |
| | | | AATC GA | | |
| GAM34 | LOC120892 | 3' | TGCAATTTTTTTTACCAAAGA 2987 | C__ T | |
| | | | TCTTTGGTA AAAATT CA | | |
| | | | | | |
| | | | AGAAACCAT TTTTAA GT | | |
| | | | TTT C | | |
| GAM34 | LOC155434 | 3' | TTGTGTGATTTTCGTACCAA 3376 | A TT | |
| | | | TTTGGTAC AAA TCACACAA | | |
| | | | | | |
| | | | AAACCATG TTT AGTGTGTT | | |
| | | | C _ | | |
| GAM34 | LOC169966 | 3' | ATTTTGCCTTTACCAAAGA 3252 | _____ | |
| | | | TCTTTGGTA CAAAAT | | |
| | | | | | |
| | | | AGAAACCAT GTTTTA | | |
| | | | TTCC | | |
| GAM34 | LOC221272 | 3' | TGTCTGCTCTGTACCAGAGA 3616 | AAATTT C | |
| | | | TCTTTGGTACA CA ACA | | |
| | | | | | |
| | | | AGAGACCATGT GT TGT | | |
| | | | CTC__ C | | |
| GAM34 | LOC221968 | 3' | TTGTGTGAAATTTTGTGCGAA 3569 | GT | |
| | | | TTTG ACAAATTTACACAA | | |
| | | | | | |
| | | | AAGC TGTTTTAAAGTGTGTT | | |
| | | | _____ | | |
| GAM34 | LOC86651 | 5' | TTGTGTGAAAGATGTTTCATAC 2830 | CA _____ | |
| | CAAGGA | | CTTTGGTA AAAT TTCACACAA | | |
| | | | | | |
| | | | GGAACCAT TTTG AAGTGTGTT | | |
| | | | AC TAGA | | |
| GAM34 | LOC90322 | 3' | GAGATTCCATACTAAAGA 2632 | CAA | |
| | | | TCTTTGGTA AATTTC | | |
| | | | | | |
| | | | AGAAATCAT TTAGAG | | |
| | | | ACC | | |
| GAM35 | MYO1E | 5' | ATGGAGTCCCCTCTAGGGTT 1168 | ATC A A | |
| | | | GACC GA GG GACTCCAT | | |
| | | | | | |

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|-------|-----------|----|-----------------------------|--------|-------|
| | | | TTGG CT CC CTGAGGTA | | |
| | | | GAT C _ | | |
| GAM35 | ROCK2 | 3' | ATGAAGTCTTTTAACAGTCTC 2737 | CATCGA | C |
| | | | GAGAC AGGAGACT CAT | | |
| | | | | | |
| | | | CTCTG TTTTCTGA GTA | | |
| | | | ACAA_ A | | |
| GAM35 | MGC15937 | 5' | GAGTTTCTTCTTCAAGGTCTCA 2383 | ATC | _ |
| | | | TGAGACC GAAGGAGA CTC | | |
| | | | | | |
| | | | ACTCTGG CTTCTTCT GAG | | |
| | | | AA_ TT | | |
| GAM35 | STK16 | 5' | GAGCTCTTCGGTAGCCTCA 2937 | ACC | G A |
| | | | TGAG ATCGAAG AG CTC | | |
| | | | | | |
| | | | ACTC TGGCTTC TC GAG | | |
| | | | CGA _ _ | | |
| GAM35 | LOC148029 | 5' | GGAGTCTCCATCCTCA 3116 | ACCATC | A |
| | | | TGAG GA GGAGACTCC | | |
| | | | | | |
| | | | ACTC CT CCTCTGAGG | | |
| | | | _ A | | |
| GAM35 | LOC169436 | 5' | TGGAGTTCAATGAGCTCA 3261 | AC C | AGGAG |
| | | | TGAG CAT GA ACTCCA | | |
| | | | | | |
| | | | ACTC GTA CT TGAGGT | | |
| | | | GA A _ | | |
| GAM35 | LOC256267 | 3' | ATGGAGTCTCCCTCTGTC 3713 | CATC | A |
| | | | GAC GA GGAGACTCCAT | | |
| | | | | | |
| | | | CTG CT CCTCTGAGGTA | | |
| | | | T_ C | | |
| GAM35 | LOC257426 | 3' | GAGTCCTTCGGTGGCCTCA 2755 | A | GA |
| | | | TGAG CCATCGAAGGA CTC | | |
| | | | | | |
| | | | ACTC GGTGGCTTCCT GAG | | |
| | | | C _ | | |
| GAM35 | LOC92466 | 3' | ATGGAGTCTCCCTCTGTC 2858 | CATC | A |
| | | | GAC GA GGAGACTCCAT | | |
| | | | | | |
| | | | CTG CT CCTCTGAGGTA | | |
| | | | T_ C | | |
| GAM36 | MME | 3' | AAAAAAAGTTACAGAAATA 785 | AA | |
| | | | TATTTTTTGTA ACTTTTTTT | | |
| | | | | | |
| | | | ATAAAGACAT TGAAAAAAA | | |
| | | | _ | | |
| GAM36 | MME | 3' | AAAAAAAGTTACAGAAATA 1377 | AA | |
| | | | TATTTTTTGTA ACTTTTTTT | | |
| | | | | | |

ATAAAGACAT TGAAAAAAAA

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|---------------------------|--------------|----|-----------------------|------|------|
| GAM36 | MME | 3' | AAAAAAAGTTACAGAAATA | 1378 | AA |
| TATTTTTGT ACTTTTTT | | | | | |
| | | | | | |
| ATAAAGACAT TGAAAAAAAA | | | | | |
| | | | | | |
| GAM36 | MME | 3' | AAAAAAAGTTACAGAAATA | 1379 | AA |
| TATTTTTGT ACTTTTTT | | | | | |
| | | | | | |
| ATAAAGACAT TGAAAAAAAA | | | | | |
| | | | | | |
| GAM36 | DKFZP434C212 | 3' | AAAAAGTACACAGAAATATT | 2832 | AAA |
| AATATTTTGT ACTTTTT | | | | | |
| | | | | | |
| TTATAAAGACA TGAAAAA | | | | | |
| CA_ | | | | | |
| GAM36 | FLJ11275 | 3' | TAAATGGGATTATAAAAAATA | 1821 | A TT |
| TT AATATTTTGTAAA CT TTTTA | | | | | |
| | | | | | |
| TTATAAAAATATTT GG AAAAT | | | | | |
| A GT | | | | | |
| GAM36 | GOLPH3 | 3' | TAAAAAAGTTTACTGCCATA | 1981 | TTTT |
| TT AATAT GTAAACTTTTTTTA | | | | | |
| | | | | | |
| TTATA CATTTTGAAAAAAT | | | | | |
| CCGT | | | | | |
| GAM36 | KIAA0563 | 5' | TAAAAAAGGAGCAAAAGTAT | 1565 | AAAA |
| ATATTTTGT CTTTTTTA | | | | | |
| | | | | | |
| TATGAAAACG GAAAAAAT | | | | | |
| AG_ | | | | | |
| GAM36 | TAF2 | 3' | AGAAAGTTTGACAAAAATA | 997 | A |
| TATTTTGT AAACTTTT | | | | | |
| | | | | | |
| ATAAAAACA TTTGAAAGA | | | | | |
| G | | | | | |
| GAM36 | LOC147071 | 5' | TAAAAAAGGAGCAAAAGTAT | 2965 | AAAA |
| ATATTTTGT CTTTTTTA | | | | | |
| | | | | | |
| TATGAAAACG GAAAAAAT | | | | | |
| AG_ | | | | | |
| GAM36 | LOC147639 | 5' | AAAAGTGCTGCAAAAATATT | 3110 | AA |
| AATATTTTGT ACTTTT | | | | | |
| | | | | | |
| TTATAAAAACGT TGAAAA | | | | | |
| CG | | | | | |
| GAM36 | LOC201173 | 5' | TAAAAAAGGAGCAAAAGTAT | 3405 | AAAA |
| ATATTTTGT CTTTTTTA | | | | | |
| | | | | | |

| | | | | |
|-------|--------------|----|---------------------------|------|
| | | | TATGAAAACG GAAAAAAT | |
| | | | AG__ | |
| GAM36 | LOC201220 | 5' | TAAAAAAGGAGCAAAAGTAT 3406 | AAAA |
| | | | ATATTTTTGT CTTTTTTA | |
| | | | | |
| | | | TATGAAAACG GAAAAAAT | |
| | | | AG__ | |
| GAM37 | MME | 3' | AAAAAAAGTTACAGAAATA 785 | AA |
| | | | TATTTTTGTA ACTTTTTT | |
| | | | | |
| | | | ATAAAGACAT TGAAAAAA | |
| | | | — | |
| GAM37 | MME | 3' | AAAAAAAGTTACAGAAATA 1377 | AA |
| | | | TATTTTTGTA ACTTTTTT | |
| | | | | |
| | | | ATAAAGACAT TGAAAAAA | |
| | | | — | |
| GAM37 | MME | 3' | AAAAAAAGTTACAGAAATA 1378 | AA |
| | | | TATTTTTGTA ACTTTTTT | |
| | | | | |
| | | | ATAAAGACAT TGAAAAAA | |
| | | | — | |
| GAM37 | MME | 3' | AAAAAAAGTTACAGAAATA 1379 | AA |
| | | | TATTTTTGTA ACTTTTTT | |
| | | | | |
| | | | ATAAAGACAT TGAAAAAA | |
| | | | — | |
| GAM37 | DKFZP434C212 | 3' | AAAAAGTACACAGAAATATT 2832 | AAA |
| | | | AATATTTTGT ACTTTT | |
| | | | | |
| | | | TTATAAAGACA TGAAAA | |
| | | | CA_ | |
| GAM37 | FLJ11275 | 3' | TAAATGGGATTATAAAAATA 1821 | A TT |
| | TT | | AATATTTTGTAAA CT TTTTA | |
| | | | | |
| | | | TTATAAAAATATTT GG AAAAT | |
| | | | A GT | |
| GAM37 | GOLPH3 | 3' | TAAAAAAGTTTACTGCCATA 1981 | TTTT |
| | TT | | AATAT GTAAACTTTTTTTA | |
| | | | | |
| | | | TTATA CATTTTGAAAAAAT | |
| | | | CCGT | |
| GAM37 | KIAA0563 | 5' | TAAAAAAGGAGCAAAAGTAT 1565 | AAAA |
| | | | ATATTTTTGT CTTTTTTA | |
| | | | | |
| | | | TATGAAAACG GAAAAAAT | |
| | | | AG__ | |
| GAM37 | TAF2 | 3' | AGAAAGTTTGACAAAATA 997 | A |
| | | | TATTTTTGT AAACTTTT | |
| | | | | |

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|-------|---------------|----|-----------------------------|------|------|
| | | | ATAAAAACA TTTGAAAGA | | |
| | | | G | | |
| GAM37 | LOC147071 | 5' | TAAAAAAAGGAGCAAAAGTAT 2965 | AAAA | |
| | | | ATATTTTGT CTTTTTTA | | |
| | | | | | |
| | | | TATGAAAACG GAAAAAAT | | |
| | | | AG__ | | |
| GAM37 | LOC147639 | 5' | AAAAGTGCTGCAAAAATATT 3110 | AA | |
| | | | AATATTTTGTA ACTTTT | | |
| | | | | | |
| | | | TTATAAAAACGT TGAAAA | | |
| | | | CG | | |
| GAM37 | LOC201173 | 5' | TAAAAAAAGGAGCAAAAGTAT 3405 | AAAA | |
| | | | ATATTTTGT CTTTTTTA | | |
| | | | | | |
| | | | TATGAAAACG GAAAAAAT | | |
| | | | AG__ | | |
| GAM37 | LOC201220 | 5' | TAAAAAAAGGAGCAAAAGTAT 3406 | AAAA | |
| | | | ATATTTTGT CTTTTTTA | | |
| | | | | | |
| | | | TATGAAAACG GAAAAAAT | | |
| | | | AG__ | | |
| GAM38 | MARK1 | 3' | TATAATAAACATGATTGCTTA 1857 | TA | TAC |
| | A | | TTA CGATC GTTTATTATA | | |
| | | | | | |
| | | | AAT GTTAG CAAATAATAT | | |
| | | | TC TA_ | | |
| GAM39 | DKK1 | 3' | AAAATACTAGCTTATTTTCTGA 1417 | _ | TAA |
| | | | TCAGAAAG AGGTT TATTTT | | |
| | | | | | |
| | | | AGTCTTTT TTCGA ATAAAA | | |
| | | | A TC_ | | |
| GAM39 | KERA | 3' | AAAATATTGAATGCTTTCT 1349 | AG | |
| | | | AGAAAG GTTTAATATTTT | | |
| | | | | | |
| | | | TCTTTC TAAGTTATAAAA | | |
| | | | G_ | | |
| GAM39 | PPP1R12A | 3' | AAAATACTACATCTTTCTGG 931 | G | TTAA |
| | | | TCAGAAAGA GT TATTTT | | |
| | | | | | |
| | | | GGTCTTTCT CA ATAAAA | | |
| | | | A TC__ | | |
| GAM39 | S100B | 3' | AAAATTGAAAACCTCTTTC 1284 | AAT | |
| | | | GAAAGAGGTTT ATTTT | | |
| | | | | | |
| | | | CTTTCTCCAAA TAAAA | | |
| | | | AGT | | |
| GAM39 | DKFZP564I0422 | 3' | AAAATATTGCATTCTTCTGAT 2196 | A | GTT |
| | | | ATCAGAA GAG TAATATTTT | | |
| | | | | | |

| | | | | |
|-------|-----------|----|-----------------------------|---------|
| | | | TAGTCTT CTT GTTATAAAA | |
| | | | _ AC_ | |
| GAM39 | EML4 | 3' | AAAATGTTTCCTCTTTCT 1876 | TTT |
| | | | AGAAAGAGG AATATTTT | |
| | | | | |
| | | | TCTTTCTCC TTGTAAAA | |
| | | | T__ | |
| GAM39 | FLJ21657 | 3' | AAAATATTTTACTCTGCCTGAT 1990 | AA GTTT |
| | | | ATCAG AGAG AATATTTT | |
| | | | | |
| | | | TAGTC TCTC TTATAAAA | |
| | | | CG ATT_ | |
| GAM39 | KIAA1054 | 3' | AAAATGGTACCTCTTTC 2820 | TTAA |
| | | | GAAAGAGGT TATTTT | |
| | | | | |
| | | | CTTTCTCCA GTAAAA | |
| | | | TG__ | |
| GAM39 | SEMA3E | 5' | AAAATACAGCTTCTTCCTGA 1431 | A TAA |
| | | | TCAG AAGAGGTT TATTTT | |
| | | | | |
| | | | AGTC TTCTTCGA ATAAAA | |
| | | | C C__ | |
| GAM39 | LOC130507 | 3' | AAAATATTAAGATAACTTTCTG 3011 | AGG_ |
| | | | CAGAAAG TTTAATATTTT | |
| | | | | |
| | | | GTCTTTC GAATTATAAAA | |
| | | | AATA | |
| GAM39 | LOC148145 | 5' | AAAATATTAACCTGGACCTGA 3296 | AAAG |
| | | T | ATCAG AGGTTTAATATTTT | |
| | | | | |
| | | | TAGTC TCCAAATTATAAAA | |
| | | | CAGG | |
| GAM40 | DKK1 | 3' | AAAATACTAGCTTATTTTCTGA 1417 | _ TAA |
| | | | TCAGAAAG AGGTT TATTTT | |
| | | | | |
| | | | AGTCTTTT TTCGA ATAAAA | |
| | | | A TC_ | |
| GAM40 | KERA | 3' | AAAATATTGAATGCTTTCT 1349 | AG |
| | | | AGAAAG GTTTAATATTTT | |
| | | | | |
| | | | TCTTTC TAAGTTATAAAA | |
| | | | G_ | |
| GAM40 | PPP1R12A | 3' | AAAATACTACATCTTTCTGG 931 | G TTAA |
| | | | TCAGAAAGA GT TATTTT | |
| | | | | |
| | | | GGTCTTTCT CA ATAAAA | |
| | | | A TC__ | |
| GAM40 | S100B | 3' | AAAATTGAAAACCTCTTTC 1284 | AAT |
| | | | GAAAGAGGTTT ATTTT | |
| | | | | |

CTTTCTCCAAA TAAAA
AGT

GAM40 DKFZP564I0422 3' AAAATATTGCATTCTTCTGAT 2196 A GTT
ATCAGAA GAG TAATATTTT
||||| ||| |||||||
TAGTCTT CTT GTTATAAAA
_ AC_

GAM40 EML4 3' AAAATGTTTCCTCTTTCT 1876 TTT
AGAAAGAGG AATATTTT
||||| |||||||
TCTTTCTCC TTGTAAAA
T__

GAM40 FLJ21657 3' AAAATATTTTACTCTGCCTGAT 1990 AA GTTT
ATCAG AGAG AATATTTT
|||| ||| |||||||
TAGTC TCTC TTATAAAA
CG ATT_

GAM40 KIAA1054 3' AAAATGGTACCTCTTTC 2820 TTAA
GAAAGAGGT TATTTT
||||| |||||
CTTTCTCCA GTAAAA
TG__

GAM40 SEMA3E 5' AAAATACAGCTTCTTCCTGA 1431 A TAA
TCAG AAGAGGTT TATTTT
||| ||||||| |||||
AGTC TTCTTCGA ATAAAA
C C__

GAM40 LOC130507 3' AAAATATTAAGATAACTTTTCTG 3011 AGG_
CAGAAAG TTTAATATTTT
||||| |||||||
GTCTTTC GAATTATAAAA
AATA

GAM40 LOC148145 5' AAAATATTAAACCTGGACCTGA 3296 AAAG
T ATCAG AGGTTTAATATTTT
|||| |||||||
TAGTC TCCAAATTATAAAA
CAGG

GAM41 DKK1 3' AAAATACTAGCTTATTTTCTGA 1417 _ TAA
TCAGAAAG AGGTT TATTTT
||||| ||||| |||||
AGTCTTTT TTCGA ATAAAA
A TC_

GAM41 KERA 3' AAAATATTGAATGCTTTCT 1349 AG
AGAAAG GTTTAATATTTT
||||| |||||||
TCTTTC TAAGTTATAAAA
G_

GAM41 PPP1R12A 3' AAAATACTACATCTTTCTGG 931 G TTAA
TCAGAAAGA GT TATTTT
||||| || |||||

| | | | | |
|-------|---------------|----|-----------------------------|---------|
| | | | GGTCTTTCT CA ATAAAA | |
| | | | A TC__ | |
| GAM41 | S100B | 3' | AAAATTGAAAACCTCTTTC 1284 | AAT |
| | | | GAAAGAGGTTT ATTTT | |
| | | | | |
| | | | CTTTCTCCAAA TAAAA | |
| | | | AGT | |
| GAM41 | DKFZP564I0422 | 3' | AAAATATTGCATTCTTCTGAT 2196 | A GTT |
| | | | ATCAGAA GAG TAATATTTT | |
| | | | | |
| | | | TAGTCTT CTT GTTATAAAA | |
| | | | _ AC_ | |
| GAM41 | EML4 | 3' | AAAATGTTTCCTCTTTCT 1876 | TTT |
| | | | AGAAAGAGG AATATTTT | |
| | | | | |
| | | | TCTTTCTCC TTGTAAAA | |
| | | | T__ | |
| GAM41 | FLJ21657 | 3' | AAAATATTTTACTCTGCCTGAT 1990 | AA GTTT |
| | | | ATCAG AGAG AATATTTT | |
| | | | | |
| | | | TAGTC TCTC TTATAAAA | |
| | | | CG ATT_ | |
| GAM41 | KIAA1054 | 3' | AAAATGGTACCTCTTTC 2820 | TTAA |
| | | | GAAAGAGGT TATTTT | |
| | | | | |
| | | | CTTTCTCCA GTAAAA | |
| | | | TG__ | |
| GAM41 | SEMA3E | 5' | AAAATACAGCTTCTTCCTGA 1431 | A TAA |
| | | | TCAG AAGAGGTT TATTTT | |
| | | | | |
| | | | AGTC TTCTTCGA ATAAAA | |
| | | | C C__ | |
| GAM41 | LOC130507 | 3' | AAAATATTAAGATAACTTTCTG 3011 | AGG_ |
| | | | CAGAAAG TTTAATATTTT | |
| | | | | |
| | | | GTCTTTC GAATTATAAAA | |
| | | | AATA | |
| GAM41 | LOC148145 | 5' | AAAATATTAACCTGGACCTGA 3296 | AAAG |
| | | T | ATCAG AGGTTTAATATTTT | |
| | | | | |
| | | | TAGTC TCCAAATTATAAAA | |
| | | | CAGG | |
| GAM42 | DKK1 | 3' | AAAATACTAGCTTATTTTCTGA 1417 | _ TAA |
| | | | TCAGAAAG AGGTT TATTTT | |
| | | | | |
| | | | AGTCTTTT TTCGA ATAAAA | |
| | | | A TC_ | |
| GAM42 | KERA | 3' | AAAATATTGAATGCTTTCT 1349 | AG |
| | | | AGAAAG GTTTAATATTTT | |
| | | | | |

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|-------|---------------|----|-----------------------------|---------|
| | | | TCTTTC TAAGTTATAAAA | |
| | | | G_ | |
| GAM42 | PPP1R12A | 3' | AAAATACTACATCTTTCTGG 931 | G TTAA |
| | | | TCAGAAAGA GT TATTTT | |
| | | | | |
| | | | GGTCTTTCT CA ATAAAA | |
| | | | A TC__ | |
| GAM42 | S100B | 3' | AAAATTGAAAACCTCTTTC 1284 | AAT |
| | | | GAAAGAGGTTT ATTTT | |
| | | | | |
| | | | CTTTCTCCAAA TAAAA | |
| | | | AGT | |
| GAM42 | DKFZP564I0422 | 3' | AAAATATTGCATTCTTCTGAT 2196 | A GTT |
| | | | ATCAGAA GAG TAATATTTT | |
| | | | | |
| | | | TAGTCTT CTT GTTATAAAA | |
| | | | _ AC_ | |
| GAM42 | EML4 | 3' | AAAATGTTTCCTCTTTCT 1876 | TTT |
| | | | AGAAAGAGG AATATTTT | |
| | | | | |
| | | | TCTTTCTCC TTGTAAAA | |
| | | | T__ | |
| GAM42 | FLJ21657 | 3' | AAAATATTTTACTCTGCCTGAT 1990 | AA GTTT |
| | | | ATCAG AGAG AATATTTT | |
| | | | | |
| | | | TAGTC TCTC TTATAAAA | |
| | | | CG ATT_ | |
| GAM42 | KIAA1054 | 3' | AAAATGGTACCTCTTTC 2820 | TTAA |
| | | | GAAAGAGGT TATTTT | |
| | | | | |
| | | | CTTTCTCCA GTAAAA | |
| | | | TG__ | |
| GAM42 | SEMA3E | 5' | AAAATACAGCTTCTTCCTGA 1431 | A TAA |
| | | | TCAG AAGAGGTT TATTTT | |
| | | | | |
| | | | AGTC TTCTTCGA ATAAAA | |
| | | | C C__ | |
| GAM42 | LOC130507 | 3' | AAAATATTAAGATAACTTTCTG 3011 | AGG_ |
| | | | CAGAAAG TTTAATATTTT | |
| | | | | |
| | | | GTCTTTC GAATTATAAAA | |
| | | | AATA | |
| GAM42 | LOC148145 | 5' | AAAATATTAACCTGGACCTGA 3296 | AAAG |
| | | T | ATCAG AGGTTTAATATTTT | |
| | | | | |
| | | | TAGTC TCCAAATTATAAAA | |
| | | | CAGG | |
| GAM43 | DKK1 | 3' | AAAATACTAGCTTATTTTCTGA 1417 | _ TAA |
| | | | TCAGAAAG AGGTT TATTTT | |
| | | | | |

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|-------|---------------|----|-----------------------------|---------|
| | | | AGTCTTTT TTCGA ATAAAA | |
| | | | A TC_ | |
| GAM43 | KERA | 3' | AAAATATTGAATGCTTTCT 1349 | AG |
| | | | AGAAAG GTTTAATATTTT | |
| | | | | |
| | | | TCTTTC TAAGTTATAAAA | |
| | | | G_ | |
| GAM43 | PPP1R12A | 3' | AAAATACTACATCTTTCTGG 931 | G TTAA |
| | | | TCAGAAAGA GT TATTTT | |
| | | | | |
| | | | GGTCTTTCT CA ATAAAA | |
| | | | A TC__ | |
| GAM43 | S100B | 3' | AAAATTGAAAACCTCTTTC 1284 | AAT |
| | | | GAAAGAGGTTT ATTTT | |
| | | | | |
| | | | CTTTCTCCAAA TAAAA | |
| | | | AGT | |
| GAM43 | DKFZP564I0422 | 3' | AAAATATTGCATTCTTCTGAT 2196 | A GTT |
| | | | ATCAGAA GAG TAATATTTT | |
| | | | | |
| | | | TAGTCTT CTT GTTATAAAA | |
| | | | _ AC_ | |
| GAM43 | EML4 | 3' | AAAATGTTTCCTCTTTCT 1876 | TTT |
| | | | AGAAAGAGG AATATTTT | |
| | | | | |
| | | | TCTTTCTCC TTGTAAAA | |
| | | | T__ | |
| GAM43 | FLJ21657 | 3' | AAAATATTTTACTCTGCCTGAT 1990 | AA GTTT |
| | | | ATCAG AGAG AATATTTT | |
| | | | | |
| | | | TAGTC TCTC TTATAAAA | |
| | | | CG ATT_ | |
| GAM43 | KIAA1054 | 3' | AAAATGGTACCTCTTTC 2820 | TTAA |
| | | | GAAAGAGGT TATTTT | |
| | | | | |
| | | | CTTTCTCCA GTAAAA | |
| | | | TG__ | |
| GAM43 | SEMA3E | 5' | AAAATACAGCTTCTTCCTGA 1431 | A TAA |
| | | | TCAG AAGAGGTT TATTTT | |
| | | | | |
| | | | AGTC TTCTTCGA ATAAAA | |
| | | | C C__ | |
| GAM43 | LOC130507 | 3' | AAAATATTAAGATAACTTTCTG 3011 | AGG_ |
| | | | CAGAAAG TTTAATATTTT | |
| | | | | |
| | | | GTCTTTC GAATTATAAAA | |
| | | | AATA | |
| GAM43 | LOC148145 | 5' | AAAATATTAAACCTGGACCTGA 3296 | AAAG |
| | | | T ATCAG AGGTTTAATATTTT | |
| | | | | |

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|-------|---------------|----|-----------------------------|----------------------|--|
| | | | | TAGTC TCCAAATTATAAAA | |
| | | | | CAGG | |
| GAM44 | DKK1 | 3' | AAAATACTAGCTTATTTTCTGA 1417 | _ TAA | |
| | | | TCAGAAAG AGGTT TATTTT | | |
| | | | | | |
| | | | AGTCTTTT TTCGA ATAAAA | | |
| | | | A TC_ | | |
| GAM44 | KERA | 3' | AAAATATTGAATGCTTTCT 1349 | AG | |
| | | | AGAAAG GTTTAATATTTT | | |
| | | | | | |
| | | | TCTTTC TAAGTTATAAAA | | |
| | | | G_ | | |
| GAM44 | PPP1R12A | 3' | AAAATACTACATCTTTCTGG 931 | G TTAA | |
| | | | TCAGAAAGA GT TATTTT | | |
| | | | | | |
| | | | GGTCTTTCT CA ATAAAA | | |
| | | | A TC__ | | |
| GAM44 | S100B | 3' | AAAATTGAAAACCTCTTTC 1284 | AAT | |
| | | | GAAAGAGGTTT ATTTT | | |
| | | | | | |
| | | | CTTTCTCCAAA TAAAA | | |
| | | | AGT | | |
| GAM44 | DKFZP564I0422 | 3' | AAAATATTGCATTCTTCTGAT 2196 | A GTT | |
| | | | ATCAGAA GAG TAATATTTT | | |
| | | | | | |
| | | | TAGTCTT CTT GTTATAAAA | | |
| | | | _ AC_ | | |
| GAM44 | EML4 | 3' | AAAATGTTTCCTCTTTCT 1876 | TTT | |
| | | | AGAAAGAGG AATATTTT | | |
| | | | | | |
| | | | TCTTTCTCC TTGTAAAA | | |
| | | | T_ | | |
| GAM44 | FLJ21657 | 3' | AAAATATTTTACTCTGCCTGAT 1990 | AA GTTT | |
| | | | ATCAG AGAG AATATTTT | | |
| | | | | | |
| | | | TAGTC TCTC TTATAAAA | | |
| | | | CG ATT_ | | |
| GAM44 | KIAA1054 | 3' | AAAATGGTACCTCTTTC 2820 | TTAA | |
| | | | GAAAGAGGT TATTTT | | |
| | | | | | |
| | | | CTTTCTCCA GTAAAA | | |
| | | | TG_ | | |
| GAM44 | SEMA3E | 5' | AAAATACAGCTTCTTCCTGA 1431 | A TAA | |
| | | | TCAG AAGAGGTT TATTTT | | |
| | | | | | |
| | | | AGTC TTCTTCGA ATAAAA | | |
| | | | C C_ | | |
| GAM44 | LOC130507 | 3' | AAAATATTAAGATAACTTTCTG 3011 | AGG_ | |
| | | | CAGAAAG TTTAATATTTT | | |
| | | | | | |

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|-------|---------------|----|-----------------------------|---------|
| | | | GTCTTTC GAATTATAAAA | |
| | | | AATA | |
| GAM44 | LOC148145 | 5' | AAAATATTAAACCTGGACCTGA 3296 | AAAG |
| | | T | ATCAG AGGTTTAATATTTT | |
| | | | | |
| | | | TAGTC TCCAAATTATAAAA | |
| | | | CAGG | |
| GAM45 | DKK1 | 3' | AAAATACTAGCTTATTTTCTGA 1417 | _ TAA |
| | | | TCAGAAAG AGGTT TATTTT | |
| | | | | |
| | | | AGTCTTTT TTCGA ATAAAA | |
| | | | A TC_ | |
| GAM45 | KERA | 3' | AAAATATTGAATGCTTTCT 1349 | AG |
| | | | AGAAAG GTTTAATATTTT | |
| | | | | |
| | | | TCTTTC TAAGTTATAAAA | |
| | | | G_ | |
| GAM45 | PPP1R12A | 3' | AAAATACTACATCTTTCTGG 931 | G TTAA |
| | | | TCAGAAAGA GT TATTTT | |
| | | | | |
| | | | GGTCTTTCT CA ATAAAA | |
| | | | A TC__ | |
| GAM45 | S100B | 3' | AAAATTGAAAACCTCTTTC 1284 | AAT |
| | | | GAAAGAGGTTT ATTTT | |
| | | | | |
| | | | CTTTCTCCAAA TAAAA | |
| | | | AGT | |
| GAM45 | DKFZP564I0422 | 3' | AAAATATTGCATTCTTCTGAT 2196 | A GTT |
| | | | ATCAGAA GAG TAATATTTT | |
| | | | | |
| | | | TAGTCTT CTT GTTATAAAA | |
| | | | _ AC_ | |
| GAM45 | EML4 | 3' | AAAATGTTTCCTCTTTCT 1876 | TTT |
| | | | AGAAAGAGG AATATTTT | |
| | | | | |
| | | | TCTTTCTCC TTGTAAAA | |
| | | | T_ | |
| GAM45 | FLJ21657 | 3' | AAAATATTTTACTCTGCCTGAT 1990 | AA GTTT |
| | | | ATCAG AGAG AATATTTT | |
| | | | | |
| | | | TAGTC TCTC TTATAAAA | |
| | | | CG ATT_ | |
| GAM45 | KIAA1054 | 3' | AAAATGGTACCTCTTTC 2820 | TTAA |
| | | | GAAAGAGGT TATTTT | |
| | | | | |
| | | | CTTTCTCCA GTAAAA | |
| | | | TG_ | |
| GAM45 | SEMA3E | 5' | AAAATACAGCTTCTTCCTGA 1431 | A TAA |
| | | | TCAG AAGAGGT TATTTT | |
| | | | | |

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|-------|-----------|----|-----------------------------|-----------|
| | | | AGTC TTCTTCGA ATAAAA | |
| | | | C C__ | |
| GAM45 | LOC130507 | 3' | AAAATATTAAGATAACTTTCTG 3011 | AGG_ |
| | | | CAGAAAG TTTAATATTTT | |
| | | | | |
| | | | GTCTTTC GAATTATAAAA | |
| | | | AATA | |
| GAM45 | LOC148145 | 5' | AAAATATTAACCTGGACCTGA 3296 | AAAG |
| | | | T ATCAG AGGTTTAATATTTT | |
| | | | | |
| | | | TAGTC TCCAAATTATAAAA | |
| | | | CAGG | |
| GAM46 | EFG1 | 3' | TGTCTATCTCAACTCTATT 3661 | ATC TC |
| | | | AATAGAGTT GAT AGACA | |
| | | | | |
| | | | TTATCTCAA CTA TCTGT | |
| | | | CT_ _ | |
| GAM46 | PHYH | 3' | TCTGCTATAACTCTTTCA 1281 | T CGATT |
| | | | TGAA AGAGTTAT CAGA | |
| | | | | |
| | | | ACTT TCTCAATA GTCT | |
| | | | _ TC__ | |
| GAM46 | SLC6A3 | 3' | TGTCTGTTGACCAATCTCTATT 795 | TTA__ TT |
| | CA | | TGAATAGAG TCGA CAGACA | |
| | | | | |
| | | | ACTTATCTC AGTT GTCTGT | |
| | | | TAACC _ | |
| GAM46 | H2AV | 3' | TGCCTGACAATTAGCTCTATT 2447 | TCGAT A |
| | A | | TGAATAGAGTTA TCAG CA | |
| | | | | |
| | | | ACTTATCTCGAT AGTC GT | |
| | | | TAAC_ C | |
| GAM46 | HMP19 | 3' | GTCTGAACCGATATTTCT 3408 | T A |
| | | | AGAG TATCG TTCAGAC | |
| | | | | |
| | | | TCTT ATAGC AAGTCTG | |
| | | | T C | |
| GAM46 | KIAA1726 | 3' | TGTCTGAAAGCAACCCTACTC 2786 | A A ATCGA |
| | | | GA TAG GTT TTCAGACA | |
| | | | | |
| | | | CT ATC CAA AAGTCTGT | |
| | | | C C CGA__ | |
| GAM47 | SOX11 | 3' | GTCTCACTGTTTGATCAAACCTT 992 | A ATTTT |
| | CT | | AGAGGTTT AT GTGAGAC | |
| | | | | |
| | | | TCTTCAAA TA CACTCTG | |
| | | | C GTTTGT | |
| GAM47 | CAP350 | 3' | TCTTGTAATAGTTAAACCTC 1554 | ATTT TG |
| | | | GAGGTTTAAT TTG AGA | |
| | | | | |

| | | | | | |
|-------|--------------|----|--------------------------|---------|----------|
| | | | CTCCAAATTG | AAT TCT | |
| | | | AT__ | GT | |
| GAM47 | DKFZP564A022 | 3' | TCTCACAAATATAAAACC | 2174 | A TT |
| | | | GGTTT ATATT TGTGAGA | | |
| | | | | | |
| | | | CCAAA TATAA ACACTCT | | |
| | | | A | __ | |
| GAM47 | FLJ11730 | 3' | CTCACAAAGATAAACATC | 2005 | G TAA |
| | | | GA GTT TATTTTTGTGAG | | |
| | | | | | |
| | | | CT CAA ATAGAAACACTC | | |
| | | | A | __ | |
| GAM47 | FLJ20686 | 5' | CTCACAGTCCTACTGAACCTC | 1765 | A TTT |
| | | | GAGGTTTA TA TTGTGAG | | |
| | | | | | |
| | | | CTCCAAGT AT GACACTC | | |
| | | | C CCT | | |
| GAM47 | FRSB | 3' | GTCCCAGGGAGATATTAGACCT | 1236 | G A |
| | CT | | AGAGGTTTAATATTTTT TG GAC | | |
| | | | | | |
| | | | TCTCCAGATTATAGAGG AC CTG | | |
| | | | G C | | |
| GAM47 | KIAA1600 | 3' | ACAAAAAGACTAAACCTCT | 2919 | ATA |
| | | | AGAGGTTTA TTTTTGT | | |
| | | | | | |
| | | | TCTCCAAAT AAAACA | | |
| | | | CAG | | |
| GAM47 | LOC124801 | 3' | GTCTCACATTTGGCCCAAACCT | 2996 | AATATTTT |
| | C | | GAGGTTT TGTGAGAC | | |
| | | | | | |
| | | | CTCCAAA ACACTCTG | | |
| | | | CCCGGTTT | | |
| GAM47 | LOC221035 | 3' | TCCCAGTATTAAACCT | 3593 | TTTTG A |
| | | | AGGTTTAATAT TG GA | | |
| | | | | | |
| | | | TCCAAATTATG AC CT | | |
| | | | __ C | | |
| GAM47 | LOC51611 | 3' | CGAAAAATTAAACCTCT | 1653 | AT |
| | | | AGAGGTTTAAT TTTTG | | |
| | | | | | |
| | | | TCTCCAAATTA AAAGC | | |
| | | | __ | | |
| GAM48 | AXUD1 | 3' | TTTATTCCATTTCTCTCT | 2309 | GA |
| | | | AGAGAGAAA GAATAAA | | |
| | | | | | |
| | | | TCTCTCTTT CTTATTT | | |
| | | | AC | | |
| GAM48 | BSN | 3' | ATTTTCTTTTGTCTCTCT | 1024 | G T |
| | | | AGAGAGAAA AGAA AAAAAT | | |
| | | | | | |

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|-------|---------------|----|-----------------------------|-----|-------|
| | | | TCTCTCTTT TTTT TTTTAA | | |
| | | | G C | | |
| GAM48 | DPYSL2 | 3' | AATATTTTCGTGTCTGTCTCTC 822 | A | GA TA |
| | T | | AGAGAGA AGA A AAAATATT | | |
| | | | | | |
| | | | TCTCTCT TCT T TTTTATAA | | |
| | | | G G_GC | | |
| GAM48 | EVA1 | 3' | AATGTGTTTACTCTCTTTCCTT 1250 | A | A A |
| | C | | GAG GAAAGAGA TAAA ATATT | | |
| | | | | | |
| | | | CTT CTTTCTCT ATTT TGTA | | |
| | | | C C G | | |
| GAM48 | PTMS | 3' | TTTGCTCTCTTTCTCCCT 959 | A | A |
| | | | AG GAGAAAGAGA TAAA | | |
| | | | | | |
| | | | TC CTCTTTCTCT GTTT | | |
| | | | C C | | |
| GAM48 | SELE | 3' | TTTTGTGGCTTTCTTTCT 748 | AGA | |
| | | | AGAGAGAAAAG ATAAAA | | |
| | | | | | |
| | | | TCTTTCTTTC TGTTTT | | |
| | | | GG_ | | |
| GAM48 | SLC7A6 | 3' | AATATTTTGTACCTTTCTCCT 1076 | A | AGA |
| | | | AG GAGAAAG ATAAAAATATT | | |
| | | | | | |
| | | | TC CTCTTTC TGTTTTTATAA | | |
| | | | _ CA_ | | |
| GAM48 | TGFBR2 | 5' | TTTCTTCTAGTTCTTTCT 1003 | AG | T |
| | | | AGAGAGAA AGAA AAA | | |
| | | | | | |
| | | | TCTTTCTT TCTT TTT | | |
| | | | GA C | | |
| GAM48 | DKFZP586N0721 | 5' | TTTTATTCCCTTTCCTCT 1627 | A | A |
| | | | AGAG GAAAG GAATAAAA | | |
| | | | | | |
| | | | TCTC CTTTC CTTATTTT | | |
| | | | _ C | | |
| GAM48 | DKFZp761J139 | 5' | TTTATTCTCTCTGTCTCT 2242 | GAA | |
| | | | AGAGA AGAGAATAAA | | |
| | | | | | |
| | | | TCTCT TCTCTTATTT | | |
| | | | GTC | | |
| GAM48 | FLJ10468 | 3' | TTTTATTCTCCTTTC 1779 | AAA | |
| | | | GAGAG GAGAATAAAA | | |
| | | | | | |
| | | | CTTTC CTCTTATTTT | | |
| | | | — | | |
| GAM48 | FLJ20485 | 3' | AATATTTTAAATCTCCTTTC 1874 | AAA | A_ |
| | T | | AGAGAG GAGA TAAAAATATT | | |
| | | | | | |

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|-------|----------|-----|------------------------------------|--|--|
| | | | TCTTTC CTCT ATTTTATAA | | |
| | | | ___ AAA | | |
| GAM48 | H2BFQ | 3' | ATATTTACTCTTCTGTC 2523 G AATAA | | |
| | | | GA AGAAAGAG AAATAT | | |
| | | | | | |
| | | | CT TCTTCTC TTTATA | | |
| | | | G A___ | | |
| GAM48 | KIAA0077 | 3' | TTTTATTCTCTCTCCCTTT 2774 A A | | |
| | | | AGAG GA AGAGAATAAAA | | |
| | | | | | |
| | | | TTTC CT TCTCTTATTT | | |
| | | | C C | | |
| GAM48 | KIAA0295 | 3' | TTTTTCCCTTTCTCTCT 2807 A T | | |
| | | | AGAGAGAAAG GAA AAA | | |
| | | | | | |
| | | | TCTCTCTTTC CTT TTT | | |
| | | | C T | | |
| GAM48 | KIAA0828 | 3' | AATATTTTGCTTCTTTCTTTC 3195 AATA | | |
| | | T | AGAGAGAAAGAG AAAATATT | | |
| | | | | | |
| | | | TCTTCTTTCTT TTTATAA | | |
| | | | CCG_ | | |
| GAM48 | KIAA1203 | 3' | AATATTTTATTCTTGAGTTAT 2921 GAGAAA | | |
| | | CT | AGA GAGAATAAAAAATATT | | |
| | | | | | |
| | | | TCT TTCTATTTTATAA | | |
| | | | ATTGAG | | |
| GAM48 | OSBPL8 | 3' | TTTTTATTATCCTCCTCTCT 1928 AAA G | | |
| | | | AGAGAG GA AATAAAAA | | |
| | | | | | |
| | | | TCTCTC CT TTATTTT | | |
| | | | CTC A | | |
| GAM48 | PAK6 | 3' | AATATTTTATGATTCTTCTGCT 1897 _ A AA | | |
| | | C | GAG AGAA GAG TAAAAATATT | | |
| | | | | | |
| | | | CTC TCTT CTT ATTTTATAA | | |
| | | | G _ AG | | |
| GAM48 | POLR3F | 3' | AATATTTTCACTGTTTCTTCTT 2547 A A | | |
| | | TCT | AGAGAGAA G GAATA AAAATATT | | |
| | | | | | |
| | | | TCTTCTT C CTTGT TTTATAA | | |
| | | | _ _ CAC | | |
| GAM48 | RNF11 | 3' | TTTATTCTCTTCTTCT 1495 G | | |
| | | | AGA AGAAAGAGAATAAA | | |
| | | | | | |
| | | | TCT TCTTCTCTTATTT | | |
| | | | - | | |
| GAM48 | SLC16A6 | 5' | TTTATTCTCTTCCCTTCT 1143 AGA | | |
| | | | AGAG AAGAGAATAAA | | |
| | | | | | |

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|-------|-----------|----|------------------------|------|---------|
| | | | TCTT TTCTCTTATTT | | |
| | | | CCC | | |
| GAM48 | LOC144321 | 3' | TTTTATTCCCTTCTCTC | 3267 | A A |
| | | | GAGAGAA G GAATAAAA | | |
| | | | | | |
| | | | CTCTCTT C CTTATTTT | | |
| | | | _ C | | |
| GAM48 | LOC150951 | 5' | ATATTTTATTTTCTTCCT | 3336 | A |
| | | | AG AAGAGAATAAAAATAT | | |
| | | | | | |
| | | | TC TTCTTTTATTTTATA | | |
| | | | C | | |
| GAM48 | LOC199920 | 5' | AATATTTTATTCTTTGATTCT | 3435 | AA |
| | | T | GAGAG AGAGAATAAAAATATT | | |
| | | | | | |
| | | | TTCTT TTTCTTATTTTATAA | | |
| | | | AG | | |
| GAM48 | LOC256435 | 3' | AATATTTTAAATGTTGTCTCT | 3675 | AAGAGAA |
| | | CT | AGAGAGA TAAAAATATT | | |
| | | | | | |
| | | | TCTCTCT ATTTTATAA | | |
| | | | GTTGTAA | | |
| GAM49 | ADAMTS5 | 3' | TATTTTCACAACTACTTTCTCT | 1352 | _ AATA_ |
| | | CT | AGAGAGAAAG AG AAAATA | | |
| | | | | | |
| | | | TCTCTCTTTC TC TTTTAT | | |
| | | | A AACAC | | |
| GAM49 | ADAT1 | 3' | TATTCCCAGCCTTTCTTTCTTC | 1404 | A_____ |
| | | | GAAGAGAGAAAG GAATA | | |
| | | | | | |
| | | | CTTCTTTCTTTC CTTAT | | |
| | | | CGACC | | |
| GAM49 | ADCY2 | 3' | TTTTATTTTCCTGTCTTC | 2711 | G AAA |
| | | | GAAGA AG GAGAATAAAA | | |
| | | | | | |
| | | | CTTCT TC CTTTATTTT | | |
| | | | G ____ | | |
| GAM49 | AHR | 3' | ATTTTGTACTCTCTTC | 840 | _ A |
| | | | GAAGAGAG AA GAGAAT | | |
| | | | | | |
| | | | CTTCTCTC TT TTTTAA | | |
| | | | A G | | |
| GAM49 | BSN | 3' | ATTTTCTTTTGTTCCTCTCT | 1025 | G T |
| | | | AGAGAGAAA AGAA AAAAAT | | |
| | | | | | |
| | | | TCTCTCTT TTTT TTTTAA | | |
| | | | G C | | |
| GAM49 | BSN | 3' | TCTCCCCCTTCTCTCTTC | 1026 | _____ |
| | | | GAAGAGAGAAA GAGA | | |
| | | | | | |

CTTCTCTCTTT CTCT
 CCCC
 GAM49 C7 3' TATTCCTTATTTCTCTTT 756 _ A
 GAAGAGAGA AAG GAATA
 ||||| ||| |||||
 TTTCTCTTT TTC CTTAT
 A _
 GAM49 CFTR 3' TATTCCTTTTTCTCTCCTC 753 A _
 GA GAGAGAAAGAG AATA
 || ||||| |||||
 CT CTCTCTTTTTTC TTAT
 C C
 GAM49 CHD2 3' ATATTTTTTCTGATCCCCCACT 813 AA__ GAAT_ |||
 CTCTCTTC AGA GA AAAAATA T
 || || ||||| |
 TCT CT TTTTAT A
 CACCCC AGTCT |||
 GAM49 CKN1 3' TATTTTATTCTTTCTTC 703 AG
 GAAGAGAGAA AGAATA
 ||||| |||||
 CTTCTTTCTT TTTTAT
 A_
 GAM49 CTH 5' TGTTCCTTTCTCTCTTC 867 A
 GAAGAGAG AAGAGAATA
 ||||| |||||
 CTTCTCTC TTTTCTTGT
 C
 GAM49 EVA1 3' ATTTTTATTTTTATGTCTCTC 1251 AA_
 GAGAGA GAGAATAAAAAT
 |||| |||||
 CTCTCT TTTTATTTTAA
 GTA
 GAM49 FBXL11 3' TTGTTCCCCCTCTCTCTTT 1426 AAGA
 GAAGAGAGA GAATAA
 ||||| |||||
 TTTCTCTCT CTTGTT
 CCCC
 GAM49 GATA3 3' TATTTTCCTTCTCTCTC 893 A A
 GA GAGAGAA GAGAATA
 || ||||| |||||
 CT CTCTCTT CTTTTAT
 _ C
 GAM49 GDI2 5' TTTTCCTCTCTTTCTCTT 832 AT
 GAGAGAAAGAGA AAAA
 ||||| |||||
 TTCTCTTTCTCT TTTT
 CC
 GAM49 HD 3' ATTCTCCCTTCTCTCTTT 899 A_
 GAAGAGAGAA GAGAAT
 ||||| |||||

| | | | | | |
|-------|---------|----|---------------------------|---------|--|
| | | | TTTCTCTCTT CTCTTA | | |
| | | | CC | | |
| GAM49 | HTR2C | 3' | TATTTTGTCTCCCTCCCTTC 781 | A AAA A | |
| | | | GAAG GAG GAGA TAAAAATA | | |
| | | | | | |
| | | | CTTC CTC CTCT GTTTTAT | | |
| | | | C C__ C | | |
| GAM49 | LGR6 | 3' | TTCTCTTCCCCTCTCTTC 3302 | A__ | |
| | | | GAAGAGAG AAGAGAA | | |
| | | | | | |
| | | | CTTCTCTC TTCTCTT | | |
| | | | CCC | | |
| GAM49 | LRP8 | 3' | TCTCTTATTTCTCTTTTC 2326 | ___ | |
| | | | GAAGAGAGAA AGAGA | | |
| | | | | | |
| | | | CTTTTCTCTT TCTCT | | |
| | | | TAT | | |
| GAM49 | LRP8 | 3' | TCTCTTATTTCTCTTTTC 1139 | ___ | |
| | | | GAAGAGAGAA AGAGA | | |
| | | | | | |
| | | | CTTTTCTCTT TCTCT | | |
| | | | TAT | | |
| GAM49 | MEF2C | 5' | TTTTTTTTCTCTCTCTCTCT 926 | _ A T | |
| | C | | GA AGAGAGA AGAGAA AAAAA | | |
| | | | | | |
| | | | CT TCTCTCT TCTCTT TTTT | | |
| | | | C C T | | |
| GAM49 | MSR1 | 3' | TATTTTGGTTTCTCTCT 929 | ___ | |
| | | | AGAGAGAAA GAGAATA | | |
| | | | | | |
| | | | TCTCTCTT TTTTAT | | |
| | | | GG | | |
| GAM49 | PCDH11X | 3' | TATTTTCACATTTTCTCTCT 2299 | ___ | |
| | | | AGAGAGAAA GAGAATA | | |
| | | | | | |
| | | | TCTCTCTT CTTTAT | | |
| | | | TACA | | |
| GAM49 | PCDH11X | 3' | TATTTTCACATTTTCTCTCT 2301 | ___ | |
| | | | AGAGAGAAA GAGAATA | | |
| | | | | | |
| | | | TCTCTCTT CTTTAT | | |
| | | | TACA | | |
| GAM49 | PCDH11Y | 3' | TATTTTCACATTTTCTCTCT 2303 | ___ | |
| | | | AGAGAGAAA GAGAATA | | |
| | | | | | |
| | | | TCTCTCTT CTTTAT | | |
| | | | TACA | | |
| GAM49 | PCMT1 | 3' | TATCTTCTGCTCTTTCTTC 1205 | A_ GA | |
| | | | GAAGAGAGA AGA ATA | | |
| | | | | | |

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|-------|---------------|----|----------------------------------|--|--|
| | | | CTTCTTTCT TCT TAT | | |
| | | | CG TC | | |
| GAM49 | PCNA | 3' | TATTTTTTTTCTCTATTC 939 G | | |
| | | | GAA AGAGAAAGAGAATA | | |
| | | | | | |
| | | | CTT TCTCTTTTTTTTAT | | |
| | | | A | | |
| GAM49 | PRELP | 3' | ATTCGTTTTCTCTCTCTC 950 _ A | | |
| | | | GA AGAGAGAAAG GAAT | | |
| | | | | | |
| | | | CT TCTCTCTTTT CTTA | | |
| | | | C G | | |
| GAM49 | PTMS | 3' | TTTGCTCTCTTTTCTCCCT 958 A A | | |
| | | | AG GAGAAAGAGA TAAA | | |
| | | | | | |
| | | | TC CTCTTTCTCT GTTT | | |
| | | | C C | | |
| GAM49 | SLC4A4 | 3' | TATTTTTATTCTCTTAAGTCTT 1054 GAGA | | |
| | T | | GAAGA AAGAGAATAAAAAATA | | |
| | | | | | |
| | | | TTTCT TTCTCTTATTTTAT | | |
| | | | GAA_ | | |
| GAM49 | TRPS1 | 5' | TATTCCTTTCTCTTTCTCTCT 1471 TAA | | |
| | | | AGAGAGAAAGAGAA AAATA | | |
| | | | | | |
| | | | TCTCTCTTTCTCTT TTTAT | | |
| | | | TCC | | |
| GAM49 | ARS2 | 5' | TTTTGTTGCGCTCTCTTC 1650 AAAGA | | |
| | | | GAAGAGAG GAATAAAA | | |
| | | | | | |
| | | | CTTCTCTC CTTGTTTT | | |
| | | | CG__ | | |
| GAM49 | BRD4 | 3' | TATTTTTTAATTCTCTCTTC 2368 A_ | | |
| | | | GAAGAGAGAA GAGAATA | | |
| | | | | | |
| | | | CTTCTCTCTT TTTTAT | | |
| | | | AA | | |
| GAM49 | CAPN13 | 3' | TATTTTACCTGCCTCTCTTC 2485 AA _ | | |
| | | | GAAGAGAG AG AGAATA | | |
| | | | | | |
| | | | CTTCTCTC TC TTTTAT | | |
| | | | CG CA | | |
| GAM49 | CECR6 | 3' | TTACCCTCTCCTCTCTTC 2218 AA AA | | |
| | | | GAAGAGAG AGAG TAA | | |
| | | | | | |
| | | | CTTCTCTC TCTC ATT | | |
| | | | C_ CC | | |
| GAM49 | DKFZP434I0714 | 5' | TTTTTGTTTTTCCCCCTCTTC 3362 AGAAA | | |
| | | | GAAGAG GAGAATAAAAA | | |
| | | | | | |

CTTCTC TTTTGTTTT
 CCCC_
 GAM49 DKFZP564G092 5' TATTCCTCTTTCTTTTC 1639 A A
 GAAGAGAGA AG GAATA
 ||||| || ||||
 CTTTCTTT TC CTTAT
 C _
 GAM49 DKFZp564K142 3' TATCCTCTTAACCTTCTCTTC 2231 A__ A
 GAAGAGAG AAGAG ATA
 ||||| |||| ||
 CTTCTCTT TTCTC TAT
 CCAA C
 GAM49 DKFZp566D234 3' TATTTTTTTTCTCTGTC 2612 AG
 GA AGAGAAAGAGAATA
 || |||||
 CT TCTCTTTTTTTTAT
 G_
 GAM49 DKFZP566I1024 3' TTTTAAATCTATTCTCTC 2878 _ GAA
 GAGAGAA AGA TAAAA
 ||||| || ||||
 CTCTCTT TCT ATTTT
 A AAA
 GAM49 EPI64 3' TATTTTGACATCTCTCTCTCTT 3681 A GAATA
 C GAAGAGAGA AGA AAAATA
 ||||| || ||||
 CTTCTCTCT TCT TTTTAT
 C ACAG_
 GAM49 FLJ00012 3' TATTTTTATCTCTATCTCCT 2985 A A A
 AG GAGA AGAGA TAAAAATA
 || |||| |||||
 TC CTCT TCTCT ATTTTTAT
 _ A _
 GAM49 FLJ10460 3' ATTTTATTCTACCTTTC 1778 AAAG
 GAGAG AGAATAAAAAAT
 |||| |||||
 CTTTC TCTATTTTAA
 CA_
 GAM49 FLJ10687 3' TTTATTCATTTCTCTCCTC 1793 A GA
 GA GAGAGAAA GAATAAA
 || ||||| |||||
 CT CTCTCTTT CTTATTT
 C A_
 GAM49 FLJ10738 3' TATTTTACTCTCCCTCTTC 1799 AGAAA A
 GAAGAG GAGA TAAAAATA
 |||| |||||
 CTTCTC CTCT ATTTTTAT
 C__ C
 GAM49 FLJ13158 3' TTCTCTCCCTTTCTCTTC 2109 A__
 GAAGAGAGA AGAGAA
 ||||| |||||

CTTCTCTTT TCTCTT
 CCC
 GAM49 FLJ20294 5' TATTCCTGTCTCCTCTTT 1747 _ A A
 GAAGAG AGA AG GAATA
 ||||| ||| || |||||
 TTTCTC TCT TC CTTAT
 C G _
 GAM49 FLJ21657 3' TATTCTACTTCTCTCTTC 1991 AG
 GAAGAGAGAA AGAATA
 ||||| |||||
 CTTCTCTCTT TCTTAT
 CA
 GAM49 GT650 3' TATTTCTGATTCTCCCTCTCTT 2341 AAA AA_
 C GAAGAGAG GAGAAT AAATA
 ||||| ||||| |||||
 CTTCTCTC CTCTTA TTTAT
 C_ GTC
 GAM49 HEY2 3' TATTCTCTTTTTTTTCTC 1420 AG
 GA AGAGAAAGAGAATA
 || ||||| |||||
 CT TTTTTTCTCTTAT
 CT
 GAM49 HIC2 3' ATTTTTTTTCTCTCTCTTTTC 2717 A T
 GAAGAGAGA AGAGAA AAAAAT
 ||||| ||||| |||||
 CTTTTCTCT TCTTTT TTTTA
 C _
 GAM49 HOOK3 3' ATTTTGAGGACTTTTTCTCTCT 2249 AATA_
 AGAGAGAAAGAG AAAAT
 ||||| |||||
 TCTCTCTTTTC TTTTA
 AGGAG
 GAM49 IL1RAPL1 5' TATTCTATTTTCCCCTCTCTT 1488 AAA A
 T GAAGAGAG GAGAATAA AATA
 ||||| ||||| |||||
 TTTCTCTC CTTTATT TTAT
 CC_ C
 GAM49 KALI 3' TTTTGTCTTGTCCTCTC 2347 AAA_
 GAGAG GAGAATAAAA
 |||| |||||
 CTCTC TTCTTGTTTT
 CCTG
 GAM49 KIAA0077 3' TTTTATTCTCTCTCCCTT 2773 A AA
 GAAG GAGA GAGAATAAAA
 ||| ||| |||||
 TTTC CTCT CTCTTATTT
 C _
 GAM49 KIAA0089 3' ATTTTtagcctcttttctcttc 2873 A AA
 GAAGAGAGAA GAG TAAAAAT
 ||||| ||| |||||

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|-------|----------|----|-----------------------------|-------|
| | | | CTTCTCTTTT CTC ATTTTTA | |
| | | | — CG | |
| GAM49 | KIAA0286 | 3' | TATTTTCACCCTCTTTTC 2814 | AAA |
| | | | GAAGAGAG GAGAATA | |
| | | | | |
| | | | CTTTTCTC CTTTAT | |
| | | | CCA | |
| GAM49 | KIAA0295 | 3' | TTTTTTCCTTTCTCTCT 2808 | A T |
| | | | AGAGAGAAAG GAA AAA | |
| | | | | |
| | | | TCTCTCTTTC CTT TTT | |
| | | | C T | |
| GAM49 | KIAA0342 | 3' | TATTCTCATTACTTCTCTTT 2890 | — A |
| | | | GAAGAGA G AA GAGAATA | |
| | | | | |
| | | | TTTCTCT C TT CTCTTAT | |
| | | | T A A | |
| GAM49 | KIAA0564 | 3' | TATTTTATTTTCTCCCTGCTC 2743 | — AA |
| | | | GAG AG AGAGAATAAAAATA | |
| | | | | |
| | | | CTC TC TCTTTATTTTAT | |
| | | | G CC | |
| GAM49 | KIAA0630 | 3' | TATTTTAAAAGTCTTCTCT 3465 | GAAT— |
| | CT | | AGAGAGAAAGA AAAAATA | |
| | | | | |
| | | | TCTCTCTTCT TTTTAT | |
| | | | GAAAAT | |
| GAM49 | KIAA0662 | 3' | TGTTCTCTCTCTCTCTT 3215 | A |
| | | | GAAGAGAGA AGAGAATA | |
| | | | | |
| | | | TTTCTCTCT TCTCTTGT | |
| | | | C | |
| GAM49 | KIAA0830 | 3' | TTTGCTTCTCTTTCTCCT 2866 | A — |
| | | | AG GAGAAAGAGAA TAAA | |
| | | | | |
| | | | TC CTCTTTCTCTT GTTT | |
| | | | — C | |
| GAM49 | KIAA0964 | 3' | ATTCTTATGTTTTTCTCTTTTC 1579 | GA A |
| | | | GAAGAGAGAAAGA ATAA AAT | |
| | | | | |
| | | | CTTTTCTCTTTT TATT TTA | |
| | | | G_ C | |
| GAM49 | KIAA1076 | 3' | TATTTTGGCTTTCTCTC 2723 | AGAAT |
| | | | GAGAGAAAG AAAAATA | |
| | | | | |
| | | | CTCTCTTTC TTTTAT | |
| | | | GT— | |
| GAM49 | KIAA1181 | 3' | ATTCCTCTTCTCTCTC 2817 | A — |
| | | | GAAGAGAG AAGAG AAT | |
| | | | | |

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|-------|----------|----|-----------------------------|--------|----|
| | | | CTTCTCTC TTCTC TTA | | |
| | | | C C | | |
| GAM49 | KIAA1319 | 3' | TATTTTGTCTTCTTCCTTTC 1925 | A | GA |
| | | | GAGAG AAGA ATAAAAATA | | |
| | | | | | |
| | | | CTTTC TTCT TGTTTTAT | | |
| | | | C TC | | |
| GAM49 | KIAA1522 | 3' | ATTCTCTGACCTTTCTCTCT 2708 | _____ | |
| | | | AGAGAGAA AGAGAAT | | |
| | | | | | |
| | | | TCTCTCTT TCTCTTA | | |
| | | | TCCAG | | |
| GAM49 | KIAA1906 | 3' | ATTTTATTCTCTGCTT 2971 | AA | |
| | | | GAG AGAGAATAAAAAAT | | |
| | | | | | |
| | | | TTC TCTCTTATTTTAA | | |
| | | | G_ | | |
| GAM49 | MAPK6 | 5' | TATTTTCTTCTCCCTTT 952 | A | AG |
| | | | GAAG GAGAA AGAATA | | |
| | | | | | |
| | | | TTTC CTCTT TTTTAT | | |
| | | | C CT | | |
| GAM49 | MGC13138 | 3' | TATTTTATTCTTGTGACCCTC 2332 | AGAAA_ | |
| | | | GAG GAGAATAAAAAATA | | |
| | | | | | |
| | | | CTC TTCTTATTTTAT | | |
| | | | CCAGTG | | |
| GAM49 | MGC2742 | 5' | TATTTCTTTTCTCTCTTC 2040 | AG | |
| | | | GAAGAGAGAAAG AATA | | |
| | | | | | |
| | | | CTTCTCTCTTTT TTAT | | |
| | | | CT | | |
| GAM49 | MGC32043 | 3' | TATTCCTGTTTTCTCTTT 2486 | _ A | |
| | | | GAAGAGAGAA AG GAATA | | |
| | | | | | |
| | | | TTTCTCTTTT TC CTTAT | | |
| | | | G _ | | |
| GAM49 | NFAT5 | 3' | TATTCCTTTTTCTCTTC 2452 | A | |
| | | | GAAGAGAGAAAG GAATA | | |
| | | | | | |
| | | | CTTCTCTTTTTC CTTAT | | |
| | | | C | | |
| GAM49 | OSBPL8 | 3' | TTTTTATTATCCTCCTCTCTTC 1929 | AAA G | |
| | | | GAAGAGAG GA AATAAAAA | | |
| | | | | | |
| | | | CTTCTCTC CT TTATTTT | | |
| | | | CTC A | | |
| GAM49 | RAB10 | 3' | TGTTCTGCTTTCCTCCTC 3337 | A AG _ | |
| | | | GA GAG AAAG AGAATA | | |
| | | | | | |

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|-------|-----------|----|-----------------------------|----------|--|
| | | | CT CTC TTTC TCTTGT | | |
| | | | C CT G | | |
| GAM49 | RANBP1 | 3' | TATTTTCTTTTCCTCTCTTT 969 | — | |
| | | | GAAGAGAG AAAGAGAATA | | |
| | | | | | |
| | | | TTTCTCTC TTTCTTTTAT | | |
| | | | CT | | |
| GAM49 | RASSF2 | 3' | TATTTTCACAATCCTCTCTTC 1537 | AAA— | |
| | | | GAAGAGAG GAGAATA | | |
| | | | | | |
| | | | CTTCTCTC CTTTTAT | | |
| | | | CTAACA | | |
| GAM49 | STK22D | 3' | TATTTTCATCAGCTTCTCTCT 2226 | AG AATA— | |
| | CT | | AGAGAGAA AG AAAATA | | |
| | | | | | |
| | | | TCTCTCTT TC TTTTAT | | |
| | | | CT GACTAC | | |
| GAM49 | SYNJ2 | 3' | ATTTTATAGGTTTCTCTTC 2606 | AGAGAA | |
| | | | GAAGAGAGAA TAAAAAT | | |
| | | | | | |
| | | | CTTCTCTTTT ATTTTAA | | |
| | | | GG— | | |
| GAM49 | TBLR1 | 3' | TATTCTTTTTTTCCCTTC 2079 | A | |
| | | | GAAG GAGAAAGAGAATA | | |
| | | | | | |
| | | | CTTC CTTTTTTTCTTAT | | |
| | | | C | | |
| GAM49 | TM9SF1 | 3' | TATTGCTGTTCTCTCCCTTTCT 1296 | AA AA | |
| | TC | | GAAGAGAG AGAGAATA AATA | | |
| | | | | | |
| | | | CTTCTTTC TCTCTTGT TTAT | | |
| | | | CC CG | | |
| GAM49 | ULK2 | 3' | TATTCTATCCTCTCCTCTTC 1523 | — AAG— | |
| | | | GAAGAG AGA AGAATA | | |
| | | | | | |
| | | | CTTCTC TCT TCTTAT | | |
| | | | C CCTA | | |
| GAM49 | UNC5D | 3' | TTATTCTTTCTTCCTCTTC 2393 | A — | |
| | | | GAAGAG GAA AGAGAATAA | | |
| | | | | | |
| | | | CTTCTC CTT TTTCTTATT | | |
| | | | — C | | |
| GAM49 | LOC121219 | 5' | TTATTAACCTCTCTCTTT 2988 | A — | |
| | | | GAAGAGAGAA GAG AATAA | | |
| | | | | | |
| | | | TTTCTCTCTT CTC TTATT | | |
| | | | C AA | | |
| GAM49 | LOC128077 | 3' | ATTTGTTTTCTCTTTCTTCCT 3006 | A TAA | |
| | C | | GA GAGAGAAAGAGAA AAAT | | |
| | | | | | |

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|-------|--------------|-----------------------------|-----|--------|
| | | CTCTTTCTTTCTCTT TTTA | | |
| | | C TTG | | |
| GAM49 | LOC143451 3' | TTCTCTCCTTCTCTTC 3058 | — | |
| | | GAAGAGAGAA AGAGAA | | |
| | | | | |
| | | CTTCTCTCTT TCTCTT | | |
| | | CC | | |
| GAM49 | LOC145125 3' | TTCTCTCCTTCTCTTC 3075 | — | |
| | | GAAGAGAGAA AGAGAA | | |
| | | | | |
| | | CTTCTCTCTT TCTCTT | | |
| | | CC | | |
| GAM49 | LOC149351 3' | ATTTTTCAGATCTTTCTCTTT 3131 | | GAAT |
| | | AGAGAGAAAGA AAAAAT | | |
| | | | | |
| | | TTTCTCTTTCT TTTTAA | | |
| | | AGAC | | |
| GAM49 | LOC149722 5' | TATTCTTTCTTTCTCTTC 3312 | | A |
| | | GAAGAGAGA AGAGAATA | | |
| | | | | |
| | | CTTCTCTTT TTTCTTAT | | |
| | | C | | |
| GAM49 | LOC149837 5' | TATTCCTGTCTTTCTCTCT 3318 | — | |
| | | AGAGAGAAAGA GAATA | | |
| | | | | |
| | | TCTCTCTTTCT CTTAT | | |
| | | GTC | | |
| GAM49 | LOC150054 3' | TATTCTGTCTTTCTCCTC 3323 | — — | |
| | | GAG AGAAAGA GAATA | | |
| | | | | |
| | | CTC TCTTTCT CTTAT | | |
| | | C GT | | |
| GAM49 | LOC150150 5' | TTTTGTGCCTCTCTTTCTTC 3324 | | AA A_ |
| | | GAAGAGAGA GAG ATAAAA | | |
| | | | | |
| | | CTTCTTTCT CTC TGTTTT | | |
| | | — CG | | |
| GAM49 | LOC150225 3' | TATTTTGTTTCCCTCTTC 3327 | | A G |
| | | GAAGAG GAAA AGAATA | | |
| | | | | |
| | | CTTCTC CTTT TTTTAT | | |
| | | C G | | |
| GAM49 | LOC152816 3' | TATTTTATCCTCAACCTCTT 3364 | | AAA A |
| | | GAGAG GAG ATAAAAATA | | |
| | | | | |
| | | TTCTC CTC TATTTTAT | | |
| | | CAA C | | |
| GAM49 | LOC155038 3' | ATTGCGTTTCTCTTTCTCCTTC 3198 | | A TAAA |
| | | GAAG GAGAAAGAGAA AAT | | |
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|-------|--------------|----------------------------|--------|
| | | CTTC CTCTTTCTCTT TTA | |
| | | — TGCG | |
| GAM49 | LOC158629 3' | TATTTTCTTTCCCTCTC 3394 | A A |
| | | GA GAG GAAAGAGAATA | |
| | | | |
| | | CT CTC CTTTCTTTTAT | |
| | | — C | |
| GAM49 | LOC158943 3' | TATTTTCTTTTCCTCTCTT 2572 | — |
| | | GAAGAGAG AAAGAGAATA | |
| | | | |
| | | TTTCTCTC TTTCTTTTAT | |
| | | CT | |
| GAM49 | LOC170082 3' | ATTCTTTTCCCTCTCTTTTC 3254 | — |
| | | GAAGAGAGA AAGAGAAT | |
| | | | |
| | | CTTTTCTCT TTTCTTA | |
| | | CCCC | |
| GAM49 | LOC199920 5' | TATTTTATTCTTTGATTCTTC 3436 | AGAA |
| | | GAAGAG AGAGAATAAAAATA | |
| | | | |
| | | CTTCTT TTTCTTATTTTAT | |
| | | AG— | |
| GAM49 | LOC219667 3' | ATTTTGTATCTCTCTTC 3516 | AAGAG |
| | | GAAGAGAGA AATAAAAT | |
| | | | |
| | | CTTCTCTCT TTGTTTTTA | |
| | | A— | |
| GAM49 | LOC220279 5' | TATTTTCTTCCCTACCTCTCT 3653 | A— |
| | TC | GAAGAGAG AAGAGAATA | |
| | | | |
| | | CTTCTCTC TTCTTTTAT | |
| | | CATCCCC | |
| GAM49 | LOC221830 3' | TATTTTCTTTTCTTTCTTC 3567 | — |
| | | GAAGAGAGAAA GAGAATA | |
| | | | |
| | | CTTCTTTCTTT CTTTAT | |
| | | T | |
| GAM49 | LOC222166 3' | ATTTTACCTTCTCTCTT 3635 | AG— |
| | | GAAGAGAGAA AGAAT | |
| | | | |
| | | TTTCTCTCTT TTTA | |
| | | CCA | |
| GAM49 | LOC254440 3' | TTCTCTCCTTCTCTCTC 3729 | — |
| | | GAAGAGAGAA AGAGAA | |
| | | | |
| | | CTTCTCTCTT TCTCTT | |
| | | CC | |
| GAM49 | LOC51123 3' | ATTTTATGCTGTTCCCTCTT 2571 | A AG A |
| | | AAGAG GAA AG ATAAAAAT | |
| | | | |

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|-------|----------|------|----------------------------|--------|--------|
| | | | TTCTC CTT TC TATTTTTA | | |
| | | | C G_ G | | |
| GAM49 | LOC51596 | 5' | TATTTTCCAAGTTTCTCTCTC 1651 | A | _____ |
| | | | GA GAGAGAAA GAGAATA | | |
| | | | | | |
| | | | CTCTCTCTT CTTTAT | | |
| | | | _ GAAC | | |
| GAM49 | LOC84570 | 5' | TTTCGTTTTCTCTCTCTC 2257 | AA | TA |
| | | | GAAGAGAGA GAGAA AAA | | |
| | | | | | |
| | | | CTTCTCTCT CTTT TTT | | |
| | | | C_ GC | | |
| GAM49 | LOC92710 | 5' | TATTTTTATGCCTCTGTCTC 2885 | A | A_ |
| | | | GAGA AGAG ATAAAAATA | | |
| | | | | | |
| | | | CTCT TCTC TATTTTTAT | | |
| | | | G CG | | |
| GAM50 | FANCF | 3' | GTCCCTTTAAAGCATTGA 1997 | ATATAT | |
| | | | TCAATGTTTTAAA GGAC | | |
| | | | | | |
| | | | AGTTACGAAATTT CCTG | | |
| | | | C_____ | | |
| GAM50 | GPR65 | 5' | TCCACCCTTTAAAGCATTGA 2544 | A | TATA |
| | | | TCAATGTTTT AAA TGGA | | |
| | | | | | |
| | | | AGTTACGAAA TTT ACCT | | |
| | | | A CCC_ | | |
| GAM50 | LMNB1 | 3' | TGTCCATACACTTTGTTGCA 1226 | TT | ATA |
| | | | TGT TAAA TATGGACA | | |
| | | | | | |
| | | | ACG GTTT ATACCTGT | | |
| | | | TT CAC | | |
| GAM50 | MEN1 | 5' | CATAATATTTTAAACATT 3600 | _ | |
| | | | AATGTTTTAAATAT ATG | | |
| | | | | | |
| | | | TTACAAAATTTTATA TAC | | |
| | | | A | | |
| GAM50 | PLAG1 | 3' | TGTCCATATACCAGATTTAAAA 944 | A_____ | |
| | | TATT | AATGTTTTAAA TATATGGACA | | |
| | | | | | |
| | | | TTATAAAATTT ATATACCTGT | | |
| | | | AGACC | | |
| GAM50 | S100A11 | 3' | TGTCACCTTTTTTAAACATGA 1231 | A | TATATG |
| | | | TCA TGTTTTAAAA GACA | | |
| | | | | | |
| | | | AGT ACAAATTTT CTGT | | |
| | | | _ TTCA_ | | |
| GAM50 | SLC9A6 | 3' | TCCAGTTAGAACATTGA 1290 | AATATA | |
| | | | TCAATGTTTTAA TGGA | | |
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|-------|----------|----|------------------------|------|-----------|
| | | | AGTTACAAGATT | ACCT | |
| | | | G_____ | | |
| GAM50 | SOD2 | 3' | TCCATATACTTTGGGGACTTG | 766 | T TA _ |
| | | | CAA GTTT AAA TATATGGA | | |
| | | | | | |
| | | | GTT CAGG TTT ATATACCT | | |
| | | | _ GG C | | |
| GAM50 | BIRC2 | 5' | TATATTTTTTAAAACATTGA | 2784 | T |
| | | | TCAATGTTTTTAAAA ATATG | | |
| | | | | | |
| | | | AGTTACAAAATTTT TATAT | | |
| GAM50 | CXorf1 | 5' | TGTCCATAGAAAAAATATT | 1145 | AAAATA |
| | | | AATGTTTT TATGGACA | | |
| | | | | | |
| | | | TTATAAAA ATACCTGT | | |
| | | | AAG_____ | | |
| GAM50 | KIAA0367 | 3' | TGTCCCACAATGCCTAAAACAT | 2787 | AAATATAT_ |
| | | | TGA TCAATGTTTTA GGACA | | |
| | | | | | |
| | | | AGTTACAAAAT CCTGT | | |
| | | | CCGTAACAC | | |
| GAM50 | KIAA1321 | 3' | TCCTTGAGCTTTAAAGCATTGA | 2627 | ATATAT |
| | | | TCAATGTTTTTAAA GGA | | |
| | | | | | |
| | | | AGTTACGAAATTT CCT | | |
| | | | CGAGTT | | |
| GAM50 | KIAA1718 | 3' | TGTATTTTAAAATATTGA | 2686 | |
| | | | TCAATGTTTTTAAAATATA | | |
| | | | | | |
| | | | AGTTATAAAAATTTTATGT | | |
| GAM50 | KIAA1789 | 5' | TGTCCCTGCCCTAGAAACATTG | 2781 | AAAATATAT |
| | | | A TCAATGTTTT GGACA | | |
| | | | | | |
| | | | AGTTACAAAG CCTGT | | |
| | | | ATCCCGTC_ | | |
| GAM50 | PRO2964 | 3' | CAAGTATTTTAAAACACTG | 1842 | A A |
| | | | CA TGTTTTTAAAATAT TG | | |
| | | | | | |
| | | | GT ACAAATTTTATG AC | | |
| | | | C A | | |
| GAM50 | SLC17A6 | 3' | TGTCCATACACAGAAACAT | 1912 | AAAATA |
| | | | ATGTTTT TATGGACA | | |
| | | | | | |
| | | | TACAAAG ATACCTGT | | |
| | | | ACAC_____ | | |
| GAM50 | TRAF3 | 5' | CATTTTATTTTAAAACGTTGA | 2542 | T_ |
| | | | TCAATGTTTTTAAAATA ATG | | |
| | | | | | |

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|-------|-----------|----|-----------------------------|-----------|
| | | | AGTTGCAAAATTTTAT TAC | |
| | | | TT | |
| GAM50 | LOC151361 | 3' | TGTCTGTGTTTTTAAAC 3344 | T |
| | | | GTTTTAAAA ATATGGACA | |
| | | | | |
| | | | CAAAATTTT TGTGTCTGT | |
| | | | — | |
| GAM50 | LOC158714 | 3' | TCCACACATTTAAACATTGA 3224 | ATATA |
| | | | TCAATGTTTTTAAA TGGA | |
| | | | | |
| | | | AGTTACAAAATTT ACCT | |
| | | | ACAC_ | |
| GAM50 | LOC219667 | 3' | TATACCTTAGAACATTGA 3518 | AA |
| | | | TCAATGTTTTTAA TATA | |
| | | | | |
| | | | AGTTACAAGATT ATAT | |
| | | | CC | |
| GAM50 | LOC91565 | 3' | TCCATTTTAAACATT 2749 | ATAT |
| | | | AATGTTTTTAAA ATGGA | |
| | | | | |
| | | | TTACAAAATTT TACCT | |
| | | | — | |
| GAM51 | C1orf1 | 5' | TATGCTGACAGAAGAACCA 809 | CC A A |
| | | | TGGTTCTTT GT CA CATA | |
| | | | | |
| | | | ACCAAGAAG CA GT GTAT | |
| | | | A_ _ C | |
| GAM51 | LRAT | 3' | AGTATGCATACATAAAAGCAAC 2556 | _ CC_ CAA |
| | CA | | TGGTTCTTT GTA CATACT | |
| | | | | |
| | | | ACCAA GAAA CAT GTATGA | |
| | | | C ATA AC_ | |
| GAM51 | MYBL1 | 3' | AGTATGTTATACAAATGCCA 2679 | TCTTCC C |
| | | | TGGT GTA AACATACT | |
| | | | | |
| | | | ACCG CAT TTGTATGA | |
| | | | TAAA_ A | |
| GAM51 | KIAA1028 | 3' | TATGTCTGCATTGAAAAGAACC 3547 | C TA_ _ |
| | A | | TGGTTCTTT CG CA ACATA | |
| | | | | |
| | | | ACCAAGAAA GT GT TGTAT | |
| | | | A TAC C | |
| GAM51 | MGC2488 | 3' | TGTAGTGGAAGAAGCAT 2045 | G _ |
| | | | ATG TTCTTTCCG TACA | |
| | | | | |
| | | | TAC AAGAAAGGT ATGT | |
| | | | G G | |
| GAM52 | CX3CR1 | 3' | ACTGCCTACTGCATCGAGTCA 2891 | TCCCTTAA |
| | | | TGACTCG TAGGCAGT | |
| | | | | |

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|-------|-----------|----|-------------------------|---------------------|-----------|
| | | | ACTGAGC | ATCCGTCA | |
| | | | TACGTC__ | | |
| GAM52 | WNT14 | 3' | CTGCAAGGGACGAGTC | 1014 | AATAG |
| | | | GACTCGTCCCTT | GCAG | |
| | | | | | |
| | | | CTGAGCAGGGAA | CGTC | |
| GAM52 | FLJ20275 | 3' | TACTGCCTTCATAAAGATCAAGT | 1745 | CGTCC AT_ |
| | | | CA | TGACT CTTA AGGCAGTA | |
| | | | | | |
| | | | ACTGA | GAAT TCCGTCAT | |
| | | | ACTA_ | ACT | |
| GAM52 | FLJ22390 | 5' | TACTGCCTATCAAACG | 2002 | CCC A |
| | | | CGT TT | ATAGGCAGTA | |
| | | | | | |
| | | | GCA | AA TATCCGTCAT | |
| | | | __ | C | |
| GAM53 | LOC120864 | 5' | CAAGGTCCAAACTGATATAA | 2986 | CGTAG |
| | | | TTGTATCAGTTT | TCTTG | |
| | | | | | |
| | | | AATATAGTCAAA | GGAAC | |
| | | | CCT__ | | |
| GAM54 | KIAA0626 | 3' | AACATCAGGGTGCAGAATTGAT | 1954 | C_ A_ |
| | | | ATCGATTC | CAT TGATGTT | |
| | | | | | |
| | | | TAGTTAAG | GTG ACTACAA | |
| | | | AC | GG | |
| GAM54 | KIAA1239 | 3' | AACATCATGATTATTGATG | 2914 | TCCCA |
| | | | CATCGAT | TATGATGTT | |
| | | | | | |
| | | | GTAGTTA | GTACTACAA | |
| | | | TTA__ | | |
| GAM54 | LOC201475 | 5' | AACATCATATATTTTGATGTTA | 3428 | TTCCC |
| | | | TAACATCGA | ATATGATGTT | |
| | | | | | |
| | | | ATTGTAGTT | TATACTACAA | |
| | | | TTA__ | | |
| GAM55 | ARCN1 | 3' | CCCATTTCCTTCCAGTCA | 844 | GAAGT CA |
| | | | TGATTGGA | AGGAAA GG | |
| | | | | | |
| | | | ACTGACCT | TCCTTT CC | |
| | | | __ | AC | |
| GAM55 | CTSK | 3' | TCCTACTTTGCTTCTCTCCACC | 736 | AT |
| | | | CA | TG TGGAGA AGTAGGA | |
| | | | | | |
| | | | AC | ACCTCT TCATCCT | |
| | | | CC | CTTCGTT | |
| GAM55 | HMG20A | 3' | TCCTATTTCCCTGCCATCA | 1800 | T__ A |
| | | | TGAT | GG GAAGTAGGA | |
| | | | | | |

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|-------|----------|----|-----------------------------|-----------|--|
| | | | ACTA CC CTTTATCCT | | |
| | | | CCGT _ | | |
| GAM55 | PRDM2 | 3' | TCCTGTTTCCCACCCAG 1415 | AGAA A | |
| | | | TTGG GT GGAAACAGGA | | |
| | | | | | |
| | | | GACC CA CCTTTGTCCT | | |
| | | | ____ C | | |
| GAM55 | RNMT | 3' | CCTGCCTATCCTCTCCGATCA 1060 | A_ AAA | |
| | | | TGATTGGAGA GTAGG CAGG | | |
| | | | | | |
| | | | ACTAGCCTCT TATCC GTCC | | |
| | | | CC ____ | | |
| GAM55 | SCAP1 | 3' | TCCCACTCCCTACTTCTGCCA 1052 | _ AAACA | |
| | | | TGG AGAAGTAGG GGA | | |
| | | | | | |
| | | | ACC TCTTCATCC CCT | | |
| | | | G CTCAC | | |
| GAM55 | USH3A | 5' | CCTATTTTATTTCTCCATCA 2355 | T AAC | |
| | | | TGAT GGAGAAGTAGGA AGG | | |
| | | | | | |
| | | | ACTA CCTCTTTATTT TCC | | |
| | | | _ A_ | | |
| GAM55 | VAT1 | 3' | TCCTGTTTCCCACCTCCTTCTC 1292 | TA____ | |
| | C | | GGAGAAG GGAAACAGGA | | |
| | | | | | |
| | | | CCTCTTC CCTTTGTCCT | | |
| | | | CTCCAC | | |
| GAM55 | AIF1 | 5' | CCTGCTGAAAACCCTCCAGTCA 2297 | A_____ | |
| | | | TGATTGGAG AGTAGG | | |
| | | | | | |
| | | | ACTGACCTC TCGTCC | | |
| | | | CCAAAAG | | |
| GAM55 | CPLX1 | 3' | CCTGTTTCTCCTCCATTCA 1317 | T AAGTA | |
| | | | TGA TGGAG GGAAACAGG | | |
| | | | | | |
| | | | ACT ACCTC TCTTTGTCC | | |
| | | | T C_ | | |
| GAM55 | CXYorf1 | 3' | CCTGTTCCCCACCTCCCGGCTC 3228 | _ A A A A | |
| | | | GA TTGG GA GT GG AACAGG | | |
| | | | | | |
| | | | CT GGCC CT CA CC TTGTCC | | |
| | | | C _ C C C | | |
| GAM55 | FLJ12221 | 3' | CCCACCCTTGCTCTCCAATTA 2637 | A AAACA | |
| | | | TGATTGGAGA GTAGG GG | | |
| | | | | | |
| | | | ATTAACCTCT CGTTC CC | | |
| | | | _ CCAC_ | | |
| GAM55 | FLJ20207 | 3' | CCTGCCCTGCTTCCCCACCCA 1741 | AT A AAA | |
| | | | TG TGG GAAGTAGG CAGG | | |
| | | | | | |

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|-------|-------------|------------------------|------|-------|-------|
| | | AC ACC CTTCTGTC | GTCC | | |
| | | CC C C__ | | | |
| GAM55 | FLJ22215 3' | CCTGCCCCCTACCCTGTTCTCC | 3715 | ___ | AAA |
| | | GGAGAA GTAGG CAGG | | | |
| | | | | | |
| | | CCTCTT CATCC GTCC | | | |
| | | GTCC CCC | | | |
| GAM55 | FLJ31547 3' | TCCCATAATTTCTCCCGCAATC | 2511 | ___ | A__ |
| | A | TGATT GGAGAAGT GGA | | | |
| | | | | | |
| | | ACTAA CCTCTTTA CCT | | | |
| | | CGC ATAC | | | |
| GAM55 | HSCBCIP1 3' | TCCTACCTATGTCTTCTCCAAT | 3449 | ___ | AAAC |
| | | ATTGGAGAAG TAGG AGGA | | | |
| | | | | | |
| | | TAACCTCTTC ATCC TCCT | | | |
| | | TGT A__ | | | |
| GAM55 | KIAA0515 5' | TCCTACCAGAACTCCTCCGATC | 2670 | A A__ | AAAC |
| | A | TGATTGGAG AGT GG AGGA | | | |
| | | | | | |
| | | ACTAGCCTC TCA CC TCCT | | | |
| | | C AGA A__ | | | |
| GAM55 | KIAA1514 3' | CCTGCTCAACTTCTCCA | 1877 | A | AAA |
| | | TGGAGAAGT GG CAGG | | | |
| | | | | | |
| | | ACCTCTTCA CT GTCC | | | |
| | | A C__ | | | |
| GAM55 | KIAA1553 3' | TCCTCACTTCTCCATCCA | 3544 | AT | _ |
| | | TG TGGAGAAGT AGGA | | | |
| | | | | | |
| | | AC ACCTCTTCA TCCT | | | |
| | | CT C | | | |
| GAM55 | KIAA1656 3' | CCCACTTCCTTCCAGTCA | 2730 | ___ | A |
| | | TGATTGGA GAAGT GG | | | |
| | | | | | |
| | | ACTGACCT CTTCA CC | | | |
| | | TC C | | | |
| GAM55 | KIAA1877 3' | CCTACCTTATTTCTCCAGCCA | 2741 | AT | AAAC |
| | | TG TGGAGAAGTAGG AGG | | | |
| | | | | | |
| | | AC ACCTCTTTATTC TCC | | | |
| | | CG CA__ | | | |
| GAM55 | MTCH1 3' | CCCGTCTACCCCTCCAGTCA | 1493 | AA | AAACA |
| | | TGATTGGAG GTAGG GG | | | |
| | | | | | |
| | | ACTGACCTC CATCT CC | | | |
| | | CC GC__ | | | |
| GAM55 | N-PAC 3' | CCGCCCTCACCCCTCCAATC | 2902 | AA _ | AAACA |
| | | GATTGGAG GTAGG GG | | | |
| | | | | | |

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|-------|-----------|----|-------------------------|------|-----------|
| | | | CTAACCTC CA TCC CC | | |
| | | | CC C CG__ | | |
| GAM55 | SEMA4B | 5' | CCTGTTTCCCACCTCC | 2839 | AA A |
| | | | GGAG GT GGAAACAGG | | |
| | | | | | |
| | | | CCTC CA CCTTTGTCC | | |
| | | | __ C | | |
| GAM55 | SPRY1 | 3' | CCTGTTTCCCACCTTCTCT | 2709 | TA_ |
| | | | GGAGAAG GGAAACAGG | | |
| | | | | | |
| | | | TCTCTC CCTTTGTCC | | |
| | | | CAC | | |
| GAM55 | WS-3 | 5' | CCTGCCAGGCTCTCCAATC | 1312 | A A_ AAA |
| | | | GATTGGAGA GT GG CAGG | | |
| | | | | | |
| | | | CTAACCTCT CG CC GTCC | | |
| | | | _ GA _ | | |
| GAM55 | LOC123242 | 5' | TCTGTACCTTCTCCATCCA | 3030 | AT TAGGAA |
| | | | TG TGGAGAAG ACAGG | | |
| | | | | | |
| | | | AC ACCTCTC TGTCT | | |
| | | | CT CA__ | | |
| GAM55 | LOC127702 | 3' | CCTGCCACAACCTTCTCCAAAC | 3024 | A A__ AAA |
| | A | | TG TTGGAGAAGT GG CAGG | | |
| | | | | | |
| | | | AC AACCTCTTCA CC GTCC | | |
| | | | A ACA C__ | | |
| GAM55 | LOC146745 | 5' | TCCTGCCACCATTCTCCAACC | 3099 | A A AAA |
| | A | | TG TTGGAGAAGT GG CAGGA | | |
| | | | | | |
| | | | AC AACCTCTTTA CC GTCCT | | |
| | | | C _ ACC | | |
| GAM55 | LOC147791 | 3' | CCCATTCCTAACCTCCAATC | 3294 | AAG A CA |
| | | | GATTGGAG TAGG AA GG | | |
| | | | | | |
| | | | CTAACCTC ATCC TT CC | | |
| | | | CA_ C AC | | |
| GAM55 | LOC196892 | 3' | TCCTGGTGATTCTTCTCCAATC | 3417 | TAGGAAA |
| | A | | TGATTGGAGAAG CAGGA | | |
| | | | | | |
| | | | ACTAACCTCTTC GTCCT | | |
| | | | TTAGTG_ | | |
| GAM55 | LOC200093 | 3' | CCTGTTCCCCACCTCCCGGCTC | 2648 | _ A A A A |
| | | | GA TTGG GA GT GG AACAGG | | |
| | | | | | |
| | | | CT GGCC CT CA CC TTGTCC | | |
| | | | C _ C C C | | |
| GAM55 | LOC201243 | 5' | TCCTGCCACCATTCTCCAACC | 3426 | A A AAA |
| | A | | TG TTGGAGAAGT GG CAGGA | | |
| | | | | | |

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|-------|-----------|----|------------------------------|-----------|--------|
| | | | AC AACCTCTTTA CC GTCCT | | |
| | | | C _ ACC | | |
| GAM55 | LOC219404 | 3' | CCTGCTCCCTACTTCCTGGCA 3606 | A TG A | AAA |
| | | | TG T G GAAGTAGG CAGG | | |
| | | | | | |
| | | | AC G C CTTTCATCC GTCC | | |
| | | | _GT _ CTC | | |
| GAM55 | LOC222066 | 3' | TCCTGCAAACCCACCTTCTCCAA 3574 | TA AAA_ | |
| | | | TCA TGATTGGAGAAG GG CAGGA | | |
| | | | | | |
| | | | ACTAACCTCTTC CC GTCCT | | |
| | | | CA AAAC | | |
| GAM55 | LOC253001 | 5' | TCTGTACCTTCTCCATCCA 3698 | AT | TAGGAA |
| | | | TG TGGAGAAG ACAGG | | |
| | | | | | |
| | | | AC ACCTCTTC TGTCT | | |
| | | | CT CA_ | | |
| GAM55 | LOC91040 | 3' | CCTGTTCCCCACCTCCCGGCTC 2700 | _ A A A A | |
| | | | GA TTGG GA GT GG AACAGG | | |
| | | | | | |
| | | | CT GGCC CT CA CC TTGTCC | | |
| | | | C _ C C C | | |
| GAM56 | GCNT2 | 5' | TCTCGGGATGAAACGGAATCGA 831 | _____ A | |
| | | | TCGATTCCGT CC AGA | | |
| | | | | | |
| | | | AGCTAAGGCA GG TCT | | |
| | | | AAGTAG C | | |
| GAM56 | BLP1 | 3' | TTACCTTGCAGACGGAATGA 2222 | G _ A | |
| | | | TC ATTCCGTC CAAG TGA | | |
| | | | | | |
| | | | AG TAAGGCAG GTTC ATT | | |
| | | | _ AC C | | |
| GAM56 | BLP1 | 3' | TTACCTTGCAGACGGAATGA 2371 | G _ A | |
| | | | TC ATTCCGTC CAAG TGA | | |
| | | | | | |
| | | | AG TAAGGCAG GTTC ATT | | |
| | | | _ AC C | | |
| GAM56 | LOC143914 | 5' | TCACTCAAACGGAATCGA 3062 | CCA A | |
| | | | TCGATTCCGT AG TGA | | |
| | | | | | |
| | | | AGCTAAGGCA TC ACT | | |
| | | | AAC _ | | |
| GAM56 | LOC253891 | 5' | CACTGGGACGGAATCGG 3654 | A A | |
| | | | TCGATTCCGTCC AG TG | | |
| | | | | | |
| | | | GGCTAAGGCAGG TC AC | | |
| | | | G _ | | |
| GAM57 | ADSS | 3' | GAAACAAATGATGAAAACAT 2925 | CCTGTT | |
| | | | ATGT TCATTTGTTTC | | |
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|-------|-----------|----|-----------------------------|--------|-------|
| | | | TACA AGTAAACAAAG | | |
| | | | AAAGT_ | | |
| GAM57 | CASP6 | 3' | GAAACAAAATCCTCAGGAAATT 2305 | G | TTTCA |
| | A | | TAAT TCCTG TTTGTTTC | | |
| | | | | | |
| | | | ATTA AGGAC AAACAAAG | | |
| | | | A TCCTA | | |
| GAM57 | CASP6 | 3' | GAAACAAAATCCTCAGGAAATT 810 | G | TTTCA |
| | A | | TAAT TCCTG TTTGTTTC | | |
| | | | | | |
| | | | ATTA AGGAC AAACAAAG | | |
| | | | A TCCTA | | |
| GAM57 | CKTSF1B1 | 3' | AAGTGGATAAACAGAACATT 1445 | C | C TG |
| | | | AATGT CTGTTT ATT TTT | | |
| | | | | | |
| | | | TTACA GACAAA TAG GAA | | |
| | | | A _ GT | | |
| GAM57 | F2R | 3' | AAACAATGCAGTACAGGACAT 879 | TTCAT_ | |
| | | | ATGTCCTGT TTGTTT | | |
| | | | | | |
| | | | TACAGGACA AACAAA | | |
| | | | TGACGT | | |
| GAM57 | GPRK7 | 3' | GGAAACAAATGTTTCTGACATT 2476 | CTGTTT | |
| | | | AATGTC CATTTGTTTCC | | |
| | | | | | |
| | | | TTACAG GTAAACAAAGG | | |
| | | | TCTTT_ | | |
| GAM57 | NLGN1 | 3' | AAACAAATGAGATGGAC 1591 | T | |
| | | | GTCC GTTTCATTTGTTT | | |
| | | | | | |
| | | | CAGG TAGAGTAAACAAA | | |
| | | | _ | | |
| GAM57 | APC10 | 5' | GGAAACTGTAACAGGACATT 1574 | T TTT | |
| | | | AATGTCCTGTT CA GTTTCC | | |
| | | | | | |
| | | | TTACAGGACAA GT CAAAGG | | |
| | | | T _ | | |
| GAM57 | C20orf139 | 3' | GGAACAAAAACAGGACATTA 3319 | CAT | |
| | | | TAATGTCCTGTTT TTGTTTC | | |
| | | | | | |
| | | | ATTACAGGACAAA AACAAAGG | | |
| | | | _ | | |
| GAM57 | FLJ11186 | 3' | GAAGCCCGAAACAAGACATTA 1818 | C ATTT | |
| | | | TAATGTC TGTTTC GTTTC | | |
| | | | | | |
| | | | ATTACAG ACAAAG CGAAG | | |
| | | | A CC_ | | |
| GAM57 | FLJ22116 | 5' | GGAATTGCGGAAAACAGGAC 2073 | CA _ | |
| | | | GTCCTGTTT TTTGT TTCC | | |
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CAGGACAAA AGGCG AAGG
 — TT
 GAM57 FLJ32978 3' AAACAAATGAAATCAACA 2487 CCT
 TGT GTTTCATTTGTTT
 ||| |||||
 ACA TAAAGTAAACAAA
 AC_

GAM57 KIAA1164 3' GGAAACAAAACAAAAC 2862 CC CA_
 GT TGTTC TTTGTTTCC
 || ||||| |||||
 CA ACAA AAACAAAGG
 AA ACA

GAM57 KIAA1762 3' AAAGAGAGAAACGGACA 2668 T A G
 TGTCC GTTTC TTT TTT
 ||||| ||||| ||| |||
 ACAGG CAAAG AGA AAA
 — — G

GAM57 KIAA1918 5' GAAAGGAGACAGAACATTA 2969 C ATTTG
 TAATGT CTGTTTC TTTC
 ||||| ||||| |||||
 ATTACA GACAGAG AAAG
 A G____

GAM57 POPX1 3' GGAAACAAACTTCAGGTCA 1583 T TTTCA
 TG CCTG TTTGTTTCC
 || ||||| |||||
 AC GGAC AAACAAAGG
 T TTC__

GAM57 PRO0800 3' AAACAAAGAGACAGGAATTA 1852 G A
 TAAT TCCTGTTTC TTTGTTT
 ||||| ||||| |||||
 ATTA AGGACAGAG AAACAAA

GAM57 LOC142779 3' GGAGTAACAAAATAGGACATTA 3050 CATT _
 TAATGTCCTGTTT TGTT TCC
 ||||| ||||| |||||
 ATTACAGGATAAA ACAA AGG
 — TG

GAM57 LOC143274 5' GGAAACAAAACAAAAGGA 3053 G CA
 TCCT TTT TTTGTTTCC
 ||||| ||||| |||||
 AGGA AAA AAACAAAGG
 — AC

GAM57 LOC154089 3' AAACAAATACTGAGACAG 3186 _
 CTGTTTCA TTTGTTT
 ||||| |||||
 GACAGAGT AAACAAA
 CAT

GAM57 LOC169679 3' AGCATATGAAGACAGGACAT 3404 _ T
 ATGTCCTGTTT CAT TGTT
 ||||| ||||| |||||

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|-------|-----------|----|-----------------------------|----------|
| | | | TACAGGACAGA GTA ACGA | |
| | | | A T | |
| GAM57 | LOC202052 | 5' | GAAACAAATACCCAGAAGACA 3484 | ___ TTTC |
| | | | TGTC CTG ATTTGTTTC | |
| | | | | |
| | | | ACAG GAC TAAACAAAG | |
| | | | AA CCA_ | |
| GAM57 | LOC256021 | 3' | GAAACGAGAACAATGACATTA 3708 | C_ CAT |
| | | | TAATGTC TGTTT TTGTTTC | |
| | | | | |
| | | | ATTACAG ACAAG AGCAAAG | |
| | | | TA ____ | |
| GAM57 | LOC91650 | 5' | AAACAAAACATCTCAGGACAT 2765 | TTTCA_ |
| | | | ATGTCCTG TTTGTTT | |
| | | | | |
| | | | TACAGGAC AAACAAA | |
| | | | TCTACA | |
| GAM57 | LOC91752 | 5' | AAGTCAAATAAAACAGGACA 2777 | C _ |
| | | | TGTCCTGTTT ATTTG TTT | |
| | | | | |
| | | | ACAGGACAAA TAAAC GAA | |
| | | | A T | |
| GAM58 | DRD1 | 3' | ATTAAC TCCGTTTCCAAATACA 774 | GCTCCT |
| | | | TGTAT AGCGGAGTTAAT | |
| | | | | |
| | | | ACATA TTGCCTCAATTA | |
| | | | AACCT_ | |
| GAM58 | KIAA0182 | 3' | AAGTCCTAGGAGCACACA 2931 | A GC G |
| | | | TGT TGCTCCTA GGA TT | |
| | | | | |
| | | | ACA ACGAGGAT CCT AA | |
| | | | C _ G | |
| GAM58 | SSH2 | 3' | AGCCCCAGGAGCATACA 2626 | AGC A |
| | | | TGTATGCTCCT GG GTT | |
| | | | | |
| | | | ACATACGAGGA CC CGA | |
| | | | C_ _ | |
| GAM58 | LOC90918 | 5' | ATTAAATCCAGGAACATATA 2687 | C AGC G |
| | | | TGTATG TCCT GGA TTAAT | |
| | | | | |
| | | | ATATAC AGGA CCT AATTA | |
| | | | A _ A | |
| GAM59 | EHHADH | 3' | TATGAATCATACATACACTC 877 | TCTC_ |
| | | | GGGTGTAT ATTCATA | |
| | | | | |
| | | | CTCACATA TAAGTAT | |
| | | | CATAC | |
| GAM59 | ADAM9 | 3' | TATGAATGAAAACAAAACACC 1063 | A C_ |
| | | | GGTGT TT TCATTGATA | |
| | | | | |

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|-------|--------------|----|-----------------------------|--------|---------|
| | | | CCACA AA AGTAAGTAT | | |
| | | | A CAAA | | |
| GAM59 | BCAR3 | 3' | ATGAATGAAAATACATCT 1036 | C | |
| | | | GGGTGTATT TCATTCAT | | |
| | | | | | |
| | | | TCTACATAA AGTAAGTA | | |
| | | | A | | |
| GAM59 | XAP135 | 5' | AATGGCCACCTGATGA 1809 | TATTC | |
| | | | TCATCGGGTG TCATT | | |
| | | | | | |
| | | | AGTAGTCCAC GGTA | | |
| | | | C | | |
| GAM59 | XAP135 | 5' | AATGGCCACCTGATGA 2408 | TATTC | |
| | | | TCATCGGGTG TCATT | | |
| | | | | | |
| | | | AGTAGTCCAC GGTA | | |
| | | | C | | |
| GAM59 | LOC252983 | 5' | ATGAATAAAAATACATCTACTG 3668 | TC | CTC |
| | | | CA GGGTGTATT ATTCAT | | |
| | | | | | |
| | | | GT TCTACATAA TAAGTA | | |
| | | | CA AAA | | |
| GAM60 | MGC5242 | 5' | CCTTACAATCCGAGACTA 2042 | | |
| | | | TGGTCTCGGATT AGG | | |
| | | | | | |
| | | | ATCAGAGCCTAA TCC | | |
| | | | CAT | | |
| GAM60 | LOC197259 | 3' | GCCAATCAAGACCAGAA 3422 | CG | A |
| | | | TTCTGGTCT GATT GGC | | |
| | | | | | |
| | | | AAGACCAGA CTAA CCG | | |
| | | | A _ _ | | |
| GAM61 | DKFZP564I052 | 3' | ATGGATGAAGATGATGACCGAT 2759 | A _ | ATA |
| | | | ATCG TCAT ATCT TCATCCAT | | |
| | | | | | |
| | | | TAGC AGTA TAGA AGTAGGTA | | |
| | | | C G _ | | |
| GAM61 | KIAA0825 | 3' | ATGGACAATACTATTGGTCGAT 2588 | TATCTA | CA |
| | | | ATCGATCA TAT TCCAT | | |
| | | | | | |
| | | | TAGCTGGT ATA AGGTA | | |
| | | | TATC_ AC | | |
| GAM61 | KIAA0976 | 3' | ATGATGTATATTATCGAT 1588 | C TC | |
| | | | ATCGAT ATA TATATCAT | | |
| | | | | | |
| | | | TAGCTA TAT ATGTAGTA | | |
| | | | T _ | | |
| GAM61 | PLAC3 | 3' | ATGGAAGGGGAAATATGATAGA 2853 | G | CTATA A |
| | T | | ATC ATCATAT TC TCCAT | | |
| | | | | | |

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|-------|---------------|----|------------------------|-------------|----------|---------|---|
| | | | | TAG TAGTATA | GG AGGTA | | |
| | | | A | AAGG_ A | | | |
| GAM61 | LOC147991 | 5' | ATGTATATAGATATGATC | 3115 | | | - |
| | | | GATCATATCTATAT CAT | | | | |
| | | | | | | | |
| | | | CTAGTATAGATATA GTA | | | | |
| | | | T | | | | |
| GAM62 | HDAC7A | 3' | CTCTGGCAAAGTCTTCAA | 1628 | | CTT | |
| | | | TTGAAGACT CCAGAG | | | | |
| | | | | | | | |
| | | | AACTTCTGA GGTCTC | | | | |
| | | | AAC | | | | |
| GAM62 | HDAC7A | 3' | CTCTGGCAAAGTCTTCAA | 1700 | | CTT | |
| | | | TTGAAGACT CCAGAG | | | | |
| | | | | | | | |
| | | | AACTTCTGA GGTCTC | | | | |
| | | | AAC | | | | |
| GAM62 | LTBP1 | 3' | TCTCAAATGAAAAAGTCTTCGA | 764 | | C C _ | |
| | | | TTGAAGACT TT CA GAGA | | | | |
| | | | | | | | |
| | | | AGCTTCTGA AA GT CTCT | | | | |
| | | | A A AAA | | | | |
| GAM62 | PDGFB | 3' | CTGGGAGAAGGTCTCCAA | 941 | | A _ | |
| | | | TTG AGAC TCTTCCAG | | | | |
| | | | | | | | |
| | | | AAC TCTG AGAGGGTC | | | | |
| | | | C GA | | | | |
| GAM62 | PRDM4 | 3' | CTTACAGAAGAGTCTCTAA | 1427 | | A CA_ | |
| | | | TTG AGACTCTTC GAG | | | | |
| | | | | | | | |
| | | | AAT TCTGAGAAG TTC | | | | |
| | | | C ACA | | | | |
| GAM62 | SIRT6 | 3' | TTCTGGAAAAGTCCTCAA | 1695 | | A C | |
| | | | TTGA GACT TTCCAGAG | | | | |
| | | | | | | | |
| | | | AACT CTGA AAGGTCTT | | | | |
| | | | C A | | | | |
| GAM62 | XYLB | 3' | TCTCTGGAAGAATTTCCAA | 1187 | | A C | |
| | | | TTG AGA TCTTCCAGAGA | | | | |
| | | | | | | | |
| | | | AAC TTT AGAAGGTCTCT | | | | |
| | | | C A | | | | |
| GAM62 | DKFZP434N093 | 3' | TGTAAACAGAAGGTCTTCAA | 3147 | | T CAGAG | |
| | | | TTGAAGAC CTTC ACG | | | | |
| | | | | | | | |
| | | | AACTTCTG GAAG TGT | | | | |
| | | | _ ACAA | | | | |
| GAM62 | DKFZP547E1010 | 5' | TTTCCAGAAGGGTCTCCAA | 2768 | | A CA | |
| | | | TTG AGACTCTTC GAGA | | | | |
| | | | | | | | |

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|-------|---------------|----|-------------------------------|------|------|---------|
| | | | AAC TCTGGGAAG CTTT | | | |
| | | | C AC | | | |
| GAM62 | DKFZP547E1010 | 5' | TTTCCAGAAGGGTCTCCAA | 1640 | A | CA |
| | | | TTG AGACTCTTC GAGA | | | |
| | | | | | | |
| | | | AAC TCTGGGAAG CTTT | | | |
| | | | C AC | | | |
| GAM62 | FLJ13942 | 3' | TTGAGATGGAAGAGTCTTTAA | 2067 | | GAGA |
| | | | TTGAAGACTCTTCCA CGA | | | |
| | | | | | | |
| | | | AATTTCTGAGAAGGT GTT | | | |
| | | | AGA_ | | | |
| GAM62 | FLJ14596 | 3' | TCATCTGGGAGTCCCCAA | 2282 | AA | TT _ |
| | | | TTG GACTC CCAGA GA | | | |
| | | | | | | |
| | | | AAC CTGAG GGTCT CT | | | |
| | | | CC _ A | | | |
| GAM62 | HRLP5 | 3' | TTCTGGAAGAATCTACAA | 2364 | A | C |
| | | | TTG AGA TCTTCCAGAG | | | |
| | | | | | | |
| | | | AAC TCT AGAAGGTCTT | | | |
| | | | A A | | | |
| GAM62 | KCNS1 | 3' | CGTTGGAAGAGTCTT | 917 | | GAG |
| | | | AAGACTCTTCCA ACG | | | |
| | | | | | | |
| | | | TTCTGAGAAGGT TGC | | | |
| | | | _____ | | | |
| GAM62 | KIAA0992 | 5' | TCTCTGGAGTCTTCAA | 1662 | | TCT |
| | | | TTGAAGAC TCCAGAGA | | | |
| | | | | | | |
| | | | AACTTCTG AGGTCTCT | | | |
| | | | _____ | | | |
| GAM62 | KIAA1975 | 5' | TATCATCTCTGGAAGTTGAGAG | 2982 | A | _____ C |
| | | | CCTCCAA G CTCT TCCAGAGA GAT A | | | |
| | | | | | | |
| | | | C GAGA AGGTCTCT CTA T | | | |
| | | | C GTTGA A | | | |
| GAM62 | MGC5590 | 3' | TCTCAGAAAGTCTTCAA | 2049 | C | CA |
| | | | TTGAAGACT TTC GAGA | | | |
| | | | | | | |
| | | | AACTTCTGA AAG CTCT | | | |
| | | | _ A_ | | | |
| GAM62 | SIAT8C | 5' | TCTTGAAGAATCTCAA | 1648 | A | C G |
| | | | TTGA GA TCTTCCA AGA | | | |
| | | | | | | |
| | | | AACT CT AGAAGGT TCT | | | |
| | | | _ A _ | | | |
| GAM62 | LOC149706 | 3' | ATCACCTCTGGAGCCCTTTCA | 3313 | ACTC | AC |
| | | | TGAAG TTCCAGAG GAT | | | |
| | | | | | | |

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|-------|-----------|----|-------------------------------|-----------|--|
| | | | ACTTT GAGGTCTC CTA | | |
| | | | CCC_ CA | | |
| GAM62 | LOC160292 | 3' | CTCTGGAAAGCCTTCAA 3399 | A C | |
| | | | TTGAAG CT TTCCAGAG | | |
| | | | | | |
| | | | AACTTC GA AAGGTCTC | | |
| | | | C _ | | |
| GAM62 | LOC203378 | 3' | GTTTCTAAAGAGTCTTCAA 3491 | CC | |
| | | | TTGAAGACTCTT AGAGAC | | |
| | | | | | |
| | | | AACTTCTGAGAA TCTTTG | | |
| | | | A_ | | |
| GAM62 | LOC204200 | 5' | CTCTGGAAAGGTCTCCAA 3493 | A TC | |
| | | | TTG AGAC TTCCAGAG | | |
| | | | | | |
| | | | AAC TCTG AAGGTCTC | | |
| | | | C GA | | |
| GAM62 | LOC255265 | 5' | CGTACGGAAAAGTCTTCA 3672 | C AGAG | |
| | | | TGAAGACT TTCC ACG | | |
| | | | | | |
| | | | ACTTCTGA AAGG TGC | | |
| | | | A CA__ | | |
| GAM63 | FLJ10737 | 3' | AGATGTTTTTATTTTATATTAT 1797 | TCCCA_ | |
| | | | TA TAATAATATAAAAT ATCT | | |
| | | | | | |
| | | | ATTATTATATTTTA TAGA | | |
| | | | TTTTTG | | |
| GAM64 | COX15 | 3' | AACAGTCCCAGAATGACCCCA 1104 | C AAATC T | |
| | | | TGGGGTTA TCT GCT GTT | | |
| | | | | | |
| | | | ACCCCAAGT AGA TGA CAA | | |
| | | | A CCC__ _ | | |
| GAM64 | SH2D1A | 3' | AACAAGCCTCCTTTTAAAGTAA 920 | C TC__ | |
| | | | CCCTA TGGGGTTACT TAAA GCTTGTT | | |
| | | | | | |
| | | | ATCCCAATGA ATTT CGAACAA | | |
| | | | A TCCTC | | |
| GAM64 | FLJ12994 | 3' | ACAAGCAAATGTAAGTCCA 2017 | TCTAAATC | |
| | | | TGGGGTTAC GCTTGT | | |
| | | | | | |
| | | | ACCTCAATG CGAACA | | |
| | | | TAAA__ | | |
| GAM64 | FLJ12994 | 3' | ACAAGCAAATGTAAGTCCA 3081 | TCTAAATC | |
| | | | TGGGGTTAC GCTTGT | | |
| | | | | | |
| | | | ACCTCAATG CGAACA | | |
| | | | TAAA__ | | |
| GAM65 | FGFR2 | 3' | ACCCTGTCATTACGTCAACGC 712 | _ _ | |
| | | | GCGT GGC AATGACAGGGT | | |
| | | | | | |

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|-------|-----------|----|-----------------------------|----|---------|
| | | | CGCA CTG TTACTGTCCCA | | |
| | | | A CA | | |
| GAM65 | FGFR2 | 3' | ACCCTGTCATTACGTCAACGC 2023 | — | — |
| | | | GCGT GGC AATGACAGGGT | | |
| | | | | | |
| | | | CGCA CTG TTACTGTCCCA | | |
| | | | A CA | | |
| GAM65 | FGFR2 | 3' | ACCCTGTCATTACGTCAACGC 2024 | — | — |
| | | | GCGT GGC AATGACAGGGT | | |
| | | | | | |
| | | | CGCA CTG TTACTGTCCCA | | |
| | | | A CA | | |
| GAM65 | FGFR2 | 3' | ACCCTGTCATTACGTCAACGC 2026 | — | — |
| | | | GCGT GGC AATGACAGGGT | | |
| | | | | | |
| | | | CGCA CTG TTACTGTCCCA | | |
| | | | A CA | | |
| GAM65 | FGFR2 | 3' | ACCCTGTCATTACGTCAACGC 2027 | — | — |
| | | | GCGT GGC AATGACAGGGT | | |
| | | | | | |
| | | | CGCA CTG TTACTGTCCCA | | |
| | | | A CA | | |
| GAM65 | FGFR2 | 3' | ACCCTGTCATTACGTCAACGC 2028 | — | — |
| | | | GCGT GGC AATGACAGGGT | | |
| | | | | | |
| | | | CGCA CTG TTACTGTCCCA | | |
| | | | A CA | | |
| GAM65 | MMP19 | 5' | ACCAAGGCTGCCACGCTCTAA 2010 | T | ATGACAG |
| | | | TTAG AGCGTGGCA GGT | | |
| | | | | | |
| | | | AATC TCGCACCGT CCA | | |
| | | | — CGGAA— | | |
| GAM66 | ARHGEF12 | 3' | AATAATGTCATTCTCAATTAA 1619 | TA | |
| | | | TTAATTG AATGATATTATT | | |
| | | | | | |
| | | | AATTAAC TTACTGTAATAA | | |
| | | | TC | | |
| GAM66 | OS4 | 3' | AATATTTGTATTACTTACAATT 1239 | A | TAT |
| | AA | | TTAATTGTAA TGATAT TATT | | |
| | | | | | |
| | | | AATTAACATT ATTATG ATAA | | |
| | | | C TTT | | |
| GAM66 | LOC148289 | 3' | AATAATAACATATACAATTAA 3300 | A | A |
| | | | TTAATTGTA ATG TATTATT | | |
| | | | | | |
| | | | AATTAACAT TAC ATAATAA | | |
| | | | A A | | |
| GAM66 | LOC253160 | 3' | AATAATAACATATACAATTAA 3714 | A | A |
| | | | TTAATTGTA ATG TATTATT | | |
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|-------|-----------|----|------------------------|------|----------|
| | | | AATTAACAT TAC ATAATAA | | |
| | | | A A | | |
| GAM67 | GAN | 3' | TGAGTGTGGTACATTAAC | 1975 | A CA _ |
| | | | AG TAA TACCACAC CA | | |
| | | | | | |
| | | | TC ATT ATGGTGTG GT | | |
| | | | A AC A | | |
| GAM67 | IDH3A | 3' | AAAGAGTGAATGTGGTATATTT | 1222 | TAAC C_ |
| | CT | | AGA ATACCACA CATTTTTT | | |
| | | | | | |
| | | | TCT TATGGTGT GTGAGAAA | | |
| | | | TTA_ AA | | |
| GAM67 | PEX1 | 3' | AAAAAATGGTGTCTATGAATTT | 749 | TAA_ CC |
| | CT | | AGA CATA ACACCATTTTTT | | |
| | | | | | |
| | | | TCT GTAT TGTGGTAAAAAA | | |
| | | | TTAA C_ | | |
| GAM67 | PYGO2 | 3' | AAAAATTGGGATATGTTATCT | 2676 | CCACA T |
| | | | AGATAACATA CCA TTTTT | | |
| | | | | | |
| | | | TCTATTGTAT GGT AAAAA | | |
| | | | AG__ T | | |
| GAM67 | FLJ21477 | 3' | TGGCGTGAGATGTTATCT | 2142 | AC A |
| | | | AGATAACAT CAC CCA | | |
| | | | | | |
| | | | TCTATTGTA GTG GGT | | |
| | | | GA C | | |
| GAM67 | NS1-BP | 3' | AAAAAATGGTGTTTTATCT | 2953 | CATACC |
| | | | AGATAA ACACCATTTTTT | | |
| | | | | | |
| | | | TCTATT TGTGGTAAAAAA | | |
| | | | T_____ | | |
| GAM67 | UNC5D | 5' | AAAAAAGCTGTAATATGTTATC | 2391 | CC CCA |
| | T | | AGATAACATA ACA TTTTTT | | |
| | | | | | |
| | | | TCTATTGTAT TGT AAAAAA | | |
| | | | AA CG_ | | |
| GAM67 | LOC257451 | 3' | AAAAATTGGGATATGTTATCT | 3678 | CCACA T |
| | | | AGATAACATA CCA TTTTT | | |
| | | | | | |
| | | | TCTATTGTAT GGT AAAAA | | |
| | | | AG__ T | | |
| GAM68 | CHAC | 3' | TGCCCATATGTCCATTTAT | 1612 | AGAT |
| | | | ATAAGTGGACATAT GCA | | |
| | | | | | |
| | | | TATTTACCTGTATA CGT | | |
| | | | CC__ | | |
| GAM68 | GGCX | 3' | CTGCACCCTGCCACTTGT | 778 | A TATAGA |
| | | | ATAAGTGG CA TGCAG | | |
| | | | | | |

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|-------|----------|----|-------------------------|-------|-----------|
| | | | TGTTCAACC GT | ACGTC | |
| | | | _ CCC _ | | |
| GAM68 | ITPKB | 3' | TCTGCATCTGTCCAC | 911 | TATA |
| | | | GTGGACA GATGCAGA | | |
| | | | | | |
| | | | CACCTGT CTACGTCT | | |
| | | | | | |
| GAM68 | KCNAB1 | 3' | TCTAATGTTATGTCCACTTA | 2584 | |
| | | | TAAGTGGACATA TAGA | | |
| | | | | | |
| | | | ATTCACCTGTAT ATCT | | |
| | | | TGTA | | |
| GAM68 | KLRC4 | 5' | CTGTCAAAATATACACCACTTA | 1451 | ACA GA_ _ |
| | T | | ATAAGTGG TATA TG CAG | | |
| | | | | | |
| | | | TATTCACC ATAT AC GTC | | |
| | | | AC_ AAA T | | |
| GAM68 | MLF2 | 3' | TCTGCATCTACTGACTTG | 1212 | _ ACATA |
| | | | TAAGT GG TAGATGCAGA | | |
| | | | | | |
| | | | GTTCA TC ATCTACGTCT | | |
| | | | G _ | | |
| GAM68 | NR1I2 | 3' | TCTGCATCCATTTGAACAC | 1067 | GA T A |
| | | | GTG CA AT GATGCAGA | | |
| | | | | | |
| | | | CAC GT TA CTACGTCT | | |
| | | | AA T C | | |
| GAM68 | NR1I2 | 3' | TCTGCATCCATTTGAACAC | 1971 | GA T A |
| | | | GTG CA AT GATGCAGA | | |
| | | | | | |
| | | | CAC GT TA CTACGTCT | | |
| | | | AA T C | | |
| GAM68 | CEP3 | 3' | TTCTACATCAGATGTTGTCACT | 1304 | _ ATA C |
| | TAT | | ATAAGTG GACAT GATG AGAA | | |
| | | | | | |
| | | | TATTCAC TTGTA CTAC TCTT | | |
| | | | TG GA_ A | | |
| GAM68 | FHX | 3' | TCATGGATCATGTCCAC | 1825 | ATA G _ |
| | | | GTGGACAT GAT CA GA | | |
| | | | | | |
| | | | CACCTGTA CTA GT CT | | |
| | | | _ G A | | |
| GAM68 | FLJ10352 | 3' | TTCTGCATCTACAACTCAACAT | 2233 | GACATA_ |
| | TTA | | TAAGTG TAGATGCAGAA | | |
| | | | | | |
| | | | ATTTAC ATCTACGTCTT | | |
| | | | AACTCAAC | | |
| GAM68 | FLJ22127 | 3' | TCGAGTCCATATGTCCAC | 2008 | A GCA |
| | | | GTGGACATAT GAT GA | | |
| | | | | | |

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|-------|-----------|----|-----------------------------|-----|-------|
| | | | CACCTGTATA CTG CT | | |
| | | | C AG_ | | |
| GAM68 | GDAP1L1 | 3' | TCTGCATCCATGCCAC 2043 | A | ATA |
| | | | GTGG CAT GATGCAGA | | |
| | | | | | |
| | | | CACC GTA CTACGTCT | | |
| | | | _ C_ | | |
| GAM68 | H-L(3)MBT | 3' | TCTGCTCTCTACCCACT 2230 | ACA | T T |
| | | | AGTGG TA AGA GCAGA | | |
| | | | | | |
| | | | TCACC AT TCT CGTCT | | |
| | | | C_ C _ | | |
| GAM68 | KIAA1340 | 3' | TCTAAGCTATGCCCATTTAT 2846 | A | ___ |
| | | | ATAAGTGG CATA TAGA | | |
| | | | | | |
| | | | TATTTACC GTAT ATCT | | |
| | | | C CGA | | |
| GAM68 | KNSL7 | 3' | TTCTGCATCCATATACACCCT 1905 | T | AC_ A |
| | | | AG GG ATAT GATGCAGAA | | |
| | | | | | |
| | | | TC CC TATA CTACGTCTT | | |
| | | | _ ACA C | | |
| GAM68 | P5-1 | 3' | CTCCATTTATGTACCCAC 1322 | AC | C |
| | | | GTGG ATATAGATG AG | | |
| | | | | | |
| | | | CACC TGTATTTAC TC | | |
| | | | CA C | | |
| GAM68 | PP1044 | 5' | CTGCATCTTTACCTATATCCAT 1956 | C | T___ |
| | TTA | | TAAGTGGA ATA AGATGCAG | | |
| | | | | | |
| | | | ATTTACCT TAT TCTACGTC | | |
| | | | A CCATT | | |
| GAM68 | SIRPB1 | 3' | TGCATGTGTCCACTTA 1272 | | ATAG |
| | | | TAAGTGGACAT ATGCA | | |
| | | | | | |
| | | | ATTCACCTGTG TACGT | | |
| | | | _____ | | |
| GAM68 | LOC148811 | 3' | CTGCATCTCTCCCCTTA 3126 | T | CATAT |
| | | | TAAG GGA AGATGCAG | | |
| | | | | | |
| | | | ATTC CCT TCTACGTC | | |
| | | | C C_ | | |
| GAM68 | LOC149711 | 3' | TCCATATGTCTATCCACTTA 3315 | ___ | A |
| | | | TAAGTGGA CATAT GA | | |
| | | | | | |
| | | | ATTCACCT GTATA CT | | |
| | | | ATCT C | | |
| GAM68 | LOC150630 | 5' | CTGCATCTTCTGCCACT 3332 | A | TAT |
| | | | AGTGG CA AGATGCAG | | |
| | | | | | |

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|-------|------------------|------------------------|------|-----------|
| | | TCACC GT TCTACGTC | | |
| | | _ CT_ | | |
| GAM68 | LOC150819 5' | CTGCATTTTAGTCCAAC | 3333 | _ ATAT |
| | | AGT GGAC AGATGCAG | | |
| | | | | |
| | | TCA CCTG TTTACGTC | | |
| | | A AT_ | | |
| GAM68 | LOC154877 3' | TCTGCATCCATTCCACT | 3373 | CAT A |
| | | AGTGGA AT GATGCAGA | | |
| | | | | |
| | | TCACCT TA CTACGTCT | | |
| | | _ C | | |
| GAM68 | LOC158327 3' | TTCTGCAGGGACACCACTTAT | 3216 | ACATATAGA |
| | | ATAAGTGG TGCAGAA | | |
| | | | | |
| | | TATTCACC ACGTCTT | | |
| | | ACAGGG_ | | |
| GAM68 | LOC196540 3' | TCTGCATCCATGTACTCC | 3467 | C_ A |
| | | GGA ATAT GATGCAGA | | |
| | | | | |
| | | CCT TGTA CTACGTCT | | |
| | | CA C | | |
| GAM68 | LOC220394 5' | TCTCAGAATATGTCCAT | 3581 | AGA C |
| | | GTGGACATAT TG AGA | | |
| | | | | |
| | | TACCTGTATA AC TCT | | |
| | | AG_ _ | | |
| GAM68 | LOC254428 3' | CTGTTGACCCATGTCCACCTAT | 3677 | A ATAGAT |
| | | ATA GTGGACAT GCAG | | |
| | | | | |
| | | TAT CACCTGTA TGTC | | |
| | | C CCCAGT | | |
| GAM68 | LOC92405 3' | TTCTGTTACACATGTCTACTTA | 2848 | ATAGAT |
| | | TAAGTGGACAT GCAGAA | | |
| | | | | |
| | | ATTCATCTGTA TGTCTT | | |
| | | CACAT_ | | |
| GAM69 | DKFZP434G1411 3' | TAGGTTGATACATGTATCA | 3554 | AA |
| | | TGATACATGTATTAA TA | | |
| | | | | |
| | | ACTATGTACATAGTT AT | | |
| | | GG | | |
| GAM69 | DKFZP564I052 3' | GAAAGTATTCCTATCATGTAT | 2760 | T TAA |
| | | ATACATG AT AATACTTTC | | |
| | | | | |
| | | TATGTAC TA TTATGAAAG | | |
| | | _ TCC | | |
| GAM69 | KLHL8 3' | AAAGTATTTGTTACATAATCA | 2639 | AC TTA |
| | | TGAT ATGTA AAATACTTT | | |
| | | | | |

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|-------|-----------|----|-----------------------------|---------|-----|
| | | | ACTA TACAT TTTATGAAA | | |
| | | | A_ TG_ | | |
| GAM69 | XLKD1 | 3' | AAAGTGCCATTAACAAATGTAT 1323 | GTA | AA_ |
| | CA | | TGATACAT TTAA TACTTT | | |
| | | | | | |
| | | | ACTATGTA AATT GTGAAA | | |
| | | | AAC ACC | | |
| GAM69 | LOC51003 | 3' | GAGGCACTTAATACATGTAT 1658 | AATA | |
| | | | ATACATGTATTAA CTT | | |
| | | | | | |
| | | | TATGTACATAATT GAG | | |
| | | | CACG | | |
| GAM70 | NEU3 | 3' | ATGATTTGTTCCATTTTAA 1319 | TA | |
| | | | TAAAAAT AACAAATCGT | | |
| | | | | | |
| | | | ATTTTAA TTGTTTAGTA | | |
| | | | CC | | |
| GAM70 | CHPT1 | 3' | AACATTTGTTTAATTTTAA 1906 | C | |
| | | | TAAAAATTAAACAAAT GTT | | |
| | | | | | |
| | | | ATTTTAAATTTGTTTA CAA | | |
| | | | - | | |
| GAM70 | LOC143310 | 3' | AATTTGTGATTTGTTTAATTT 3057 | TT_ | |
| | | | AAATTAAACAAATCG ATT | | |
| | | | | | |
| | | | TTTAATTTGTTTAGT TAA | | |
| | | | GTT | | |
| GAM70 | LOC152578 | 5' | TAATAACAAATGTTTAATTTTT 3361 | AATC | |
| | A | | TAAAAATTAAACA GTTATTA | | |
| | | | | | |
| | | | ATTTTAAATTTGT CAATAAT | | |
| | | | AAA_ | | |
| GAM71 | HNF3A | 3' | ACAGCATAATAAAATCC 2543 | C GTT | |
| | | | GGATT TGT TATGCTGT | | |
| | | | | | |
| | | | CCTAA ATA ATACGACA | | |
| | | | A _ | | |
| GAM71 | MUC12 | 3' | AGCTGCAAACACAGAGCCCA 3643 | AT TA T | |
| | | | TGG TCTGTGTT TGC GTT | | |
| | | | | | |
| | | | ACC AGACACAA ACG CGA | | |
| | | | CG _ T | | |
| GAM71 | OGN | 3' | ACAGCATTACAAAATCC 2307 | C TTT | |
| | | | GGATT TGTG ATGCTGT | | |
| | | | | | |
| | | | CCTAA ACAT TACGACA | | |
| | | | A _ | | |
| GAM71 | OGN | 3' | ACAGCATTACAAAATCC 1467 | C TTT | |
| | | | GGATT TGTG ATGCTGT | | |
| | | | | | |

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| | | | CCTAA ACAT TACGACA | | | |
| | | | A _ | | | |
| GAM71 | OGN | 3' | ACAGCATTACAAAATCC 2059 | C | TTT | |
| | | | GGATT TGTG ATGCTGT | | | |
| | | | | | | |
| | | | CCTAA ACAT TACGACA | | | |
| | | | A _ | | | |
| GAM71 | PTPRA | 3' | AGATAAACACAAAATCCAT 962 | C | G | |
| | | | ATGGATT TGTGTTTAT CT | | | |
| | | | | | | |
| | | | TACCTAA ACACAAATA GA | | | |
| | | | A _ | | | |
| GAM71 | PTPRA | 3' | AGATAAACACAAAATCCAT 2389 | C | G | |
| | | | ATGGATT TGTGTTTAT CT | | | |
| | | | | | | |
| | | | TACCTAA ACACAAATA GA | | | |
| | | | A _ | | | |
| GAM71 | PTPRA | 3' | AGATAAACACAAAATCCAT 2390 | C | G | |
| | | | ATGGATT TGTGTTTAT CT | | | |
| | | | | | | |
| | | | TACCTAA ACACAAATA GA | | | |
| | | | A _ | | | |
| GAM71 | TIRAP | 3' | AGCTAGAAACAGAAAACCCAT 2344 | A_ | G T | |
| | | | ATGG TTCTGT TTTA GCT | | | |
| | | | | | | |
| | | | TACC AAGACA AGAT CGA | | | |
| | | | CAA A _ | | | |
| GAM71 | ATF3 | 3' | AGCGTTAACACAAAATCCAT 1080 | C | T | |
| | | | ATGGATT TGTGTT ATGCT | | | |
| | | | | | | |
| | | | TACCTAA ACACAA TGCGA | | | |
| | | | A T | | | |
| GAM71 | FLJ22457 | 3' | AACATCTTCAACACAGAACACA 2106 | GA | TATGC | |
| | | | TG TTCTGTGTT TGTT | | | |
| | | | | | | |
| | | | AC AAGACACAA ACAA | | | |
| | | | AC CTTCT | | | |
| GAM71 | LIPG | 3' | AGCCTAAACACAAAATTCAT 1266 | C | T | |
| | | | ATGGATT TGTGTTTA GCT | | | |
| | | | | | | |
| | | | TACTTAA ACACAAAT CGA | | | |
| | | | A C | | | |
| GAM71 | MGC4643 | 3' | AACAGCATAAACAGCTGGACC 2271 | A T_ | | |
| | | | GG TTC G TGTTTATGCTGTT | | | |
| | | | | | | |
| | | | CC AGG C ACAAATACGACAA | | | |
| | | | _ TG | | | |
| GAM71 | LOC143888 | 3' | AGTCTAAACACAAAATTCAT 3064 | C | T | |
| | | | ATGGATT TGTGTTTA GCT | | | |
| | | | | | | |

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|-------|-----------|----|------------------------------|-----|-------|
| | | | TACTTAA ACACAAAT TGA | | |
| | | | A C | | |
| GAM71 | LOC149619 | 5' | AACATCTTCAACACAGAACACA 3311 | GA | TATGC |
| | | | TG TTCTGTGTT TGTT | | |
| | | | | | |
| | | | AC AAGACACAA ACAA | | |
| | | | AC CTTCT | | |
| GAM71 | LOC91464 | 5' | AACAGCATAAAGGACCCCA 2740 | AT | GTG |
| | | | TGG TCT TTTATGCTGTT | | |
| | | | | | |
| | | | ACC AGG AAATACGACAA | | |
| | | | CC _ | | |
| GAM72 | CLDN1 | 3' | ATATTAATTAGTTTATATTA 1940 | _ | |
| | | | TAATATAAACTAAT AATAT | | |
| | | | | | |
| | | | ATTATATTTGATTA TTATA | | |
| | | | A | | |
| GAM72 | KIAA1706 | 3' | ACAGTGTTTCATAGTTTATATTA 3577 | | ATAAT |
| | | | TAATATAAACTA ATATTGT | | |
| | | | | | |
| | | | ATTATATTTGAT TGTGACA | | |
| | | | ACT_ | | |
| GAM73 | B3GALT5 | 3' | GTGCTGAAATCCACGCCAGA 2317 | A | A_ T |
| | | | TCT GCGTGGAT CAG CAC | | |
| | | | | | |
| | | | AGA CGCACCTA GTC GTG | | |
| | | | C AA _ | | |
| GAM73 | B3GALT5 | 3' | GTGCTGAAATCCACGCCAGA 1268 | A | A_ T |
| | | | TCT GCGTGGAT CAG CAC | | |
| | | | | | |
| | | | AGA CGCACCTA GTC GTG | | |
| | | | C AA _ | | |
| GAM73 | B3GALT5 | 3' | GTGCTGAAATCCACGCCAGA 2318 | A | A_ T |
| | | | TCT GCGTGGAT CAG CAC | | |
| | | | | | |
| | | | AGA CGCACCTA GTC GTG | | |
| | | | C AA _ | | |
| GAM73 | B3GALT5 | 3' | GTGCTGAAATCCACGCCAGA 2319 | A | A_ T |
| | | | TCT GCGTGGAT CAG CAC | | |
| | | | | | |
| | | | AGA CGCACCTA GTC GTG | | |
| | | | C AA _ | | |
| GAM73 | B3GALT5 | 3' | GTGCTGAAATCCACGCCAGA 2321 | A | A_ T |
| | | | TCT GCGTGGAT CAG CAC | | |
| | | | | | |
| | | | AGA CGCACCTA GTC GTG | | |
| | | | C AA _ | | |
| GAM73 | MEF2A | 3' | GTGACTGTAGTTACTTAAGA 1229 | C C | A |
| | | | TCT TAG GTGG TACAGTCAC | | |
| | | | | | |

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|-------|-----------|----|----------------------------|----------|
| | | | AGA ATT CATT ATGTCAGTG | |
| | | | — — G | |
| GAM73 | ORC2L | 3' | GTGAGAAGCCAGGCTAGAGA 1278 | G ATACAG |
| | | | TCTCTAGC TGG TCAC | |
| | | | | |
| | | | AGAGATCG ACC AGTG | |
| | | | G GAAG__ | |
| GAM73 | PART1 | 3' | CGGTGACTATATGAGAATGGA 1699 | GCGTGG C |
| | | | TCTA ATA AGTCACCG | |
| | | | | |
| | | | AGGT TAT TCAGTGGC | |
| | | | AAGAG_ A | |
| GAM73 | SLC10A1 | 3' | GTGACTGTAAACTCTATG 989 | — |
| | | | CGTGGA TACAGTCAC | |
| | | | | |
| | | | GTATCT ATGTCAGTG | |
| | | | CAA | |
| GAM73 | FUSIP1 | 3' | GTGACTGTAATATACTAGAG 1314 | CG GA |
| | | | CTCTAG TG TACAGTCAC | |
| | | | | |
| | | | GAGATC AT ATGTCAGTG | |
| | | | AT A_ | |
| GAM73 | RAI17 | 3' | GTGACTGTGGAGCCTGAGA 3515 | T C GGA |
| | | | TCTC AG GT TACAGTCAC | |
| | | | | |
| | | | AGAG TC CG GTGTCAGTG | |
| | | | — — AG_ | |
| GAM73 | LOC115811 | 5' | GGTAACTGTGGCTAGGGA 2442 | GTGGA C |
| | | | TCTCTAGC TACAGT ACC | |
| | | | | |
| | | | AGGGATCG GTGTCA TGG | |
| | | | — — — — — A | |
| GAM73 | LOC256946 | 3' | GTGACTGTAATATACTAGAG 3657 | CG GA |
| | | | CTCTAG TG TACAGTCAC | |
| | | | | |
| | | | GAGATC AT ATGTCAGTG | |
| | | | AT A_ | |
| GAM74 | PEX3 | 3' | AATATAGATATTTTATATAC 1044 | — |
| | | | GTATGTA TATCTATATT | |
| | | | | |
| | | | CATATAT ATAGATATAA | |
| | | | TTT | |
| GAM74 | PKD2L2 | 3' | TTAATATGAGACATACTG 1497 | ATATC |
| | | | CAGTATGT TATATTAA | |
| | | | | |
| | | | GTCATACA GTATAATT | |
| | | | GA__ | |
| GAM74 | BA108L7.2 | 3' | ATGCATATACATACATGATA 2179 | _ C |
| | | | TATCA GTATGTATAT TAT | |
| | | | | |

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|-------|------------|----|------------------------------|------|-----|
| | | | ATAGT CATACATATA GTA | | |
| | | | A C | | |
| GAM74 | IDI1 | 3' | TTAATGTATTATATACACTGAT 2776 | A | TC |
| | | A | TATCAGT TGTATA TATATTAA | | |
| | | | | | |
| | | | ATAGTCA ATATAT ATGTAATT | | |
| | | | C T_ | | |
| GAM74 | PRO0899 | 5' | AGTGTTTTACACATACTGAT 1846 | A | TCT |
| | | | ATCAGTATGT TA ATATT | | |
| | | | | | |
| | | | TAGTCATACA AT TGTGA | | |
| | | | C TT_ | | |
| GAM74 | SEC14L1 | 3' | TGGTAATACAATACTGATA 980 | _ | AT |
| | | | TATCAGTAT GTAT CTA | | |
| | | | | | |
| | | | ATAGTCATA CATA GGT | | |
| | | | A AT | | |
| GAM74 | LOC130074 | 3' | TTAACATAGAATGTTTACTGAT 3045 | TG A | A |
| | | A | TATCAGTA TAT TCTAT TTAA | | |
| | | | | | |
| | | | ATAGTCAT GTA AGATA AATT | | |
| | | | TT _ C | | |
| GAM74 | LOC222159 | 5' | AGACCATGCATACTGATA 3633 | A_ | |
| | | | TATCAGTATGTAT TCT | | |
| | | | | | |
| | | | ATAGTCATACGTA AGA | | |
| | | | CC | | |
| GAM75 | RNF28 | 3' | AAGGAACTTTTGTATAATA 2263 | A | |
| | | | TATTATACAAAA TTTTTT | | |
| | | | | | |
| | | | ATAATATGTTTT AAGGAA | | |
| | | | C | | |
| GAM75 | SWAP70 | 3' | GAAATAAAAAATTATTTGTATAA 2916 | AAT | |
| | | T | ATTATACAAA TTTTATTTC | | |
| | | | | | |
| | | | TAATATGTTT AAAAATAAAG | | |
| | | | ATT | | |
| GAM75 | bA430M15.1 | 3' | AAAAATTTTTGTATAATG 3072 | | |
| | | | TATTATACAAAAATTTTT | | |
| | | | | | |
| | | | GTAATATGTTTTTAAAAA | | |
| GAM76 | PSG1 | 3' | TTTGATTCGGATGTTATA 1337 | GT | |
| | | | TATAACATC AATCAAA | | |
| | | | | | |
| | | | ATATTGTAG TTAGTTT | | |
| | | | GC | | |
| GAM76 | RALB | 3' | TTTTGAACTACAGATGTTGTA 968 | _ | A_ |
| | | | TATAACATC GTA TCAAAA | | |
| | | | | | |

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|-------|-----------|----|-----------------------------|---------|
| | | | ATGTTGTAG CAT AGTTTT | |
| | | | A CA | |
| GAM76 | CEACAM8 | 3' | TTTGATTGGGATGTTATA 859 | G |
| | | | TATAACATC TAATCAAA | |
| | | | | |
| | | | ATATTGTAG GTTAGTTT | |
| | | | G | |
| GAM76 | LAT1-3TM | 3' | TTTTGGTGGCTCGATGTTA 2183 | TA__ |
| | | | TAACATCG ATCAAAA | |
| | | | | |
| | | | ATTGTAGC TGGTTTT | |
| | | | TCGG | |
| GAM76 | LAT1-3TM | 5' | TTTTGGTGGCTCGATGTTA 2827 | TA__ |
| | | | TAACATCG ATCAAAA | |
| | | | | |
| | | | ATTGTAGC TGGTTTT | |
| | | | TCGG | |
| GAM76 | MCFP | 5' | TTTTGGCTACTGATGTTA 1863 | _ AT |
| | | | TAACATC GTA CAAAA | |
| | | | | |
| | | | ATTGTAG CAT GTTTT | |
| | | | T CG | |
| GAM76 | MGC26651 | 3' | TTTTGATGTGAAAGATGTTATA 2489 | GTA__ |
| | | | TATAACATC ATCAAAA | |
| | | | | |
| | | | ATATTGTAG TAGTTTT | |
| | | | AAAGTG | |
| GAM76 | LOC197423 | 5' | TTTTGGTGGCTCGATGTTA 3090 | TA__ |
| | | | TAACATCG ATCAAAA | |
| | | | | |
| | | | ATTGTAGC TGGTTTT | |
| | | | TCGG | |
| GAM76 | LOC220565 | 5' | TTTTGGTGGCTCGATGTTA 3495 | TA__ |
| | | | TAACATCG ATCAAAA | |
| | | | | |
| | | | ATTGTAGC TGGTTTT | |
| | | | TCGG | |
| GAM77 | FLJ13215 | 3' | GAATATTCTACCTAAATAT 2126 | G A |
| | | | ATA TTAG TAGAATATTC | |
| | | | | |
| | | | TAT AATC ATCTTATAAG | |
| | | | A C | |
| GAM77 | PTP4A1 | 3' | CTAATGAATTGAGCACATCTAA 1027 | AGAAT__ |
| | T | | GTTAGAT ATTCATTAG | |
| | | | | |
| | | | TAATCTA TAAGTAATC | |
| | | | CACGAGT | |
| GAM77 | SDFR1 | 3' | TGGTAATATTCTATGCAACTAT 1430 | AG C |
| | | | ATAGTT ATAGAATATT ATTA | |
| | | | | |

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|-------|------------|----|-----------------------------|--------|------|
| | | | TATCAA TATCTTATAA TGGT | | |
| | | | CG _ | | |
| GAM77 | SDFR1 | 3' | TGGTAATATTCTATGCAACTAT 1718 | AG | C |
| | | | ATAGTT ATAGAATATT ATTA | | |
| | | | | | |
| | | | TATCAA TATCTTATAA TGGT | | |
| | | | CG _ | | |
| GAM77 | LOC221133 | 3' | CTAATGAAGAGAATATTTAAC 3608 | GAATA | |
| | | | GTTAGATA TTCATTAG | | |
| | | | | | |
| | | | CAATTTAT AAGTAATC | | |
| | | | AAGAG | | |
| GAM78 | DJ667H12.2 | 3' | TTATGCCATGAACATGCCA 1884 | CGATAA | |
| | | | TGGTATGTTCA GTATAA | | |
| | | | | | |
| | | | ACCGTACAAGT CGTATT | | |
| | | | AC_____ | | |
| GAM78 | KIAA1799 | 3' | TTATACTTAGAACTTACCA 3003 | T | ACGA |
| | | | TGGTA GTTC TAAGTATAA | | |
| | | | | | |
| | | | ACCAT CAAG ATTCATATT | | |
| | | | T _____ | | |
| GAM78 | PPP1R3B | 3' | TTTATGTAAACATACCA 2071 | C | G |
| | | | TGGTATGTT AC ATAAG | | |
| | | | | | |
| | | | ACCATACAA TG TATTT | | |
| | | | A _ | | |
| GAM78 | LOC144840 | 3' | ATTTCTCGTGAACACCCA 3071 | TA | T |
| | | | TGG TGTTACAG AAGT | | |
| | | | | | |
| | | | ACC ACAAGTGCT TTTA | | |
| | | | C_ C | | |
| GAM78 | LOC158674 | 3' | ATTTCCCGTGAACACCCA 3222 | TA | AT |
| | | | TGG TGTTACAG AAGT | | |
| | | | | | |
| | | | ACC ACAAGTGC TTTA | | |
| | | | C_ CC | | |
| GAM78 | LOC245757 | 3' | ATTTCCCGTGAACACCCA 3496 | TA | AT |
| | | | TGG TGTTACAG AAGT | | |
| | | | | | |
| | | | ACC ACAAGTGC TTTA | | |
| | | | C_ CC | | |
| GAM78 | LOC81034 | 3' | ATTTATCGTAAACATCCA 2164 | T | C |
| | | | TGG ATGTT ACGATAAGT | | |
| | | | | | |
| | | | ACC TACAA TGCTATTTA | | |
| | | | _ A | | |
| GAM79 | DTNB | 3' | CTAATATCCAGAATCTACAAAG 2316 | TA | A G |
| | A | | TCTTT AGA TT TGGATATTAG | | |
| | | | | | |

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|-------|-----------|----|-----------------------------|--------|
| | | | AGAAA TCT AA ACCTATAATC | |
| | | | CA _ G | |
| GAM79 | SP100 | 3' | AGTAAATACAATTTTAAAA 993 | GA |
| | | | TTTTAAGAATTGTG TATT | |
| | | | | |
| | | | AAAATTTTAAACAT ATGA | |
| | | | AA | |
| GAM79 | KIAA1229 | 3' | AATATCCAGAATCTACAAAGA 2620 | TA A G |
| | | | TCTTT AGA TT TGGATATT | |
| | | | | |
| | | | AGAAA TCT AA ACCTATAA | |
| | | | CA _ G | |
| GAM79 | LOC144776 | 3' | AATATTCAATATTCTTAAAGA 3070 | T TG |
| | | | TCTTT AAGAAT TGGATATT | |
| | | | | |
| | | | AGAAA TTCTTA ACTTATAA | |
| | | | _ TA | |
| GAM79 | LOC199775 | 5' | CTAATTCTTCAATTCTTAA 3432 | T T |
| | | | TTAAGAATTG GGA ATTAG | |
| | | | | |
| | | | AATTCTTAAC TCT TAATC | |
| | | | T _ | |
| GAM79 | LOC222236 | 3' | GTCTACAATTCCCAAAGA 3651 | AA |
| | | | TCTTTT GAATTGTGGAT | |
| | | | | |
| | | | AGAAAA CTTAACATCTG | |
| | | | CC | |
| GAM80 | CHRNA1 | 3' | TTATTATTGATGATAAGA 701 | C _ |
| | | | TCT ATCATCAG AATAA | |
| | | | | |
| | | | AGA TAGTAGTT TTATT | |
| | | | A A | |
| GAM80 | TNFSF9 | 3' | ATTTATTCTGAGCCTGAG 1062 | TCA |
| | | | CTCA TCAGAATAAAT | |
| | | | | |
| | | | GAGT AGTCTTATTTA | |
| | | | CCG | |
| GAM80 | AKT3 | 3' | ATTTATTTTGTAGTGATGAGAA 1214 | C__ |
| | | | TTCTCATCAT AGAATAAAT | |
| | | | | |
| | | | AAGAGTAGTG TTTTATTTA | |
| | | | ATT | |
| GAM80 | FLJ10103 | 3' | TTGTTTACTGATGAGAA 1773 | TCA |
| | | | TTCTCATCA GAATAA | |
| | | | | |
| | | | AAGAGTAGT TTTGTT | |
| | | | CA_ | |
| GAM80 | FLJ22582 | 3' | TTTTGTAAATGATGAGAA 2132 | __ |
| | | | TTCTCATCAT CAGAA | |
| | | | | |

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|-------|-----------|----|---------------------------|------|----------|
| | | | AAGAGTAGTA GTTTT | | |
| | | | AAT | | |
| GAM80 | KIAA1371 | 3' | ATTCTAGAAATGGTGAGAA 3454 | — | — |
| | | | TTCTCATCA TC AGAAT | | |
| | | | | | |
| | | | AAGAGTGGT AG TCTTA | | |
| | | | AA A | | |
| GAM80 | MACF1 | 3' | ATTTATTCTGAACGGGAGAA 2308 | ATCA | |
| | | | TTCTC TCAGAATAAAT | | |
| | | | | | |
| | | | AAGAG AGTCTTATTTA | | |
| | | | GGCA | | |
| GAM80 | MACF1 | 3' | ATTTATTCTGAACGGGAGAA 1403 | ATCA | |
| | | | TTCTC TCAGAATAAAT | | |
| | | | | | |
| | | | AAGAG AGTCTTATTTA | | |
| | | | GGCA | | |
| GAM80 | MGC16824 | 3' | TTATTCTGACAATGAAGA 1910 | — | CA |
| | | | TCT CAT TCAGAATAA | | |
| | | | | | |
| | | | AGA GTA AGTCTTATT | | |
| | | | A AC | | |
| GAM80 | NR2C1 | 3' | ATTTATTCTTGGTGAAGA 1006 | A | — |
| | | | TC TCATCA GAATAAAT | | |
| | | | | | |
| | | | AG AGTGGT CTTATTTA | | |
| | | | A T | | |
| GAM80 | P450RAI-2 | 3' | ATTTATTCACTGATAGAGAA 1887 | — | TCA |
| | | | TTCTC ATCA GAATAAAT | | |
| | | | | | |
| | | | AAGAG TAGT CTTATTTA | | |
| | | | A CA_ | | |
| GAM80 | LOC152715 | 5' | ATTTGGCTGATGATGGAA 3174 | T | AA |
| | | | TTC CATCATCAG TAAAT | | |
| | | | | | |
| | | | AAG GTAGTAGTC GTTTA | | |
| | | | _ G_ | | |
| GAM80 | LOC222166 | 3' | ATTCTGTGGGCTGATGAGAA 3634 | T | _____ |
| | | | TTCTCATCA CAGAAT | | |
| | | | | | |
| | | | AAGAGTAGT GTCTTA | | |
| | | | CGGGT | | |
| GAM80 | LOC257042 | 3' | ATTCTGAGTGATGATGAA 3719 | — | — |
| | | | TTC TCATCA TCAGAAT | | |
| | | | | | |
| | | | AAG AGTAGT AGTCTTA | | |
| | | | T G | | |
| GAM81 | CORO2B | 5' | TTCTGTTGCCCAAGCTGG 2694 | — | GAG TAAA |
| | | | CC GCT TGG CAACAGAA | | |
| | | | | | |

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|-------|---------|----|-----------------------------|----------|------|
| | | | GG CGA ACC GTTGTCTT | | |
| | | | T ____ C____ | | |
| GAM81 | EFNB2 | 3' | GTTCTGTTACCCAGGGCTCTGC 1084 | T ____ | AACA |
| | | | GC GAGT GGTA ACAGAAC | | |
| | | | | | |
| | | | CG CTCG CCAT TGTCTTG | | |
| | | | T GGAC ____ | | |
| GAM81 | GCGR | 5' | TCTGCTGCTCTGCCACTCAGC 714 | AA_ A | |
| | | | GCTGAGTGGTA CA CAGA | | |
| | | | | | |
| | | | CGACTCACCGT GT GTCT | | |
| | | | CTC C | | |
| GAM81 | HMOX1 | 3' | GTTCTGTTGTTTTTATAGCAGG 901 | G AGTGGT | |
| | G | | CC CTG AAACAACAGAAC | | |
| | | | | | |
| | | | GG GAC TTTGTTGTCTTG | | |
| | | | _ GATATT | | |
| GAM81 | HS3ST2 | 3' | GTTCTGTTGCTATGAACACAGC 1267 | A GGTA | AAA |
| | | | GCTG GT CAACAGAAC | | |
| | | | | | |
| | | | CGAC CA GTTGTCTTG | | |
| | | | A AGTATC | | |
| GAM81 | PIM2 | 3' | CTGTTGTTACCCCAAGG 2550 | GC AGT A | |
| | | | CC TG GGTA CAACAG | | |
| | | | | | |
| | | | GG AC CCATT GTTGTC | | |
| | | | A_ C__ _ | | |
| GAM81 | PIP5K1B | 5' | TCTGTTGCTACTAAGC 1034 | G TAAA | |
| | | | GCT AGTGG CAACAGA | | |
| | | | | | |
| | | | CGA TCATC GTTGTCT | | |
| | | | A ____ | | |
| GAM81 | RBM3 | 3' | TTCTGTTGTGTCTCATACAG 2887 | A TAA | |
| | | | CTG GTGG ACAACAGAA | | |
| | | | | | |
| | | | GAC TACT TGTTGTCTT | | |
| | | | A CTG | | |
| GAM81 | SMAC | 3' | CTGTCTCCCCACTCAGTGG 1889 | TAAACA | |
| | | | CCGCTGAGTGG ACAG | | |
| | | | | | |
| | | | GGTGA CTACC TGTC | | |
| | | | CCTC__ | | |
| GAM81 | SMAC | 3' | CTGTCTCCCCACTCAGTGG 2459 | TAAACA | |
| | | | CCGCTGAGTGG ACAG | | |
| | | | | | |
| | | | GGTGA CTACC TGTC | | |
| | | | CCTC__ | | |
| GAM81 | SMAC | 3' | CTGTCTCCCCACTCAGTGG 2460 | TAAACA | |
| | | | CCGCTGAGTGG ACAG | | |
| | | | | | |

GGTGACTCACC TGTC
CCTC__

GAM81 SOST 3' TTCTGCCCACCACTCACGG 2148 C AAACAA
CCG TGAGTGGT CAGAA
||| ||||| |||||
GGC ACTCACCA GTCTT
_ CCC__

GAM81 ZNF10 5' TCTGCTGTCACTCAAGG 1626 GC GTAA A
CC TGAGTG ACA CAGA
|| ||||| ||| |||||
GG ACTCAC TGT GTCT
A_ _ C

GAM81 ABCA10 5' TTCTGTTAGTTACTCA 2373 GTAA _
TGAGTG AC AACAGAA
||||| || |||||
ACTCAT TG TTGTCTT
_ A

GAM81 H2AFJ 3' GTTCTGCTATTTACTCTGTGG 1807 T TAAACAA
CCGC GAGTGG CAGAAC
||||| |||||
GGTG CTCATT GTCTTG
T TATC__

GAM81 HSH2 3' GTTCTGTTGTCTAAAAGC 2289 GAG TAA
GCT TGG ACAACAGAAC
||| ||| |||||
CGA ATC TGTTGTCTTG
AA_ _

GAM81 KIAA1024 3' TTCTGTTGTTCCACCATTAAGGG 2841 G G A
G CC CT AGTGGT AACAACAGAA
|| || ||||| |||||
GG GA TTACCA TTGTTGTCTT
G A C

GAM81 KIAA1399 3' GTTCTGCTATTTCCAATCAGTC 2881 C G T CAA
A C GCTGA TGG AAA CAGAAC
| ||||| ||| |||||
A TGA CT ACC TTT GTCTTG
C A _ ATC

GAM81 MIC2L1 3' TCTGTTGTGTCAGAGGCTCACGG 2205 C GGTA
CCG TGAGT ACAACAGA
||| ||||| |||||
GGC ACTCG TGTTGTCT
_ GAGAC

GAM81 RASGRF2 3' TTCTGTTAGAACTCAGGG 2590 G GGTAAC
CC CTGAGT AACAGAA
|| ||||| |||||
GG GACTCA TTGTCTT
_ AGA__

GAM81 TJP2 3' CTGTTACTTGCTTCAGTGG 2534 GT AC
CCGCTGA GGTAAC AACAG
||||| ||||| |||||

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|-------|-----------|----|------------------------|-----------|----------|-----------|----|----|
| | | | GGTGA | CT | TCGTT | TTGTC | | |
| | | | __ | | CA | | | |
| GAM81 | LOC202020 | 3' | TTCTGTTGCCTAAGGCAGC | 3459 | AG_ | TAAA | | |
| | | | GCTG | TGG | CAACAGAA | | | |
| | | | | | | | | |
| | | | CGAC | ATC | GTTGTCTT | | | |
| | | | GGA | C__ | | | | |
| GAM81 | LOC220766 | 5' | TCTGGATTTCACCACTCAGAGG | 3499 | G | AAACAA | | |
| | | | CC | CTGAGTGGT | CAGA | | | |
| | | | | | | | | |
| | | | GG | GA | CTCACCA | GTCT | | |
| | | | A | CTTTAG | | | | |
| GAM81 | LOC256277 | 3' | CTGTTGTTTCAGCAGTG | 3664 | AG | TAA | | |
| | | | CGCTG | TGG | ACAACAG | | | |
| | | | | | | | | |
| | | | GTGAC | ACT | TGTTGTC | | | |
| | | | G_ | __ | | | | |
| GAM81 | LOC256337 | 3' | CTGTTGTTTCAGCAGTG | 3663 | AG | TAA | | |
| | | | CGCTG | TGG | ACAACAG | | | |
| | | | | | | | | |
| | | | GTGAC | ACT | TGTTGTC | | | |
| | | | G_ | __ | | | | |
| GAM82 | PTCRA | 3' | ATGACTGAGAACATTAAA | 2433 | ATC | | | |
| | | | TTTAAT | CTCAGTCAT | | | | |
| | | | | | | | | |
| | | | AAATTA | GAGTCAGTA | | | | |
| | | | CAA | | | | | |
| GAM82 | PUNC | 3' | ATGACTTGGAAGTGAAGTAAAC | 3469 | ATA | TC | | |
| | | | GTTAGTTTA | TCC | AGTCAT | | | |
| | | | | | | | | |
| | | | CAATCAAGT | AGG | TCAGTA | | | |
| | | | CA_ | T_ | | | | |
| GAM82 | KIAA0940 | 3' | ACTGATATATTATAAACTAAC | 1586 | __ | CC | | |
| | | | GTTAGTTTA | ATAT | TCAGT | | | |
| | | | | | | | | |
| | | | CAATCAAAT | TATA | AGTCA | | | |
| | | | AT | T_ | | | | |
| GAM82 | RGS18 | 3' | ATGACTGAGAAATAAGATCCAC | 2398 | TA | AA | C | |
| | | | GT | GTTT | TAT | CTCAGTCAT | | |
| | | | | | | | | |
| | | | CA | TAGA | ATA | GAGTCAGTA | | |
| | | | CC | __ | A | | | |
| GAM83 | ATP12A | 3' | CCCTGCAGTGCAGACATCGTCA | 846 | A | A | C | TT |
| | A | | TTGATGAT | TCT | CAT | GT | GG | |
| | | | | | | | | |
| | | | AACTGCTA | AGA | GTG | CG | CC | |
| | | | C | C | A | TC | | |
| GAM83 | CRYGS | 3' | CCAAATAGGCATCATCAA | 1722 | AT | ACATC | | |
| | | | TTGATGAT | CT | GTTTGG | | | |
| | | | | | | | | |

AACTACTA GA TAAACC
 CG _____
 GAM83 LPIN2 3' TCCAAAGTTAATTGTAAACATC 1514 ATC TCG____
 ATCAG TTGATGAT TACA TTTGGA
 ||||| ||| |||||
 GACTACTA ATGT AAACCT
 CAA TAATTG
 GAM83 KIAA1786 3' TCCATGCTGTAGATACCA 2738 A TC T
 TG TATCTACA GT TGGG
 || ||||| || |||||
 AC ATAGATGT CG ACCT
 C _ T
 GAM83 LOC222008 3' CCAAGTTAGATGTCATCAA 3629 CATCG
 TTGATGATATCTA TTTGG
 ||||| |||||
 AACTACTGTAGAT GAACC
 T____
 GAM83 LOC90639 5' TCTGAACACAGATATCATCAG 2663 ACATC TG
 TTGATGATATCT GTT GA
 ||||| ||| ||
 GACTACTATAGA CAA CT
 CA____ GT
 GAM84 AP1B1 3' GTCAGGATTGAAAGCTG 803 C ATA
 TAGCTTTCA TC TGAC
 ||||| || |||||
 GTCGAAAGT AG ACTG
 T G____
 GAM84 IQGAP1 3' GTCATTTAGAAGTGGAAGCTA 2840 _AT_
 TAGCTTTCACT C ATGAC
 ||||| | |||||
 ATCGAAGGTGA G TACTG
 A ATT
 GAM84 PDE6A 3' GTCATAGGATTTGAAAGCTG 744 C_ A
 TAGCTTTCA TC TATGAC
 ||||| || |||||
 GTCGAAAGT AG ATACTG
 TT G
 GAM84 PTEN 3' CATATAAATGTGGAGGCTA 728 TC____
 TAGCTTTCAC ATATG
 ||||| |||||
 ATCGGAGGTG TATAC
 TAAA
 GAM84 SH3GL2 3' TCATGTGGAGTGAAAGGC 985 _ _
 GC TTTCACCTC ATATGA
 || ||||| |||||
 CG AAAGTGAG TGTACT
 G G
 GAM84 C1orf16 3' CATGGGAAGTGAAAGCTG 1567 _A
 TAGCTTTCACT C TATG
 ||||| | |||||

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|-------|--------------|----|----------------------|------|--------|
| | | | GTCGAAAGTGA G GTAC | | |
| | | | A G | | |
| GAM84 | DKFZp547A023 | 3' | GTCATATAAATGAGTGAAA | 2956 | _____ |
| | | | TTTCACTCA TATGAC | | |
| | | | | | |
| | | | AAAGTGAGT ATACTG | | |
| | | | AAAT | | |
| GAM84 | FLJ11850 | 5' | GTCATATGTGGCAGCT | 2001 | T TC |
| | | | AGCT TCAC ATATGAC | | |
| | | | | | |
| | | | TCGA GGTG TATACTG | | |
| | | | C _ | | |
| GAM84 | FLJ12888 | 3' | GTCATATTTTTGAAAGTTA | 2115 | CTC |
| | | | TAGCTTTCA ATATGAC | | |
| | | | | | |
| | | | ATTGAAAGT TATACTG | | |
| | | | TTT | | |
| GAM84 | FLJ21596 | 3' | GTCATTGCATGGTGAAAGC | 2092 | T _ |
| | | | GCTTTCAC CAT ATGAC | | |
| | | | | | |
| | | | CGAAAGTG GTA TACTG | | |
| | | | _ CGT | | |
| GAM84 | KIAA1878 | 3' | GTCACAGATTTTGAAAGCTA | 3539 | C_ ATA |
| | | | TAGCTTTCA TC TGAC | | |
| | | | | | |
| | | | ATCGAAAGT AG ACTG | | |
| | | | TTT AC_ | | |
| GAM84 | NXPH3 | 3' | GTCATGGGAGGAAGCTA | 2728 | A TA |
| | | | TAGCTTTC CTCA TGAC | | |
| | | | | | |
| | | | ATCGAAGG GGGT ACTG | | |
| | | | A _ | | |
| GAM84 | SS18L1 | 3' | GTCATATGAATGTTGAGC | 2719 | T_ C |
| | | | GCTT CA TCATATGAC | | |
| | | | | | |
| | | | CGAG GT AGTATACTG | | |
| | | | TT A | | |
| GAM84 | SYT13 | 3' | CAGATGCAGAGAAAGCTA | 3605 | A _ A |
| | | | TAGCTTTC CT CAT TG | | |
| | | | | | |
| | | | ATCGAAAG GA GTA AC | | |
| | | | A C G | | |
| GAM84 | LOC134301 | 3' | GTCATATGTTAAAGAGCTA | 3016 | CACT |
| | | | TAGCTTT CATATGAC | | |
| | | | | | |
| | | | ATCGAGA GTATACTG | | |
| | | | AATT | | |
| GAM84 | LOC151438 | 3' | GTCATTTCTGATGAAAGCTG | 3346 | C T_ |
| | | | TAGCTTTCA TCA ATGAC | | |
| | | | | | |

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|-------|-----------|----|--------------------------|-----------|--|
| | | | GTCGAAAGT AGT TACTG | | |
| | | | _ CTT | | |
| GAM84 | LOC158696 | 3' | TCATATGAAGAAAGCTA 3223 | AC | |
| | | | TAGCTTTC TCATATGA | | |
| | | | | | |
| | | | ATCGAAAG AGTATACT | | |
| | | | A_ | | |
| GAM84 | LOC221975 | 3' | GTCATATGACAGGGCTG 3570 | CAC | |
| | | | TAGCTTT TCATATGAC | | |
| | | | | | |
| | | | GTCGGGA AGTATACTG | | |
| | | | C_ | | |
| GAM84 | LOC84549 | 3' | GTCAAGTGGAAAGCTA 2256 | ACT A | |
| | | | TAGCTTTC CAT TGAC | | |
| | | | | | |
| | | | ATCGAAAG GTG ACTG | | |
| | | | _ A | | |
| GAM84 | LOC90459 | 3' | TCATATAGGGTGAAAAGC 2644 | - - | |
| | | | GCTTT CACTC ATATGA | | |
| | | | | | |
| | | | CGAAA GTGGG TATACT | | |
| | | | A A | | |
| GAM84 | LOC90529 | 3' | GTCTACTGGGCGAAAGCTA 2652 | A TAT | |
| | | | TAGCTTTC CTCA GAC | | |
| | | | | | |
| | | | ATCGAAAG GGGT CTG | | |
| | | | C CAT | | |
| GAM85 | F2RL3 | 3' | TGGTGAAATCCTATCTCT 1074 | AG ATGTAA | |
| | | | AGA TAGGATT CATCA | | |
| | | | | | |
| | | | TCT ATCCTAA GTGGT | | |
| | | | CT A_____ | | |
| GAM85 | RAP1B | 3' | ATGTTACAACACTACTTT 1642 | GATTA | |
| | | | GAAGTAG TGTAACAT | | |
| | | | | | |
| | | | TTTCATC ACATTGTA | | |
| | | | A_____ | | |
| GAM85 | SLC6A12 | 3' | TTGCCATCCTGCTTCT 988 | TAT | |
| | | | AGAAGTAGGAT GTAA | | |
| | | | | | |
| | | | TCTTCGTCCTA CGTT | | |
| | | | C_ | | |
| GAM85 | ALDH5A1 | 3' | TGCAAATCCTACCCCTG 799 | AA A | |
| | | | CAG GTAGGATT TGTA | | |
| | | | | | |
| | | | GTC CATCCTAA ACGT | | |
| | | | CC _ | | |
| GAM85 | C20orf112 | 3' | TGATGTTAGAATCCCAC 2379 | A ATG | |
| | | | GT GGATT TAACATCA | | |
| | | | | | |

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|-------|---------------|----|--------------------------|------|--------|---------|
| | | | CA CCTAA ATTGTAGT | | | |
| | | | C G__ | | | |
| GAM85 | DICER1 | 3' | GATGCCACATAGTCTTGC | 2152 | AA | |
| | | | GTAGGATTATGT CATC | | | |
| | | | | | | |
| | | | CGTTCTGATACA GTAG | | | |
| | | | CC | | | |
| GAM85 | DKFZP566G1424 | 5' | TGATGTTAGAATCCAC | 3320 | A | ATG |
| | | | GT GGATT TAACATCA | | | |
| | | | | | | |
| | | | CA CCTAA ATTGTAGT | | | |
| | | | C G__ | | | |
| GAM85 | FLJ10858 | 3' | ATGTTTGGTCCTCCTCTG | 1805 | A T | TGT |
| | | | CAGA G AGGATTA AACAT | | | |
| | | | | | | |
| | | | GTCT C TCCTGGT TTGTA | | | |
| | | | _ C _ | | | |
| GAM85 | FLJ13265 | 3' | TGATGTTACTTGCCACCTACTT | 2100 | ATTAT_ | |
| | C | | GAAGTAGG GTAACATCA | | | |
| | | | | | | |
| | | | CTTCATCC CATTGTAGT | | | |
| | | | ACCGTT | | | |
| GAM85 | FLJ22282 | 3' | TGATGTGGAAACCTACTTCTG | 2089 | A | ATGTA |
| | | | CAGAAGTAGG TT ACATCA | | | |
| | | | | | | |
| | | | GTCTTCATCC AA TGTAGT | | | |
| | | | A GG__ | | | |
| GAM85 | GBTS1 | 3' | GATGTTGCCTCCTCTCCTG | 2516 | A T | TTAT |
| | | | CAG AG AGGA GTAACATC | | | |
| | | | | | | |
| | | | GTC TC TCCT CGTTGTAG | | | |
| | | | C _ C__ | | | |
| GAM85 | KIAA0193 | 3' | TGATGTCCTAGTCCTACCACT | 1545 | AA | TGTA |
| | | | AG GTAGGATTA ACATCA | | | |
| | | | | | | |
| | | | TC CATCCTGAT TGTAGT | | | |
| | | | AC CC__ | | | |
| GAM85 | KIAA1030 | 3' | TGATGCCCTGTCCTCACCTCTG | 3597 | A _ | TATGTAA |
| | | | CAGA GT AGGAT CATCA | | | |
| | | | | | | |
| | | | GTCT CA TCCTG GTAGT | | | |
| | | | C C TCCC__ | | | |
| GAM85 | OR7C1 | 3' | ATGTTTCATGCATCCATACTTC | 1719 | _ _ | T |
| | TG | | CAGAAGTA GGAT TATG AACAT | | | |
| | | | | | | |
| | | | GTCTTCAT CCTA GTAC TTGTA | | | |
| | | | A C T | | | |
| GAM85 | PRO2214 | 3' | TATGTAAATCCTACTTTTG | 1834 | _ | |
| | | | CAGAAGTAGGATT ATGTA | | | |
| | | | | | | |

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|-------|-----------|----|-----------------------------|-----|----------|
| | | | GTTTTTCATCCTAA TGTAT | | |
| | | | A | | |
| GAM85 | SMCR5 | 3' | ACATGGGGAGATCCTACCTCT 2502 | A | _____ |
| | | | AGA GTAGGATT ATGT | | |
| | | | | | |
| | | | TCT CATCCTAG TACA | | |
| | | | C AGGGG | | |
| GAM85 | SSH1 | 3' | ACATTAAGTCCTACCTCTG 1869 | A | ___ |
| | | | CAGA GTAGGATT ATGT | | |
| | | | | | |
| | | | GTCT CATCCTGA TACA | | |
| | | | C AT | | |
| GAM85 | TERA | 3' | TGGATCATCTCTACTTCTG 1948 | | _ T G |
| | | | CAGAAGTAG GAT AT TA | | |
| | | | | | |
| | | | GTCTTCATC CTA TA GT | | |
| | | | T C G | | |
| GAM85 | WBSCR23 | 5' | ATATAGTGAGACCCTATTTCT 2131 | | _____ |
| | | | AGAAGTAGG ATTATGT | | |
| | | | | | |
| | | | TCTTTATCC TGATATA | | |
| | | | CAGAG | | |
| GAM85 | LOC134637 | 3' | ATGTTACATGCACCTTC 3017 | AGT | AT |
| | | | GA AGG TATGTAACAT | | |
| | | | | | |
| | | | CT TCC GTACATTGTA | | |
| | | | ___ AC | | |
| GAM85 | LOC146745 | 5' | GATGCCGAGGACATCTTACTCC 3098 | A | TATGTAA_ |
| | TG | | CAG AGTAGGAT CATC | | |
| | | | | | |
| | | | GTC TCATTCTA GTAG | | |
| | | | C CAGGAGCC | | |
| GAM85 | LOC153416 | 3' | ATGTTACAACACTACTTT 2573 | | GATTA |
| | | | GAAGTAG TGTAACAT | | |
| | | | | | |
| | | | TTTCATC ACATTGTA | | |
| | | | A_____ | | |
| GAM85 | LOC157867 | 5' | TGATTCAACAATCTTACTCCTG 3383 | A | TA AAC |
| | | | CAG AGTAGGAT TGT ATCA | | |
| | | | | | |
| | | | GTC TCATTCTA ACA TAGT | | |
| | | | C _ ACT | | |
| GAM85 | LOC201243 | 5' | GATGCCGAGGACATCTTACTCC 3425 | A | TATGTAA_ |
| | TG | | CAG AGTAGGAT CATC | | |
| | | | | | |
| | | | GTC TCATTCTA GTAG | | |
| | | | C CAGGAGCC | | |
| GAM86 | OSR1 | 3' | CGTTAGTAAACTTACTTCATA 1188 | AG_ | CT |
| | | | TATGAAGTAA TAT ACG | | |
| | | | | | |

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|-------|-----------|----|------------------------------|--------|---------|
| | | | ATACTTCATT ATG TGC | | |
| | | | CAA AT | | |
| GAM86 | PACE4 | 5' | CGCAGGCCCTTTACTTCA 2435 | TA | A |
| | | | TGAAGTAAAG TCT CG | | |
| | | | | | |
| | | | ACTTCATTTC GGA GC | | |
| | | | CC C | | |
| GAM86 | KIAA1462 | 3' | CGTATGATTTTATTTTATA 3522 | ATC | |
| | | | TATGAAGTAAAGT TACG | | |
| | | | | | |
| | | | ATACTTTATTTTA ATGC | | |
| | | | GT_ | | |
| GAM86 | LOC145945 | 3' | TCATAGATACAATACTTTA 3280 | AA | C |
| | | | TGAAGTA GTATCTA GA | | |
| | | | | | |
| | | | ATTTTCAT CATAGAT CT | | |
| | | | AA A | | |
| GAM86 | LOC219401 | 5' | TCGTGGGCCCGCACTTCATA 3580 | AAAGTA | |
| | | | TATGAAGT TCTACGA | | |
| | | | | | |
| | | | ATACTTCA GGGTGCT | | |
| | | | CGCCC_ | | |
| GAM87 | ABCA1 | 3' | TGGTGGCAGTAACATGCAAC 1219 | T | CA |
| | | | GTT GCATGTTAC CTATCA | | |
| | | | | | |
| | | | CAA CGTACAATG GGTGGT | | |
| | | | _ AC | | |
| GAM87 | CD2AP | 3' | ATAATGGTAATAGGAAAAC 1408 | GCA | C |
| | | | GTTT TGTTACCA TAT | | |
| | | | | | |
| | | | CAAA ATAATGGT ATA | | |
| | | | AGG A | | |
| GAM87 | HHIP | 5' | TGACACTGGCACAAC TGCAAAC 1989 | T | A__ CTA |
| | GG | | CCGTTTGCA GTT CCA TCA | | |
| | | | | | |
| | | | GGCAAACGT CAA GGT AGT | | |
| | | | _ CAC CAC | | |
| GAM87 | AKAP7 | 3' | TGATAGTGTCTGCACAAC 1159 | _ | TGTTAC |
| | | | GTT TGCA CACTATCA | | |
| | | | | | |
| | | | CAA ACGT GTGATAGT | | |
| | | | C CT____ | | |
| GAM87 | AKAP7 | 3' | TGATAGTGTCTGCACAAC 1683 | _ | TGTTAC |
| | | | GTT TGCA CACTATCA | | |
| | | | | | |
| | | | CAA ACGT GTGATAGT | | |
| | | | C CT____ | | |
| GAM87 | AKAP7 | 3' | TGATAGTGTCTGCACAAC 2446 | _ | TGTTAC |
| | | | GTT TGCA CACTATCA | | |
| | | | | | |

CAA ACGT GTGATAGT
 C CT____
 GAM87 ARHGAP5 3' TTGATAATGTTGTGCAAAGG 3077 G TTAC C
 CC TTTGCATG CA TATCAA
 || ||||| || |||||
 GG AAACGTGT GT ATAGTT
 _ T__ A
 GAM87 C22orf19 3' TGACAGTGCAGTGCAAAC 1048 GTTAC A
 GTTTGCAT CACT TCA
 ||||| ||| |||
 CAAACGTG GTGA AGT
 AC__ C
 GAM87 DKFZp566D234 3' GACAGTGGTAAGTAAA 2611 ATG A
 TTTGC TTACCACT TC
 |||| ||||| ||
 AAATG AATGGTGA AG
 _ C
 GAM87 FLJ11160 3' TGACAGCGAGATGCAAGC 1815 G ACCA A
 GTTTGCAT TT CT TCA
 ||||| || ||| |||
 CGAACGTA AG GA AGT
 G C__ C
 GAM87 FLJ13089 5' TTGACAATGGTAATAATAAAAT 2899 GCA CTA
 GG CCGTTT TGTTACCA TCAA
 |||| ||||| |||
 GGTAAGT ATAATGGT AGTT
 ATA AAC
 GAM87 FLJ14297 3' ATAGTTTAAACATGCAAC 2107 T ACC
 GTT GCATGTT ACTAT
 || ||||| |||||
 CAA CGTACAA TGATA
 _ ATT
 GAM87 HSPC065 3' TGACAGTGGTAGAATAAAGG 1483 G CATG A
 CC TTTG TTACCACT TCA
 || ||| ||||| |||
 GG AAAT GATGGTGA AGT
 _ AA__ C
 GAM87 LOC150737 3' TGATAGTGGCATTATCAAATG 3149 C TTA_
 G CCGTTTG ATG CCACTATCA
 ||||| ||| ||||| |||
 GGTAAC TAT GGTGATAGT
 _ TTAC
 GAM87 LOC152185 3' ATAATGGTAATGCAAATCA 2498 C GT C
 C GTTTGCAT TACCA TAT
 | ||||| ||||| |||
 A TAAACGTA ATGGT ATA
 C _ A
 GAM88 DAAM2 3' ACCAACTGGGGAAGTGTG 3560 _ C
 TACAGTTCCTT GTT GT
 ||||| ||| ||| |||

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|-------|---------------|----|-----------------------|--------------------|-----|-----------------|
| | | | | GTGTCAAGGGG CAA CA | | |
| | | | | T C | | |
| GAM88 | FN14 | 3' | TGACTAAGGA | ACTGCAGC 1703 | A | TTC |
| | | | | GCT CAGTTCCTTG | | GTCTG |
| | | | | | | |
| | | | | CGA GTCAAGGAAT | | CAGT |
| | | | | C | | ___ |
| GAM88 | TM4SF2 | 3' | TGTTTTAAAAAGGA | ACTGCAGC 1131 | A | GTTCGTC |
| | | | | GCT CAGTTCCTT | | GACA |
| | | | | | | |
| | | | | CGA GTCAAGGAA | | TTGT |
| | | | | C | | AAATT___ |
| GAM88 | WNT3 | 3' | GTCAGACAGCAAGGA | ACTGT 2159 | | C _ |
| | | | | ACAGTTCCTTGTT | | GTC GAC |
| | | | | | | |
| | | | | TGTCAAGGAACGA | | CAG CTG |
| | | | | _ A | | |
| GAM88 | GLTP | 3' | GCCAACGAGGAACACAGC | 1686 | ACA | C |
| | | | | GCT GTTCCTTGTT | | GT |
| | | | | | | |
| | | | | CGA CAAGGAGCAA | | CG |
| | | | | CA_ | | C |
| GAM88 | PRO0149 | 5' | GTCCCAAAAAACTGTAGT | 1473 | | CC TTCGTC |
| | | | | GCTACAGTT TTG | | GAC |
| | | | | | | |
| | | | | TGATGTCAA AAC | | CTG |
| | | | | AA C_____ | | |
| GAM89 | LAMP2 | 3' | AGTACTAAAATTAATGCA | 1455 | | T |
| | | | | TGCATTAATTTT | | GTATT |
| | | | | | | |
| | | | | ACGTAATTAAAA | | CATGA |
| | | | | T | | |
| GAM89 | DKFZp762K2015 | 3' | AGAATCCATGCTAAAAATTA | 2949 | | _ T |
| | | | | TTAATTTT | | GTAT GATTCT |
| | | | | | | |
| | | | | AATTAAAAA | | CGTA CTAAGA |
| | | | | T C | | |
| GAM89 | FLJ10921 | 5' | AGAATCAATACTACA | ACTGCA 1808 | | TTAATTTT |
| | | | | TGCA | | GTATTGATTCT |
| | | | | | | |
| | | | | ACGT | | CATAACTAAGA |
| | | | | CAACAT___ | | |
| GAM89 | LOC91752 | 3' | AATCAATACAATATATGC | 2778 | | TAATTT |
| | | | | GCAT | | TTGTATTGATT |
| | | | | | | |
| | | | | CGTA | | AACATAACTAA |
| | | | | TAT___ | | |
| GAM90 | GLP1R | 3' | AGACACATGGCTATCCTAGAG | 896 | C | A |
| | | | | TTTTG | | GATAGCCATGT TCT |
| | | | | | | |

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|-------|-----------|----|-----------------------------|----------|
| | | | GAGAT CTATCGGTACA AGA | |
| | | | C C | |
| GAM90 | FLJ10891 | 3' | TACAGCCATTGCAAAACA 1806 | A CA |
| | | | TGTTTTGCGAT GC TGTA | |
| | | | | |
| | | | ACAAAACGTTA CG ACAT | |
| | | | C _ | |
| GAM90 | KIAA0781 | 3' | CAAGGCCATCACAAAGCA 2793 | C A A |
| | | | TGTTTTG GAT GCC TG | |
| | | | | |
| | | | ACGAAAC CTA CGG AC | |
| | | | A C A | |
| GAM90 | KIAA1077 | 3' | CATGGCCACCGCAGAACA 2963 | ATA |
| | | | TGTTTTGCG GCCATG | |
| | | | | |
| | | | ACAAGACGC CGGTAC | |
| | | | CAC | |
| GAM90 | PELI2 | 3' | ATACATGGGACTTCACAAACA 1950 | T C TAG_ |
| | | | TGTTT G GA CCATGTAT | |
| | | | | |
| | | | ACAAA C CT GGTACATA | |
| | | | _ A TCAG | |
| GAM91 | GPRK6 | 3' | GAGGAGCCACTGCCAAACT 898 | CTA AGA |
| | | | AGTTTGGCAG GC TTC | |
| | | | | |
| | | | TCAAACCGTC CG GAG | |
| | | | AC_ AG_ | |
| GAM91 | WWP1 | 5' | GTTTCTAGTGCCAAACTTA 3164 | G C |
| | | | TAAGTTTGGCA CTAG AGAT | |
| | | | | |
| | | | ATTCAAACCGT GATC TTTG | |
| | | | - - | |
| GAM91 | LOC144559 | 5' | TGAATCTGCCAGCACCATAACT 3067 | _ CA A |
| | T | | AAGTT TGG GCT GCAGATTCA | |
| | | | | |
| | | | TTCAA ACC CGA CGTCTAAGT | |
| | | | T A_ C | |
| GAM91 | LOC200163 | 3' | TGCTAATGCCAAACTTA 3440 | GC |
| | | | TAAGTTTGGCA TAGCA | |
| | | | | |
| | | | ATTCAAACCGT ATCGT | |
| | | | A_ | |
| GAM91 | LOC219918 | 5' | TGAATCTGCCAGCACCAGAACT 3531 | _ CA A |
| | T | | AAGT TTGG GCT GCAGATTCA | |
| | | | | |
| | | | TTCA GACC CGA CGTCTAAGT | |
| | | | A A_ C | |
| GAM91 | LOC220071 | 5' | TGAATCTGCCAGCAGCAGAACT 3603 | G A A |
| | T | | AAGTTT GC GCT GCAGATTCA | |
| | | | | |

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|-------|-----------|----|------------------------------|--------|--------|
| | | | TTCAAG CG CGA CGTCTAAGT | | |
| | | | A A C | | |
| GAM91 | LOC255515 | 3' | TGAATCTGCCAACACCAGAACT 3689 | _ | CAGCTA |
| | | T | AAGT TTGG GCAGATTCA | | |
| | | | | | |
| | | | TTCA GACC CGTCTAAGT | | |
| | | | A ACAAC_ | | |
| GAM92 | BCL11B | 3' | ACAAATATCATAAAAGGA 2020 | CC G | |
| | | | TCCT TA GATATTTGT | | |
| | | | | | |
| | | | AGGA AT CTATAAACA | | |
| | | | AA A | | |
| GAM92 | M17S2 | 5' | GATACCTACAACCTCCTAGGAAG 2213 | C | TAT A_ |
| | | A | TC TCCTAGGA TTGTA TATC | | |
| | | | | | |
| | | | AG AGGATCCT AACAT ATAG | | |
| | | | A C_ CC | | |
| GAM92 | CRFG | 3' | ATATTACAAATATTTTGAG 2775 | CT | |
| | | | CTC AGGATATTTGTAATAT | | |
| | | | | | |
| | | | GAG TTTTATAAACATTATA | | |
| | | | — | | |
| GAM92 | FLJ23360 | 5' | ATATTGCATCCCTAGAGA 2030 | _ | ATATT |
| | | | TC CTAGG TGTAATAT | | |
| | | | | | |
| | | | AG GATCC ACGTTATA | | |
| | | | A CT_ | | |
| GAM92 | KIAA0349 | 3' | ATATCACAGAGCCTGGGAG 3561 | ATA A | |
| | | | CTCCTAGG TTTGT ATAT | | |
| | | | | | |
| | | | GAGGGTCC AGACA TATA | | |
| | | | G_ C | | |
| GAM92 | PRO2325 | 5' | GATATTAACAGTCATCCTAG 1836 | AT _ | |
| | | | CTAGGAT TTGT AATATC | | |
| | | | | | |
| | | | GATCCTA GACA TTATAG | | |
| | | | CT A | | |
| GAM92 | SCYA16 | 3' | ATATTTTCTCAATCTTAGGAGG 1130 | ATTTGT | |
| | | A | TCCTCCTAGGAT AATAT | | |
| | | | | | |
| | | | AGGAGGATTCTA TTATA | | |
| | | | ACTCTT | | |
| GAM93 | DJ-1 | 3' | CGTTAGGAATCCATTCTCA 1375 | ACTAAA | |
| | | | TGAGAAT ATTCCTAACG | | |
| | | | | | |
| | | | ACTCTTA TAAGGATTGC | | |
| | | | CC_ | | |
| GAM93 | FLJ10535 | 3' | TAGGAATTTTATTCCCA 1787 | A CT | |
| | | | TG GAATA AAAATTCCTA | | |
| | | | | | |

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|-------|-----------|----|---------------------------|------|-----------|
| | | | AC CTTAT TTTTAAGGAT | | |
| | | | C _ | | |
| GAM93 | FLJ10539 | 3' | AGGATTTTAGTATCCTCA | 1788 | A T |
| | | | TGAG ATACTAAAAT CCT | | |
| | | | | | |
| | | | ACTC TATGATTTTA GGA | | |
| | | | C _ | | |
| GAM93 | PIB5PA | 3' | TTAGGAATTAAATTCTC | 2739 | ACTAA |
| | | | GAGAAT AATTCCTAA | | |
| | | | | | |
| | | | CTCTTA TTAAGGATT | | |
| | | | AA _ | | |
| GAM93 | LOC149351 | 3' | AGGAGTTTAGTATCCTTA | 3130 | A A |
| | | | TGAG ATACTAAA TTCCT | | |
| | | | | | |
| | | | ATTC TATGATTT GAGGA | | |
| | | | C _ | | |
| GAM93 | LOC157858 | 5' | AGGGGAGTGTTCTCA | 3384 | AAAA |
| | | | TGAGAATACT TTCCT | | |
| | | | | | |
| | | | ACTCTTGTGA GGGGA | | |
| | | | _____ | | |
| GAM94 | DLG5 | 5' | TGATACAGCACAATAACT | 3265 | CCAC C |
| | | | AGTTA GTGCTGTA CA | | |
| | | | | | |
| | | | TCAAT CACGACAT GT | | |
| | | | AA _ A | | |
| GAM94 | DVL3 | 3' | CAATAAATGGTAGCTATTA | 1112 | CG C |
| | | | TAATAGTTACCA TG TG | | |
| | | | | | |
| | | | ATTATCGATGGT AT AC | | |
| | | | AA A | | |
| GAM94 | ENPP3 | 3' | GTACACACAGTGACTATTA | 1173 | CAC C |
| | | | TAATAGTTAC GTG TGTAC | | |
| | | | | | |
| | | | ATTATCAGTG CAC ACATG | | |
| | | | A _ _ | | |
| GAM94 | FANCF | 3' | TGGTACAACCCAGGGGTAAACT | 1998 | _ ACGTGC_ |
| | | | ATTA TAATAGTT ACC TGTACCA | | |
| | | | | | |
| | | | ATTATCAA TGG ACATGGT | | |
| | | | A GGACCCA | | |
| GAM94 | PCDH11X | 3' | ACAGCACACAAGTGGCTATTG | 2298 | CAC_ |
| | | | TAATAGTTAC GTGCTGT | | |
| | | | | | |
| | | | GTTATCGGTG CACGACA | | |
| | | | AACA | | |
| GAM94 | PCDH11X | 3' | ACAGCACACAAGTGGCTATTG | 2300 | CAC_ |
| | | | TAATAGTTAC GTGCTGT | | |
| | | | | | |

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|-------|----------|----|-----------------------------|-----------|
| | | | GTTATCGGTG CACGACA | |
| | | | AACA | |
| GAM94 | PCDH11Y | 3' | ACAGCACACAAGTGGCTATTG 2302 | CAC_ |
| | | | TAATAGTTAC GTGCTGT | |
| | | | | |
| | | | GTTATCGGTG CACGACA | |
| | | | AACA | |
| GAM94 | FLJ10539 | 3' | TACAGTATGACAACTATT 1789 | ACCA |
| | | | AATAGTT CGTGCTGTA | |
| | | | | |
| | | | TTATCAA GTATGACAT | |
| | | | CA__ | |
| GAM94 | FLJ10898 | 3' | TAGTCATTCGTGGTAACTA 2528 | T__ |
| | | | TAGTTACCACG GCTG | |
| | | | | |
| | | | ATCAATGGTGC TGAT | |
| | | | TTAC | |
| GAM94 | KIAA0680 | 3' | TGGTACAGTATAGTACCATTA 1530 | A T CAC |
| | | | TAAT GT AC GTGCTGTACCA | |
| | | | | |
| | | | ATTA CA TG TATGACATGGT | |
| | | | C _ A__ | |
| GAM94 | KIAA1804 | 3' | GCAGTACAGTACTATTA 2868 | T CAC |
| | | | TAATAGT AC GTGCTGT | |
| | | | | |
| | | | ATTATCA TG CATGACG | |
| | | | _ A__ | |
| GAM94 | MO25 | 3' | TAGTAGTATGTA ACTATTA 1677 | C_ G |
| | | | TAATAGTTAC AC TGCTG | |
| | | | | |
| | | | ATTATCAATG TG ATGAT | |
| | | | TA _ | |
| GAM94 | RAB33B | 3' | ACAGCTGTAGTAACTAT 2190 | C T |
| | | | ATAGTTAC ACG GCTGT | |
| | | | | |
| | | | TATCAATG TGT CGACA | |
| | | | A _ | |
| GAM94 | RoXaN | 3' | TGGTACAGCACACATGTGAGC 2128 | AC C__ |
| | | | GTT CA GTGCTGTACCA | |
| | | | | |
| | | | CGA GT CACGACATGGT | |
| | | | GT ACA | |
| GAM95 | KIF13A | 3' | ACCGCAACA ACTTGGTAGGA 1979 | ATAG AT |
| | | | TCC TAC AGTTGTTGCGGT | |
| | | | | |
| | | | AGG ATG TCAACAACGCCA | |
| | | | __ GT | |
| GAM95 | LOXL3 | 3' | ACTCATCAGACCATGCACTATG 2264 | A A GT_ C |
| | GA | | TCCATAGT CAT GTT TG GGT | |
| | | | | |

AGGTATCA GTA CAG AC TCA
 C C ACT _
 GAM95 DKFZp547l014 5' CAGCTAACAATGTACTACAGA 1901 CA A _
 TC TAGTACAT GTT GTTG
 || ||||| || ||||
 AG ATCATGTA CAA CGAC
 AC A T
 GAM95 Spir-1 3' ACCATGAACTCGTACTATG 2699 AT GTTGC
 CATAGTAC AGTT GGT
 ||||| ||| ||
 GTATCATG TCAA CCA
 C_ GTA_
 GAM96 GCLC 3' AATTGTACAATACTTGCATTCC 833 CT__ C
 GGA AGTAT GTACAATT
 || |||| |||||
 CCT TCATA CATGTAA
 TACGT A
 GAM96 FLJ21324 5' AATTGTTGCCTAGTCCTGC 3513 TAT T
 GTAGGACTAG CG ACAATT
 ||||| || |||||
 CGTCCTGATC GT TGTAA
 C_ _
 GAM96 KIAA0193 3' AATTGTGATGTCCTAGTCCTAC 1543 T CG
 GTAGGACTAG AT TACAATT
 ||||| || |||||
 CATCCTGATC TG GTGTAA
 C TA
 GAM96 LOC91097 3' AATTGTTGCCTAGTCCTGC 2705 TAT T
 GTAGGACTAG CG ACAATT
 ||||| || |||||
 CGTCCTGATC GT TGTAA
 C_ _
 GAM97 ADAMTS5 3' TTCAATAGATACCACGAA 1353 GG A
 TTTGTGGTATT AT GAA
 ||||| || ||
 AAGCACCATAG TA CTT
 A_ A
 GAM97 BCRP2 3' TTCTATCCAACATTCAA 2633 T A
 TTG GGT TTGGATAGAA
 ||| || |||||
 AAC TTA AACCTATCTT
 _ C
 GAM97 IL13RA1 3' TCTACTAAACTACAAA 835 A A
 TTTGTGGT TTGG TAGA
 ||||| ||| ||||
 AAACATCA AATC ATCT
 A _
 GAM97 IL1A 3' TCTACCCATATTACAGA 2634 T A
 TTTGTGGTAT GG TAGA
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|-------|--------|----|----------------------------|--------|
| | | | AGACATTATA CC ATCT | |
| | | | C _ | |
| GAM97 | ISL1 | 3' | TCTATTTTGCCACAAG 906 | TT |
| | | | TTTGTGGTA GGATAGA | |
| | | | | |
| | | | GAACACCGT TTTATCT | |
| | | | — | |
| GAM97 | MITF | 3' | TTCTATTTTACAACACTACAAA 721 | ATT_ |
| | | | TTTGTGGT GGATAGAA | |
| | | | | |
| | | | AAACATCA TTTATCTT | |
| | | | ACAT | |
| GAM97 | NCF2 | 3' | TTCTGTGTCATACCACAA 742 | T _ |
| | | | TTGTGGTAT GG ATAGAA | |
| | | | | |
| | | | AACACCATA CT TGTCTT | |
| | | | _ G | |
| GAM97 | NEDD4L | 3' | TTCTACTCAACTACAAA 1618 | AT GA |
| | | | TTTGTGGT TG TAGAA | |
| | | | | |
| | | | AAACATCA AC ATCTT | |
| | | | _ TC | |
| GAM97 | NR3C1 | 3' | TTCTATCCTACAACAAG 717 | G TT |
| | | | TTTGT GTA GGATAGAA | |
| | | | | |
| | | | GAACA CAT CCTATCTT | |
| | | | A _ | |
| GAM97 | PDK4 | 3' | TTCTATTTTCCCCACAAA 3733 | TATT |
| | | | TTTGTGG GGATAGAA | |
| | | | | |
| | | | AAACACC TTTATCTT | |
| | | | CCT_ | |
| GAM97 | PSEN1 | 3' | TTCTACTTTGCCACAGA 1393 | TT A |
| | | | TTTGTGGTA GG TAGAA | |
| | | | | |
| | | | AGACACCGT TC ATCTT | |
| | | | T_ _ | |
| GAM97 | RAG1 | 3' | TTCTTTCCACCACAAA 746 | ATT T |
| | | | TTTGTGGT GGA AGAA | |
| | | | | |
| | | | AAACACCA CCT TCTT | |
| | | | _ T | |
| GAM97 | SYNGR1 | 3' | TTCTGTGCCCACCACAAG 1148 | ATT _ |
| | | | TTTGTGGT GG ATAGAA | |
| | | | | |
| | | | GAACACCA CC TGTCTT | |
| | | | C_ G | |
| GAM97 | TOX | 5' | TTCTTAAACAAACCACAAA 1534 | A GAT_ |
| | | | TTTGTGGT TTG AGAA | |
| | | | | |

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|-------|----------|----|----------------------------|-----|-----|
| | | | AAACACCA AAC TCTT | | |
| | | | _ AAAT | | |
| GAM97 | TRPC6 | 3' | TTCTATCCTTCTACCCAAA 1135 | T | TT_ |
| | | | TTTG GGTA GGATAGAA | | |
| | | | | | |
| | | | AAAC CCAT CCTATCTT | | |
| | | | _ CTT | | |
| GAM97 | AF9Q34 | 3' | TTCTACACACTCAGCCACAAA 2258 | AT_ | GA |
| | | | TTTGTGGT TG TAGAA | | |
| | | | | | |
| | | | AAACACCG AC ATCTT | | |
| | | | ACTC AC | | |
| GAM97 | C1QR1 | 3' | TTCCATCCTCATCACAAG 1402 | ATT | A |
| | | | TTTGTGGT GGAT GAA | | |
| | | | | | |
| | | | GAACACTA CCTA CTT | | |
| | | | CT_ C | | |
| GAM97 | FLJ10193 | 3' | TCTGACAGATACCACGAA 1775 | GGA | |
| | | | TTTGTGGTATT TAGA | | |
| | | | | | |
| | | | AAGCACCATAG GTCT | | |
| | | | ACA | | |
| GAM97 | FLJ10989 | 3' | CTATTTACTGATCACAAA 1810 | AT_ | |
| | | | TTTGTGGT TGGATAG | | |
| | | | | | |
| | | | AAACACTA ATTTATC | | |
| | | | GTC | | |
| GAM97 | FLJ20700 | 3' | TTCTACCAAAACTACAAA 1767 | A | A |
| | | | TTTGTGGT TTGG TAGAA | | |
| | | | | | |
| | | | AAACATCA AACC ATCTT | | |
| | | | A _ | | |
| GAM97 | FLJ31101 | 3' | TTCTATCTAGCACAA 1772 | GTA | |
| | | | TTGTG TTGGATAGAA | | |
| | | | | | |
| | | | AACAC GATCTATCTT | | |
| | | | — | | |
| GAM97 | KIAA0252 | 3' | TCTACTAAAACACTACAAA 2638 | A | A |
| | | | TTTGTGGT TTGG TAGA | | |
| | | | | | |
| | | | AAACATCA AATC ATCT | | |
| | | | A _ | | |
| GAM97 | KIAA0416 | 3' | TCATTTCAAACCACAAA 1638 | A | TA |
| | | | TTTGTGGT TTGGA GA | | |
| | | | | | |
| | | | AAACACCA AACTT CT | | |
| | | | _ TA | | |
| GAM97 | KIAA0445 | 5' | TCTACTAAAACACTACAAA 1519 | A | A |
| | | | TTTGTGGT TTGG TAGA | | |
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|-------|----------|----|-----------------------------|------|-------|
| | | | AAACATCA AATC ATCT | | |
| | | | A _ | | |
| GAM97 | KIAA0493 | 5' | TTCTACTTCCACCACAAG 2683 | ATT | __ |
| | | | TTTGTGGT GGA TAGAA | | |
| | | | | | |
| | | | GAACACCA CCT ATCTT | | |
| | | | __ TC | | |
| GAM97 | KIAA0753 | 3' | TCTATTTTCATACCACAAA 1553 | TG | |
| | | | TTTGTGGTAT GATAGA | | |
| | | | | | |
| | | | AAACACCATA TTATCT | | |
| | | | CT | | |
| GAM97 | KIAA0781 | 3' | TTCTGCCCCACCACAAA 2794 | ATT | A |
| | | | TTTGTGGT GG TAGAA | | |
| | | | | | |
| | | | AAACACCA CC GTCTT | | |
| | | | CC_ _ | | |
| GAM97 | KIAA0825 | 3' | TTCTATCTAACACATAA 2589 | GTA | |
| | | | TTGTG TTGGATAGAA | | |
| | | | | | |
| | | | AATAC AATCTATCTT | | |
| | | | AC_ | | |
| GAM97 | KIAA0831 | 3' | TTCTATCCGGTAGTCACAAA 1590 | | _ |
| | | | TTTGTGG TATTGGATAGAA | | |
| | | | | | |
| | | | AAACACT ATGGCCTATCTT | | |
| | | | G | | |
| GAM97 | KIAA1172 | 3' | TTCTATTTAAAAATAGCCACAA 2897 | A | _____ |
| | A | | TTTGTGGT TTGGATAGAA | | |
| | | | | | |
| | | | AAACACCG AATTTATCTT | | |
| | | | ATAAA | | |
| GAM97 | KR18 | 3' | TTCTATCCAATTTGTGAA 2325 | TG T | |
| | | | TTTG G ATTGGATAGAA | | |
| | | | | | |
| | | | AAGT T TAACCTATCTT | | |
| | | | GT_ | | |
| GAM97 | MAPK13 | 3' | TCTAACGAATTACCACAAA 953 | | __ GA |
| | | | TTTGTGGTA TTG TAGA | | |
| | | | | | |
| | | | AAACACCAT AGC ATCT | | |
| | | | TA A_ | | |
| GAM97 | MGC11386 | 3' | TCTACTAAAACTACAAA 2296 | A | A |
| | | | TTTGTGGT TTGG TAGA | | |
| | | | | | |
| | | | AAACATCA AATC ATCT | | |
| | | | A _ | | |
| GAM97 | PRO0641 | 3' | TCTGCCAATAACCACAAA 1477 | | _ A |
| | | | TTTGTGGT ATTGG TAGA | | |
| | | | | | |

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|-------|-----------|----|----------------------------|---------|
| | | | AAACACCA TAACC GTCT | |
| | | | A _ | |
| GAM97 | PRO0902 | 3' | TCTACCTTTGCCACAAG 2358 | TT A |
| | | | TTTGTGGTA GG TAGA | |
| | | | | |
| | | | GAACACCGT CC ATCT | |
| | | | TT _ | |
| GAM97 | SMAP-5 | 3' | TCTACTAAAACTACAAA 2168 | A A |
| | | | TTTGTGGT TTGG TAGA | |
| | | | | |
| | | | AAACATCA AATC ATCT | |
| | | | A _ | |
| GAM97 | SPRY4 | 3' | TCTACTAAAACTACAAA 2177 | A A |
| | | | TTTGTGGT TTGG TAGA | |
| | | | | |
| | | | AAACATCA AATC ATCT | |
| | | | _ _ | |
| GAM97 | USP24 | 3' | TCTACGATGCTACAAA 3512 | GA |
| | | | TTTGTGGTATTG TAGA | |
| | | | | |
| | | | AAACATCGTAGC ATCT | |
| | | | _ | |
| GAM97 | ZNF304 | 3' | TTCATTGTATACCACAA 1921 | TG A |
| | | | TTGTGGTAT GAT GAA | |
| | | | | |
| | | | AACACCATA TTA CTT | |
| | | | TG _ | |
| GAM97 | LOC121344 | 3' | TCTACCTCAGTTTGCCACAAA 2990 | TT___ A |
| | | | TTTGTGGTA GG TAGA | |
| | | | | |
| | | | AAACACCGT CC ATCT | |
| | | | TTGACT _ | |
| GAM97 | LOC144266 | 5' | TTCTGTCCCACCAGAAA 3065 | G ATT |
| | | | TTT TGGT GGATAGAA | |
| | | | | |
| | | | AAA ACCA CCTGTCTT | |
| | | | G C_ | |
| GAM97 | LOC145241 | 3' | CTTACGTCAGTACCACAAA 2640 | AT__ |
| | | | TTTGTGGTATTGG AG | |
| | | | | |
| | | | AAACACCATGACT TC | |
| | | | GCAT | |
| GAM97 | LOC148545 | 5' | TCTACCTCTTCTGCCACAAA 3120 | TT _ |
| | | | TTTGTGGTA GGA TAGA | |
| | | | | |
| | | | AAACACCGT TCT ATCT | |
| | | | CT CC | |
| GAM97 | LOC149073 | 5' | TTCTGATGACAAACCACAAA 3305 | A GA__ |
| | | | TTTGTGGT TTG TAGAA | |
| | | | | |

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| | | AAACACCA AAC GTCTT | |
| | | _ AGTA | |
| GAM97 | LOC149448 3' | CTGTAACAAAATACCACAAA 3309 | GG__ |
| | | TTTGTGGTATT ATAG | |
| | | | |
| | | AAACACCATAA TGTC | |
| | | AACAA | |
| GAM97 | LOC149579 5' | TCTACTAAAACTACAAA 2907 | A A |
| | | TTTGTGGT TTGG TAGA | |
| | | | |
| | | AAACATCA AATC ATCT | |
| | | A _ | |
| GAM97 | LOC152641 5' | TTCTAGGGAAACCACAAA 3173 | A GGA |
| | | TTTGTGGT TT TAGAA | |
| | | | |
| | | AAACACCA AG ATCTT | |
| | | A GG_ | |
| GAM97 | LOC169966 3' | TTCTATCATCATCTACTACAAA 3253 | TTG__ |
| | | TTTGTGGTA GATAGAA | |
| | | | |
| | | AAACATCAT CTATCTT | |
| | | CTACTA | |
| GAM97 | LOC222234 3' | TCTGTAACAAATTACCACAAA 3647 | _ G_ |
| | | TTTGTGGTA TTG ATAGA | |
| | | | |
| | | AAACACCAT AAC TGTCT | |
| | | TA AA | |
| GAM97 | LOC254058 3' | TTCTAACCACCACAAG 3735 | ATT A |
| | | TTTGTGGT GG TAGAA | |
| | | | |
| | | GAACACCA CC ATCTT | |
| | | _ A | |
| GAM97 | LOC51110 3' | TTCTGGTATACCACAAA 1657 | TGGA |
| | | TTTGTGGTAT TAGAA | |
| | | | |
| | | AAACACCATA GTCTT | |
| | | TG_ | |
| GAM97 | LOC51292 3' | TCTATCTGCACACACAAA 1698 | _ ATT |
| | | TTTGTG GT GGATAGA | |
| | | | |
| | | AAACAC CA TCTATCT | |
| | | A CG_ | |
| GAM97 | LOC92573 5' | TTCTGGCCACCACAGA 2870 | ATT A |
| | | TTTGTGGT GG TAGAA | |
| | | | |
| | | AGACACCA CC GTCTT | |
| | | _ G | |
| GAM98 | AVP 5' | AGCTCCTAGGCCAGGGCCTGTC 752 | A AGA_ |
| | | GACAG CC CCTAGGAGCT | |
| | | | |

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|-------|----------|----|-----------------------------|------------|----|--|
| | | | CTGTC GG GGATCCTCGA | | | |
| | | | C GACC | | | |
| GAM98 | HTRA3 | 3' | CTGCAGGTCTGGGCTGCCA 3457 | A A | A_ | |
| | | | TG CAG CCAGACCT GG | | | |
| | | | | | | |
| | | | AC GTC GGTCTGGA TC | | | |
| | | | C G CG | | | |
| GAM98 | LGALS3BP | 3' | AGCCCCTGGTCAGTCTG 2851 | CA T A | | |
| | | | CAGAC GACC AGG GCT | | | |
| | | | | | | |
| | | | GTCTG CTGG TCC CGA | | | |
| | | | A_ _ C | | | |
| GAM98 | MAD2L1 | 3' | TAGCTCCTTTTGACCTTCA 921 | C AC CCT | | |
| | | | TGA AG CAGA AGGAGCTA | | | |
| | | | | | | |
| | | | ACT TC GTTT TCCTCGAT | | | |
| | | | _ CA _ | | | |
| GAM98 | PYGM | 5' | TAGCTCCCTGAGCTGCCA 1230 | A AC ACCTA | | |
| | | | TG CAG CAG GGAGCTA | | | |
| | | | | | | |
| | | | AC GTC GTC CCTCGAT | | | |
| | | | C GA _ | | | |
| GAM98 | SLC35A3 | 3' | TTCTGGGTCTGATCTGTCA 1418 | C | | |
| | | | TGACAGA CAGACCTAGGA | | | |
| | | | | | | |
| | | | ACTGTCT GTCTGGGTCTT | | | |
| | | | A | | | |
| GAM98 | ATPAF1 | 3' | ATAGCTCCCAAATGATGAGTTT 2583 | _ GACCTA_ | | |
| | | | GTCA TGACAGAC CA GGAGCTAT | | | |
| | | | | | | |
| | | | ACTGTTTG GT CCTCGATA | | | |
| | | | A AGTAAAC | | | |
| GAM98 | C7orf13 | 3' | CTTAAGTCTGGTCCCTCA 2265 | CA C | | |
| | | | TGA GACCAGAC TAGG | | | |
| | | | | | | |
| | | | ACT CTGGTCTG ATTC | | | |
| | | | CC A | | | |
| GAM98 | CBLC | 3' | CTGCCAAGCCTGGTCTGTCA 1407 | AC A _ | | |
| | | | TGACAGACCAG CT GG AG | | | |
| | | | | | | |
| | | | ACTGTCTGGTC GA CC TC | | | |
| | | | C_ A G | | | |
| GAM98 | FLJ10241 | 3' | AGCTCCTGTCACCCTGTCA 1776 | ACCA CT | | |
| | | | TGACAG GAC AGGAGCT | | | |
| | | | | | | |
| | | | ACTGTC CTG TCCTCGA | | | |
| | | | CCA_ _ | | | |
| GAM98 | FLJ20651 | 3' | CCAAGCTTGGTCTGTCA 1761 | AC A | | |
| | | | TGACAGACCAG CT GG | | | |
| | | | | | | |

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|-------|-----------|----|----------------------------|----------|
| | | | ACTGTCTGGTT GA CC | |
| | | | C_ A | |
| GAM98 | KIAA1203 | 3' | CTTCAGATCCTGTCTGTCA 2922 | CA C A |
| | | | TGACAGAC GA CT GGAG | |
| | | | | |
| | | | ACTGTCTG CT GA CTTC | |
| | | | TC A _ | |
| GAM98 | PL6 | 3' | AGCTCCTGGGCGGCCCTCA 1348 | CAGA AGA |
| | | | TGA CC CCTAGGAGCT | |
| | | | | |
| | | | ACT GG GGGTCCTCGA | |
| | | | CCC_ CC_ | |
| GAM98 | SRCRB4D | 3' | AGCTCCTACCTTGGGCCCTCA 2386 | CAGA ACC |
| | | | TGA CCAG TAGGAGCT | |
| | | | | |
| | | | ACT GGTT ATCCTCGA | |
| | | | CCCG CC_ | |
| GAM98 | SYNPO2 | 3' | AGCAGCTCTGGTCTGTCA 2928 | C AGGA |
| | | | TGACAGACCAGA CT GCT | |
| | | | | |
| | | | ACTGTCTGGTCT GA CGA | |
| | | | C _ | |
| GAM98 | LOC145858 | 5' | CCTAGGTCTGGCCTTCA 3085 | C A |
| | | | TGA AG CCAGACCTAGG | |
| | | | | |
| | | | ACT TC GGTCTGGATCC | |
| | | | _ C | |
| GAM98 | LOC151162 | 5' | AGCTCCTAGAGGCTGCTCA 3338 | _ A AGAC |
| | | | TGA CAG CC CTAGGAGCT | |
| | | | | |
| | | | ACT GTC GG GATCCTCGA | |
| | | | C _ A_ | |
| GAM98 | LOC196410 | 5' | AGCTCAGAGCTGGTCTGCCA 3411 | A AC AG |
| | | | TG CAGACCAG CT GAGCT | |
| | | | | |
| | | | AC GTCTGGTC GA CTCGA | |
| | | | C _ GA | |
| GAM98 | LOC203339 | 5' | AGCTCCTAGGAATTCTCTCA 3489 | C CCAGA |
| | | | TGA AGA CCTAGGAGCT | |
| | | | | |
| | | | ACT TCT GGATCCTCGA | |
| | | | C TAA_ | |
| GAM98 | LOC203377 | 5' | AGCTCCTAGAGGCTGCTCA 3490 | _ A AGAC |
| | | | TGA CAG CC CTAGGAGCT | |
| | | | | |
| | | | ACT GTC GG GATCCTCGA | |
| | | | C _ A_ | |
| GAM99 | SEL1L | 3' | CAAGAAAATTTAAACGATCCC 1179 | AA TT |
| | AA | | TTG ATTGTTTT ATTTCTTG | |
| | | | | |

| | | | | | |
|--------|---------------|----|-----------------------------|-----------|--|
| | | | AAC TAGCAAAA TAAAAGAAC | | |
| | | | CC TT | | |
| GAM99 | DKFZP564O1863 | 3' | AAAGTAAATACAATTTCAA 2826 | TT | |
| | | | TTGAAATTGT TTTATTTT | | |
| | | | | | |
| | | | AACTTTAACA AAATGAAA | | |
| | | | T_ | | |
| GAM99 | LOC129446 | 3' | CAAGAAAAATGAGAACATTTTC 3042 | T TA | |
| | AA | | TTGAAA TGTTTT TTTTCTTG | | |
| | | | | | |
| | | | AACTTT ACAAGAG AAAAGAAC | | |
| | | | T TA | | |
| GAM100 | CYP19 | 3' | AAAAAGCAGAGGCCAAGAGTTT 705 | ATGAT_ C | |
| | G | | CAAA GCCTCTGC TTTT | | |
| | | | | | |
| | | | GTTT CGGAGACG AAAA | | |
| | | | GAGAAC A | | |
| GAM100 | CYP19 | 3' | AAAAAGCAGAGGCCAAGAGTTT 2185 | ATGAT_ C | |
| | G | | CAAA GCCTCTGC TTTT | | |
| | | | | | |
| | | | GTTT CGGAGACG AAAA | | |
| | | | GAGAAC A | | |
| GAM100 | F8 | 3' | AAAGGCAAATCATTTGGA 707 | A GCCTC | |
| | | | TCCAAA TGAT TGCCTTT | | |
| | | | | | |
| | | | AGGTTT ACTA ACGGAAA | | |
| | | | _ A_ | | |
| GAM100 | MSR1 | 3' | AAAAGGCAAAACCTTACCTTGG 2453 | AA TGCCTC | |
| | A | | TCCAA TGA TGCCTTTT | | |
| | | | | | |
| | | | AGGTT ATT ACGGAAAA | | |
| | | | CC CCAA_ | | |
| GAM100 | MSR1 | 3' | AAAAGGCAAAACCTTACCTTGG 2454 | AA TGCCTC | |
| | A | | TCCAA TGA TGCCTTTT | | |
| | | | | | |
| | | | AGGTT ATT ACGGAAAA | | |
| | | | CC CCAA_ | | |
| GAM100 | PCDHB16 | 3' | AAAAGGCAAAGGTATTAT 1931 | C | |
| | | | ATGATGCCT TGCCTTTT | | |
| | | | | | |
| | | | TATTATGGA ACGGAAAA | | |
| | | | A | | |
| GAM100 | QPCT | 3' | AAAAGTCAAGGCATCATTT 1428 | C C | |
| | | | AAATGATGCCT TG CTTTT | | |
| | | | | | |
| | | | TTTACTACGGA AC GAAAA | | |
| | | | _ T | | |
| GAM100 | TWIST | 3' | AAAGGAAAGGCATCACTATGGA 750 | AAA CTG | |
| | | | TCCA TGATGCCT CCTTT | | |
| | | | | | |

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AGGT ACTACGGA GGAAA
ATC AA_
GAM100 ATP9A 3' AAAGGCAGAGGCATCTTTCGGA 2617 A T
TCC AAA GATGCCTCTGCCTTT
||| ||| |||||
AGG TTT CTACGGAGACGGAAA
C _
GAM100 CALN1 3' CAGAAATATCATCTTGGA 2207 A CC
TCCAA ATGATG TCTG
||||| ||||| |||
AGGTT TACTAT AGAC
C AA
GAM100 FLJ23277 3' AAAAGGCAGAAATCCATTCA 2238 _ CC__
TGA TG TCTGCCTTTT
||| ||| |||||
ACT AC AGACGGAAAA
T CTAA
GAM100 KIAA0992 3' AAAAGGCAGAAACATACCTTTG 1661 ATG CC
CAAA ATG TCTGCCTTTT
||| ||| |||||
GTTT TAC AGACGGAAAA
CCA AA
GAM100 KIAA1045 3' AAAAGGCAGAACAGTTTTG 2906 GA CC
CAAAAT TG TCTGCCTTTT
||||| ||| |||||
GTTTTG AC AGACGGAAAA
_ A_
GAM100 KIAA1056 3' AAAGGCAGAGAGGCCAGGA 1575 AAAA AT _
TCC TG GCCTCT GCCTTT
||| ||| ||||| |||||
AGG AC CGGAGA CGGAAA
_ _ GA
GAM100 KIAA1323 3' AGGGGAGAGGCACATTTT 2646 A G
AAAATG TGCCTCT CCTT
||||| ||||| |||
TTTTAC ACGGAGA GGGA
_ G
GAM100 LMOD1 3' AGGTGAAAGGCATCTTTCTG 1409 A T CT_
CA AA GATGCCT GCCT
||| ||| ||||| |||
GT TT CTACGGA TGGA
C T AAG
GAM100 RNF32 3' AAAAAGTTTACCATCATTTTGG 2172 CCTCT C
A TCCAAAATGATG GC TTTT
||||| ||| |||
AGGTTTTACTAC TG AAAA
CATT_ A
GAM100 SS-56 3' AAAAAGCAGAGGCCAGTCA 2535 _ C
TGAT GCCTCTGC TTTT
||| ||||| |||

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|--------|--------------|-----------------------------|---------|---------|
| | | ACTG CGGAGACG AAAA | | |
| | | ACC A | | |
| GAM100 | LOC122792 3' | AAAAGTGCCTTGCATCATTT 2518 | | CTCT _ |
| | | AAATGATGC GC CTTTT | | |
| | | | | |
| | | TTTACTACG CG GAAAA | | |
| | | TTC_ T | | |
| GAM100 | LOC146512 3' | GCAGTGCAAACATCATTTTGGA 3094 | | CCT____ |
| | | TCCAAAATGATG CTGC | | |
| | | | | |
| | | AGGTTTTACTAC GACG | | |
| | | AAACGT | | |
| GAM100 | LOC201633 3' | CAGAGGCATCTTCTGGA 3483 | A T | |
| | | TCCA AA GATGCCTCTG | | |
| | | | | |
| | | AGGT TT CTACGGAGAC | | |
| | | C _ | | |
| GAM100 | LOC202126 3' | AAAAAGCAAGTATCATTTGGA 3486 | A CTC C | |
| | | TCCAAA TGATGC TGC TTTT | | |
| | | | | |
| | | AGGTTT ACTATG ACG AAAA | | |
| | | _ A_ A | | |
| GAM100 | LOC221755 3' | CAGAGGCGCCATCTTGGA 3563 | A A | |
| | | TCCAA ATG TGCCTCTG | | |
| | | | | |
| | | AGGTT TAC GCGGAGAC | | |
| | | C C | | |
| GAM100 | LOC257334 3' | GCAGAGGCACCATCTTGG 3734 | A A | |
| | | CCAA ATG TGCCTCTGC | | |
| | | | | |
| | | GGTT TAC ACGGAGACG | | |
| | | C C | | |
| GAM101 | ANGPT1 3' | ACTGAAACATGCTTACCAGATT 804 | | CATCTC_ |
| | CA | TGAATC TATGTTTCAGT | | |
| | | | | |
| | | ACTTAG GTACAAAGTCA | | |
| | | ACCATTC | | |
| GAM101 | GPR61 5' | ACTGAAATTCAGAAGATTCAC 3123 | | CATC AT |
| | | GTGAATC TCT GTTTCAGT | | |
| | | | | |
| | | CACTTAG AGA TAAAGTCA | | |
| | | A_ CT | | |
| GAM101 | PPP1R12B 3' | ACTGAAACCCGGAACAGATTC 2228 | | CATC AT |
| | | GAATC TCT GTTTCAGT | | |
| | | | | |
| | | CTTAG AGG CAAAGTCA | | |
| | | ACA_ CC | | |
| GAM101 | TRIM9 3' | ACTTCTATATAGAGATAGACTT 1610 | A C | TTC |
| | AC | GTGA TC ATCTCTATGT AGT | | |
| | | | | |

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|--------|-----------|----|------------------------------|----------|
| | | | CATT AG TAGAGATATA TCA | |
| | | | C A TCT | |
| GAM101 | YWHAE | 3' | ACTGAAACACAGCATGGAATTA 1329 | A CT A |
| | | | TGA TCCAT CT TGTTTCAGT | |
| | | | | |
| | | | ATT AGGTA GA ACAAAGTCA | |
| | | | A C_ C | |
| GAM101 | AKAP9 | 3' | ACTGAAATAAAAAATGACTTCAC 1242 | TC CTCTA |
| | | | GTGAA CAT TGTTTCAGT | |
| | | | | |
| | | | CACTT GTA ATAAAGTCA | |
| | | | CA AAA_ | |
| GAM101 | LOC166824 | 3' | ACTGAAACATAATCAATGGATT 3259 | CTC_ |
| | CA | | TGAATCCAT TATGTTTCAGT | |
| | | | | |
| | | | ACTTAGGTA ATACAAAGTCA | |
| | | | ACTA | |
| GAM101 | LOC254835 | 3' | TGAAGCAAGAGACAGACCCAC 3722 | AA CA A |
| | | | GTG TC TCTCT TGTTTCA | |
| | | | | |
| | | | CAC AG AGAGA ACGAAGT | |
| | | | CC AC _ | |
| GAM102 | PNPASE | 3' | CTGAGGCAGAAGAATCACTTC 2900 | GATG G |
| | | | GAAGTGATTCTTT GT TCAG | |
| | | | | |
| | | | CTTCACTAAGAAG CG AGTC | |
| | | | A_ G | |
| GAM102 | SEC24D | 3' | CAGTATCAATAAATCACTTC 1559 | CT G |
| | | | GAAGTGATT TTGATG TG | |
| | | | | |
| | | | CTTCACTAA AACTAT AC | |
| | | | AT G | |
| GAM102 | LOC131000 | 3' | CTGACCTTGAAATAAATCACTT 3037 | CT GAT T |
| | C | | GAAGTGATT TT GG GTCAG | |
| | | | | |
| | | | CTTCACTAA AA TC CAGTC | |
| | | | AT AGT _ | |
| GAM102 | LOC151658 | 5' | GAAGTCTCAAAGCATCACTTC 3349 | T T TG |
| | | | GAAGTGAT CTTTGA GG TC | |
| | | | | |
| | | | CTTCACTA GAAACT CT AG | |
| | | | C _ GA | |
| GAM102 | LOC257428 | 3' | GCACTTTCAAAGAATCATCC 3649 | A T |
| | | | A GTGATTCTTTGA GGTGT | |
| | | | | |
| | | | C TACTAAGAAACT TCACG | |
| | | | C T | |
| GAM103 | CARD15 | 3' | GTAAATAATCAGAGGGGAATAA 1983 | GGA TC |
| | A | | TTTGTT T CTGATTATTAC | |
| | | | | |

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|--------|-----------|----|-----------------------------|---------|
| | | | AAATAA G GACTAATAAATG | |
| | | | GG_ GA | |
| GAM103 | CLCN4 | 3' | AAATAACAGAAAACCCAGCAAA 861 | ATTC_ A |
| | | | TTTGTTGG CTG TTATTT | |
| | | | | |
| | | | AAACGACC GAC AATAAA | |
| | | | CAAAA _ | |
| GAM103 | FGF2 | 3' | TAAATAATTTTATAATTCAACA 885 | CCT_ |
| | AA | | TTTGTTGGATT GATTATTTA | |
| | | | | |
| | | | AAACAACCTTAA TTAATAAAT | |
| | | | TATT | |
| GAM103 | ZNF135 | 3' | TGGTGAGAAACCCAACAAA 1022 | A C G |
| | | | TTTGTTGG TT CT ATTA | |
| | | | | |
| | | | AAACAACC AA GA TGGT | |
| | | | C A G | |
| GAM103 | SEC15B | 3' | AATTAAAAATCCAACAAA 2757 | CC |
| | | | TTTGTTGGATT TGATT | |
| | | | | |
| | | | AAACAACCTAA ATTAA | |
| | | | AA | |
| GAM103 | ZNF334 | 3' | AAGTAATAAATTCCAACAAA 1780 | TTCCTG |
| | | | TTTGTTGGA ATTATTT | |
| | | | | |
| | | | AAACAACCT TAATGAA | |
| | | | TAAA__ | |
| GAM103 | LOC158954 | 3' | TGGTGAGAAATCCAACAAA 2567 | C G |
| | | | TTTGTTGGATT CT ATTA | |
| | | | | |
| | | | AAACAACCTAA GA TGGT | |
| | | | A G | |
| GAM103 | LOC219686 | 3' | GTAATTGGAAAAAATCCAATAA 3500 | C__ TG |
| | A | | TTTGTTGGATT C ATTAT | |
| | | | | |
| | | | AAATAACCTAA G TAATG | |
| | | | AAAA GT | |
| GAM103 | LOC221510 | 3' | AAATAATCAAAACCCAACA 3508 | A CC |
| | | | TGTTGG TT TGATTATTT | |
| | | | | |
| | | | ACAACC AA ACTAATAAA | |
| | | | C A_ | |
| GAM104 | PLN | 3' | TAATAGCCTACTATTGACC 947 | C _ |
| | | | GG CAATAGTAG CTATTA | |
| | | | | |
| | | | CC GTTATCATC GATAAT | |
| | | | A C | |
| GAM104 | PRRG1 | 3' | GTAATAGCTCTATCAGCC 789 | CA T |
| | | | GGC ATAG AGCTATTAC | |
| | | | | |

CCG TATC TCGATAATG
 AC _
 GAM104 LOC149320 3' GCGGCAGCTACTACTGCC 2892 CAA ATTA
 GGC TAGTAGCT CCGT
 ||| ||||| |||
 CCG ATCATCGA GGCG
 TC_ C__
 GAM104 LOC163782 5' ACGGATGCCACTATTGGGC 3234 G A TATTA
 G CCAATAGT GC CCGT
 | ||||| || |||
 C GGTTATCA CG GGCA
 G C TA__
 GAM105 FLJ12668 3' ACTTGAGCAAATAATTGGGATG 2123 CCAA AG
 A TTATCCCAATTA CT AAGT
 ||||| || |||
 AGTAGGGTTAAT GA TTCA
 AAAC G_
 GAM105 KIAA0016 3' ACTTTTAAGGTAAGTGGGATGA 1542 A AAC
 TTATCCCA TTACC TAGAAGT
 ||||| ||| |||||
 AGTAGGGT AATGG ATTTTCA
 C A__
 GAM105 ZAK 3' ACTTCCAGTTTTTGATTGGGA 1708 ACC_ A
 TCCAATT AACT GAAGT
 ||||| ||| |||||
 AGGGTTAG TTGA CTTCA
 GTTT C
 GAM105 LOC58489 3' TGGTTGGTAATGGAATAA 2952 C A
 TTAT CCA TTACCAACTA
 ||| ||| |||||
 AATA GGT AATGGTTGGT
 A _
 GAM106 IL1R1 3' AGAACATCCTCCAATTCC 782 CG A
 GGAATTGGAGG ATG TCT
 ||||| ||| |||
 CCTTAACCTCC TAC AGA
 _ A
 GAM106 SUFU 3' ATCAGTTCGCCTCCATTCC 1668 T _
 GGAAT GGAGGCGA TGAT
 ||||| ||||| |||
 CCTTA CCTCCGCT ACTA
 _ TG
 GAM106 CGRP-RCP 5' AAGATCATCGCACCCCC 1503 AATT AG
 GG GG GCGATGATCTT
 || || |||||
 CC CC CGCTACTAGAA
 _ CA
 GAM106 LOC152348 5' ATCAGTCACCACCAATTCC 3358 A C _
 GGAATTGG GG GA TGAT
 ||||| || |||

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|--------|--------------|--------------------------|---------------------|-----------|--|
| | | | CCTTAACC CC CT ACTA | | |
| | | | A A G | | |
| GAM106 | LOC158219 3' | ATCATTGCCCCCAACTCC | 3214 | A A | |
| | | GGA TTGG GGCGATGAT | | | |
| | | | | | |
| | | CCT AACC CCGTTACTA | | | |
| | | C C | | | |
| GAM106 | LOC255177 3' | AGAATCACCTCTAATCC | 3711 | A C GA | |
| | | GGA TTGGAGG GAT TCT | | | |
| | | | | | |
| | | CCT AATCTCC CTA AGA | | | |
| | | — A — | | | |
| GAM106 | LOC90522 3' | AGGCACCGCCTCCATCC | 2651 | AT A A | |
| | | GGA TGGAGGCG TG TCT | | | |
| | | | | | |
| | | CCT ACCTCCGC AC GGA | | | |
| | | — C — | | | |
| GAM107 | CEACAM4 3' | CTCTGAGTCCTGAGGAG | 860 | CC TCGT | |
| | | CTCC TAG ACTCAGAG | | | |
| | | | | | |
| | | GAGG GTC TGAGTCTC | | | |
| | | A_ C_ | | | |
| GAM107 | MGC11115 3' | CTCTGAGGCCAGGGGAGC | 2244 | AGTC A | |
| | | GCTCCCT GT CTCAGAG | | | |
| | | | | | |
| | | CGAGGGGA CG GAGTCTC | | | |
| | | CC_ _ | | | |
| GAM107 | PRO2714 5' | CTCTAAGCAACAAGGGGAGCG | 1837 | A C ACTC | |
| | | CGCTCCCCT GT GT AGAG | | | |
| | | | | | |
| | | GCGAGGGGA CA CG TCTC | | | |
| | | A A AA_ | | | |
| GAM107 | LOC147057 3' | CTCTGAGTATTGGGAAGAGAGG | 3288 | G_ C_ GTC | |
| | C | GC CTC CCTA GTACTCAGAG | | | |
| | | | | | |
| | | CG GAG GGGT TATGAGTCTC | | | |
| | | GA AA _ | | | |
| GAM107 | LOC147976 3' | CTCTGGTGTGACTAAGGAAAG | 3114 | CC _ T | |
| | | CT CCT AGTCGTAC CAGAG | | | |
| | | | | | |
| | | GA GGA TCAGTGTG GTCTC | | | |
| | | AA A _ | | | |
| GAM107 | LOC57100 3' | CTCTGAGTACCCTGGCGGGAGG | 1917 | G _ TC | |
| | C | GC CTCCC CTAG GTACTCAGAG | | | |
| | | | | | |
| | | CG GAGGG GGTC CATGAGTCTC | | | |
| | | _ C C_ | | | |
| GAM108 | E2F3 3' | ACAAACCTCGAAACGAACAGTT | 875 | TCA A A | |
| | AA | TTAGCTGTTT TC AG TTTGT | | | |
| | | | | | |

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|--------|-----------|----|-----------------------------|-----|----------|
| | | | AATTGACAAG AG TC AAACA | | |
| | | | CAA C C | | |
| GAM108 | SCML1 | 3' | ACAGAGAACCAAAACAGCTAA 1328 | | CATCAAGA |
| | | | TTAGCTGTTTT TTTGT | | |
| | | | | | |
| | | | AATCGACAAAA AGACA | | |
| | | | CCAAG__ | | |
| GAM108 | KIAA1468 | 3' | ACAAATCCTACAGTCAATAGCT 3541 | | TTCATCAA |
| | AA | | TTAGCTGTT GATTTGT | | |
| | | | | | |
| | | | AATCGATAA CTAAACA | | |
| | | | CTGACATC | | |
| GAM108 | MGC16025 | 3' | ACAAATCTCCAAGAAAACAGCT 2295 | | ATCA |
| | | | AGCTGTTTTT AGATTTGT | | |
| | | | | | |
| | | | TCGACAAAAG TCTAAACA | | |
| | | | AACC | | |
| GAM108 | LOC148545 | 3' | CTTGATAAAAACAACTAA 3119 | C C | |
| | | | TTAG TGTTTT ATCAAG | | |
| | | | | | |
| | | | AATC ACAAAA TAGTTC | | |
| | | | A A | | |
| GAM108 | LOC163669 | 5' | ACAAATCTTGACGAACAC 3233 | T A | |
| | | | GT TTC TCAAGATTTGT | | |
| | | | | | |
| | | | CA AAG AGTTCTAAACA | | |
| | | | C C | | |
| GAM108 | LOC51652 | 3' | ACAAATAAGGAAAACAGCT 1660 | | ATCAAG |
| | | | AGCTGTTTTT ATTTGT | | |
| | | | | | |
| | | | TCGACAAAAG TAAACA | | |
| | | | GAA__ | | |
| GAM109 | CXCL13 | 3' | GTTATTCAGTTATAAGTAATA 1299 | | T |
| | | | TATTATTTATAACTGA GTAAC | | |
| | | | | | |
| | | | ATAATGAATATTGACT TATTG | | |
| | | | - | | |
| GAM109 | RASGRP1 | 3' | ATCAGTGGCTTAAATAATA 1241 | | TA__ |
| | | | TATTATTTA ACTGAT | | |
| | | | | | |
| | | | ATAATAAAT TGACTA | | |
| | | | TCGG | | |
| GAM109 | HTGN29 | 3' | GGGTCATTATCACTTAAATAAT 1899 | | TAAC TA_ |
| | A | | TATTATTTA TGATG ACCC | | |
| | | | | | |
| | | | ATAATAAAT ACTAT TGGG | | |
| | | | TC__ TAC | | |
| GAM109 | KIAA1430 | 3' | GGACCACATCAGTTGCAAA 3179 | A | AA_ |
| | | | TTT TAACTGATGT CC | | |
| | | | | | |

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|--------|-----------|-----------|--------------------|----------------|---------------|
| | | AAA GTTGA | CTACA | GG | |
| | | C | CCA | | |
| GAM109 | KIAA1764 | 5' | GCTTCAGTTATAA | ATAGTA | 2850 T |
| | | | TATTATTTATAA | CTGA | GT |
| | | | | | |
| | | | ATGATAA | ATTTGACT | CG |
| | | | T | | |
| GAM109 | ZAK | 3' | TATCAGTTTCAA | ATAATA | 2428 AT |
| | | | TATTATTT | AACTGATG | |
| | | | | | |
| | | | ATAATAAA | TTGACTAT | |
| | | | CT | | |
| GAM109 | LOC151571 | 5' | GGTTATATACATCATAA | ATGA | 3348 AACTG |
| | | | TTATTTAT | ATGTAACC | |
| | | | | | |
| | | | AGTAAATA | TATATTGG | |
| | | | CTACA | | |
| GAM109 | LOC196989 | 3' | GGGCACATAGAGCTATAA | ATAA | 3470 A G_ AA |
| | | | TTATTTATA | CT ATGT | CC |
| | | | | | |
| | | | AATAAATAT | GA TACA | GG |
| | | | C GA | CG | |
| GAM109 | LOC221431 | 3' | TATATCAGGTCATAA | ATAATA | 3553 AA_ |
| | | | TATTATTTAT | CTGATGTA | |
| | | | | | |
| | | | ATAATAAATA | GACTATAT | |
| | | | CTG | | |
| GAM110 | COL12A1 | 3' | AACCTCCTTGTTT | TAGACAC | 1102 CTAGT |
| | | | GTGTCTAA | GGAGGTT | |
| | | | | | |
| | | | CACAGATT | CCTCCAA | |
| | | | TTGTT | | |
| GAM110 | COL12A1 | 3' | AACCTCCTTGTTT | TAGACAC | 2380 CTAGT |
| | | | GTGTCTAA | GGAGGTT | |
| | | | | | |
| | | | CACAGATT | CCTCCAA | |
| | | | TTGTT | | |
| GAM110 | FLJ25473 | 5' | AACCTCCGAAAGCTCAGC | CACAC | 2496 _ AA_ AG |
| | | | GTGT | CT CT TGGAGGTT | |
| | | | | | |
| | | | CACA | GA GA GCCTCCAA | |
| | | | C CTC | AA | |
| GAM111 | ANK1 | 5' | CAGCCCCAGCTGCTCCTC | CCTC | 699 A TC C A |
| | | | GAGGAGGA | TA GT GG GCTG | |
| | | | | | |
| | | | CTCCTCCT | GT CG CC CGAC | |
| | | | C _ | A C | |
| GAM111 | ANK1 | 5' | CAGCCCCAGCTGCTCCTC | CCTC | 1918 A TC C A |
| | | | GAGGAGGA | TA GT GG GCTG | |
| | | | | | |

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|--------|----------|----|-----------------------------|------------|
| | | | CTCCTCCT GT CG CC CGAC | |
| | | | C _ A C | |
| GAM111 | CDH5 | 3' | CAGCCCAGCACCCCTTCCTCG 857 | AATATC C A |
| | | | CGAGGAGG GT GG GCTG | |
| | | | | |
| | | | GCTCCTTC CG CC CGAC | |
| | | | CCCA_ A _ | |
| GAM111 | DSP | 5' | CAGCTCCGACGCAGCTCCTC 1110 | GAATAT |
| | | | GAGGAG CGTCGGAGCTG | |
| | | | | |
| | | | CTCCTC GCAGCCTCGAC | |
| | | | GAC_ | |
| GAM111 | GDF5 | 3' | AGCCCACCATTTCTCCTC 755 | ATC C A |
| | | | GAGGAGGAAT GT GG GCT | |
| | | | | |
| | | | CTCCTCTTTA CA CC CGA | |
| | | | C_ _ _ | |
| GAM111 | OGDH | 3' | CAGCTCTGGCCACAATCCTCC 3510 | ATATC |
| | | | GGAGGA GTCGGAGCTG | |
| | | | | |
| | | | CCTCCT CGGTCTCGAC | |
| | | | AACAC | |
| GAM111 | RFX2 | 3' | CAGCCCCGCGCGGCGCCTCCTC 765 | AATATC A |
| | G | | CGAGGAGG GTCGG GCTG | |
| | | | | |
| | | | GCTCCTCC CGGCC CGAC | |
| | | | GCGGC_ C | |
| GAM111 | SET7 | 5' | CAGCCCCGACTGCTCCTCCTC 2153 | A TC A |
| | | | GAGGAGGA TA GTCGG GCTG | |
| | | | | |
| | | | CTCCTCCT GT CAGCC CGAC | |
| | | | C _ C | |
| GAM111 | C17orf31 | 3' | CAGCTCCCCCTTCACCCCTCCT 1723 | AATATCGTC |
| | TG | | CGAGGAGG GGAGCTG | |
| | | | | |
| | | | GTTCTCCTC CCTCGAC | |
| | | | CCACTTCCC | |
| GAM111 | caspr5 | 5' | CAGCTCCGAAGAATCCCCCG 2396 | A A ATA G |
| | | | CG GG GGA TC TCGGAGCTG | |
| | | | | |
| | | | GC CC CCT AG AGCCTCGAC | |
| | | | _ _ A_ A | |
| GAM111 | caspr5 | 5' | CAGCTCCGAAGAATCCCCCG 2462 | A A ATA G |
| | | | CG GG GGA TC TCGGAGCTG | |
| | | | | |
| | | | GC CC CCT AG AGCCTCGAC | |
| | | | _ _ A_ A | |
| GAM111 | CECR2 | 5' | AGCCCCGCCCCCTCCTCG 2192 | AATATC T A |
| | | | CGAGGAGG G CGG GCT | |
| | | | | |

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|--------|------------------|------------------------|-----------|------------|---|
| | | GCTCCTCC | C GCC CGA | | |
| | | CC_____C | | | |
| GAM111 | DKFZP434P0111 3' | CAGCCCCGGCCCATTCCTCC | 2790 | ATC | A |
| | | GGAGGAAT GTCGG GCTG | | | |
| | | | | | |
| | | CCTCCTTA CGGCC CGAC | | | |
| | | CC_ C | | | |
| GAM111 | FLJ10634 3' | CAGCTCCAGCCATCCACCCCTC | 1791 | A AAT C C | |
| | | GAGG GG AT GT GGAGCTG | | | |
| | | | | | |
| | | CTCC CC TA CG CCTCGAC | | | |
| | | _ ACC C A | | | |
| GAM111 | FLJ32334 3' | CTCCAAAACGCTATTCCTTC | 2483 | T C__ | |
| | | GGAGGAATA CGT GGAG | | | |
| | | | | | |
| | | CTTCCTTAT GCA CCTC | | | |
| | | C AAA | | | |
| GAM111 | FLJ32894 3' | CTCTGGTTTCCTCCTC | 2491 | TATCG | |
| | | GAGGAGGAA TCGGAG | | | |
| | | | | | |
| | | CTCCTCCTT GGTCTC | | | |
| | | T_____ | | | |
| GAM111 | KIAA0711 5' | AGTTGGACACACCCCTCCTCG | 1572 | AATATC G G | |
| | | CGAGGAGG GTC GA CT | | | |
| | | | | | |
| | | GCTCCTCC CAG TT GA | | | |
| | | CCACA_ G _ | | | |
| GAM111 | KIAA1649 3' | CAGCTGGAAGACATTCCTCC | 2245 | A G GG | |
| | | GGAGGAAT TC TC AGCTG | | | |
| | | | | | |
| | | CCTCCTTA AG AG TCGAC | | | |
| | | C A G_ | | | |
| GAM111 | KIAA1649 3' | CAGCTGGAAGACATTCCTCC | 2770 | A G GG | |
| | | GGAGGAAT TC TC AGCTG | | | |
| | | | | | |
| | | CCTCCTTA AG AG TCGAC | | | |
| | | C A G_ | | | |
| GAM111 | MGC30052 3' | AGTACATCATTCCTCCTC | 2500 | ATC CGGA | |
| | | GAGGAGGAAT GT GCT | | | |
| | | | | | |
| | | CTCCTCCTTA CA TGA | | | |
| | | CTA _____ | | | |
| GAM111 | MGC4737 3' | CAGCCCCATCTCCTCCTCCTC | 2206 | ATATC C A | |
| | | GAGGAGGA GT GG GCTG | | | |
| | | | | | |
| | | CTCCTCCT TA CC CGAC | | | |
| | | CCTC_ C _ | | | |
| GAM111 | LOC115110 5' | AGCCCCGGTTCCTCCCG | 2923 | A ATCGT A | |
| | | CG GGAGGAAT CGG GCT | | | |
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| | GC CCTCCTTG GCC CGA | |
| | C _ C | |
| GAM111 LOC123242 5' | CAGCTCCACCATATTTCTCC 3029 | C C |
| | GGAGGAATAT GT GGAGCTG | |
| | | |
| | CCTCTTTATA CA CCTCGAC | |
| | C _ | |
| GAM111 LOC146237 3' | CAGCTCTCACATTCCTTC 3282 | ATC C |
| | GGAGGAAT GT GGAGCTG | |
| | | |
| | CTTCCTTA CA TCTCGAC | |
| | _ C | |
| GAM111 LOC147160 5' | CAGCCCCACTCACTCCTTCTC 3291 | ATATC C A |
| | GAGGAGGA GT GG GCTG | |
| | | |
| | CTCTTCCT CA CC CGAC | |
| | CACT_ C _ | |
| GAM111 LOC149670 5' | CAGCCCTGCCACTCCTTCCTC 3138 | _ ATATC C A |
| | GAGGA GGA GT GG GCTG | |
| | | |
| | CTCCT CCT CG CC CGAC | |
| | T CAC_ T _ | |
| GAM111 LOC155072 3' | CAGCTCCGACCACACCATCCTC 3374 | _ AATATC |
| | GAGGA GG GTCGGAGCTG | |
| | | |
| | CTCCT CC CAGCCTCGAC | |
| | A ACAC_ | |
| GAM111 LOC158828 3' | CAGCCCCGGAGCCATTCCTCC 3227 | ATCG A |
| | GGAGGAAT TCGG GCTG | |
| | | |
| | CCTCCTTA GGCC CGAC | |
| | CCGA C | |
| GAM111 LOC202868 3' | CAGCTCCGACCACACCATCCTC 3487 | _ AATATC |
| | GAGGA GG GTCGGAGCTG | |
| | | |
| | CTCCT CC CAGCCTCGAC | |
| | A ACAC_ | |
| GAM111 LOC253001 5' | CAGCTCCACCATATTTCTCC 3697 | C C |
| | GGAGGAATAT GT GGAGCTG | |
| | | |
| | CCTCTTTATA CA CCTCGAC | |
| | C _ | |
| GAM111 LOC253841 5' | CAGCCCCAGCTGCTCCTCCTC 3704 | A TC C A |
| | GAGGAGGA TA GT GG GCTG | |
| | | |
| | CTCCTCCT GT CG CC CGAC | |
| | C _ A C | |
| GAM111 LOC51177 5' | CAGCTCCGACGCCCTCCCG 1676 | A AATAT |
| | CG GGAGG CGTCGGAGCTG | |
| | | |

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|--------|-----------|--------------------------------|----|-------|
| | | GC CCTCC GCAGCCTCGAC | | |
| | | — C — | | |
| GAM111 | LOC91408 | 3' CAGCTTTTGGTAATATTCTTCC 2735 | CG | — |
| | | TC GAGGAGGAATAT TCGGA GCTG | | |
| | | | | |
| | | CTCCTTCTTATA GGTTT CGAC | | |
| | | AT T | | |
| GAM112 | KIAA1265 | 3' CCATATGAATTTTGGTATA 2896 | A | — |
| | | TATACCAGAATT ATGG | | |
| | | | | |
| | | ATATGGTTTTAA TACC | | |
| | | GTA | | |
| GAM112 | MGC2731 | 3' CCACTGATTGGCTGGTGTA 2050 | — | A |
| | | TATACCAG AATTA TGG | | |
| | | | | |
| | | ATGTGGTC TTAGT ACC | | |
| | | GG C | | |
| GAM113 | C3AR1 | 3' ACTGTCAAAGAATCAATCCA 1081 | A | GA — |
| | | TG ATTGATTCTT GGT | | |
| | | | | |
| | | AC TAACTAAGAA TCA | | |
| | | C ACTG | | |
| GAM113 | GABARAPL3 | 3' TATACCTCTCACTCATTCA 2260 | T | TTCTT |
| | | TGAAT GA GAGGTATA | | |
| | | | | |
| | | ACTTA CT CTCCATAT | | |
| | | — CACT — | | |
| GAM113 | GOLGA2LY | 5' CTCAGTGAAAACATCAATTCA 2684 | — | — |
| | | TGAATTGAT TC TTGAG | | |
| | | | | |
| | | ACTTAACTA AG GACTC | | |
| | | CAAA T | | |
| GAM113 | PEG10 | 3' TACCTCAAGTATCAATTCA 1607 | T | |
| | | TGAATTGAT CTTGAGGTA | | |
| | | | | |
| | | ACTTAACTA GAACTCCAT | | |
| | | T | | |
| GAM113 | RNF13 | 3' TGTA ACTCAAGCATCAATTCA 1376 | T | G |
| | | TGAATTGAT CTTGAG TATA | | |
| | | | | |
| | | ACTTAACTA GAACTC ATGT | | |
| | | C A | | |
| GAM113 | LOC143692 | 5' GCCTATCAGAAGTCAATTCA 3060 | CT | — |
| | | TGAATTGATT TGA GGT | | |
| | | | | |
| | | ACTTAACTGA ACT CCG | | |
| | | AG AT | | |
| GAM113 | LOC151201 | 5' GTTTATACCATTGGATTCAATT 3342 | T | TGA |
| | CA | TGAATTGA TCT GGTATAAAC | | |
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|--------|--------------|----------------------------|-------|-----|
| | | ACTTAACT AGG CCATATTTG | | |
| | | T TTA | | |
| GAM113 | LOC257431 5' | CTCAGTGAAAACATCAATTCA 3231 | _____ | — |
| | | TGAATTGAT TC TTGAG | | |
| | | | | |
| | | ACTTAACTA AG GACTC | | |
| | | CAAA T | | |
| GAM113 | LOC93259 5' | ATACCCAGGTCAATTC 2927 | TT | A |
| | | GAATTGA CTTG GGTAT | | |
| | | | | |
| | | CTTAACT GGAC CCATA | | |
| | | — — | | |
| GAM114 | SAMHD1 3' | CATCAAATCCTGCCCCCGT 2594 | AA | T |
| | | ACGGG CAGGGTTTG TG | | |
| | | | | |
| | | TGCCC GTCCTAAAC AC | | |
| | | CC T | | |
| GAM114 | LOC150864 5' | AATCAACAGGCTCCCG 3150 | ACAGG | |
| | | CGGGA GTTTGTTGATT | | |
| | | | | |
| | | GCCCT CGGACAACTAA | | |
| | | — | | |
| GAM114 | LOC257358 3' | AATCAACACCCTTGCCCC 3731 | AA | TT |
| | | GGG CAGGG TGTTGATT | | |
| | | | | |
| | | CCC GTTCC ACAACTAA | | |
| | | C_ C_ | | |
| GAM114 | LOC90288 3' | AATCTTGCTCTGTTCCC 2621 | TTGTT | |
| | | GGGAACAGGGT GATT | | |
| | | | | |
| | | CCCTTGTCTCG CTAA | | |
| | | TT_ | | |
| GAM115 | GAD1 3' | GGCTTAGTAATAGATCACGGCA 777 | A A | A T |
| | | TGC CGT ATCTATTAT GA GCC | | |
| | | | | |
| | | ACG GCA TAGATAATG TT CGG | | |
| | | _ C A _ | | |
| GAM115 | KLHL2 3' | TATAATAAATTATGTGCA 1371 | C | |
| | | TGCACGTAAT TATTATA | | |
| | | | | |
| | | ACGTGTATTA ATAATAT | | |
| | | A | | |
| GAM115 | KIAA0276 3' | CACTGTAATGTTACATGCA 2904 | C CT | A |
| | | TGCA GTAAT ATTATAG TG | | |
| | | | | |
| | | ACGT CATTG TAATGTC AC | | |
| | | A _ _ | | |
| GAM115 | LOC130814 3' | GGCACCTATAATAAATGAC 3012 | A C | A |
| | | GT AT TATTATAG TGCC | | |
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| | | CA TA ATAATATC ACGG | |
| | | G A C | |
| GAM116 | TGFB2 | 3' AATGCCTGTATATAAATATGAA 1002 | TAG C_ |
| | | TTCATATTTAT ATAC GCATT | |
| | | | |
| | | AAGTATAAATA TATG CGTAA | |
| | | ____ TC | |
| GAM116 | KIAA1223 | 3' AATGAGTCTATTAATAAATATG 2908 | ATACCG |
| | AA | TTCATATTTATTAG CATT | |
| | | | |
| | | AAGTATAAATAATT GTAA | |
| | | ATCTGA | |
| GAM116 | PRO2859 | 5' CGGTATGTAAATATGAA 1840 | TAG |
| | | TTCATATTTAT ATACCG | |
| | | | |
| | | AAGTATAAATG TATGGC | |
| | | _____ | |
| GAM116 | PSIP2 | 3' ATGCTTATACAATAAATATGAA 2324 | AG CC |
| | | TTCATATTTATT ATA GCAT | |
| | | | |
| | | AAGTATAAATAA TAT CGTA | |
| | | CA T_ | |
| GAM116 | LOC152185 | 3' AATGCAAATCAAATAAATATGA 2497 | A ACC |
| | | TCATATTTATT GAT GCATT | |
| | | | |
| | | AGTATAAATAA CTA CGTAA | |
| | | A AA_ | |
| GAM116 | LOC89953 | 3' ATGCTACTCTAATAAATAT 2437 | TACC |
| | | ATATTTATTAGA GCAT | |
| | | | |
| | | TATAAATAATCT CGTA | |
| | | CAT_ | |
| GAM116 | LOC90509 | 5' GTGTTTAATAAATATGAA 2649 | |
| | | TTCATATTTATTAGATAC | |
| | | | |
| | | AAGTATAAATAATTTGTG | |
| | | _____ | |
| GAM117 | BPNT1 | 3' CAATGAGAGATTATA 2702 | TCC |
| | | TATGA TCTCTCATTG | |
| | | | |
| | | ATATT AGAGAGTAAC | |
| | | _____ | |
| GAM117 | FLJ21709 | 3' CAATGAGGGTGTGTCATG 2235 | CCT |
| | | TATGAT CTCTCATTG | |
| | | | |
| | | GTA CTG GGGAGTAAC | |
| | | T_ | |
| GAM117 | MGC13007 | 5' CAATGAGAAAGGAGAGTA 2246 | GA C |
| | | TAT TCCT TCTCATTG | |
| | | | |

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|--------|---------------|----|-----------------------------|----------|--|
| | | | ATG AGGA AGAGTAAC | | |
| | | | AG A | | |
| GAM117 | MGC14407 | 5' | CAATGGGGGAGACATA 2294 | ATC | |
| | | | TATG CTCTCTCATTG | | |
| | | | | | |
| | | | ATAC GAGGGGGTAAC | | |
| | | | A__ | | |
| GAM117 | LOC151201 | 3' | CAATGGGGCGGTCATA 3341 | T T T | |
| | | | TATGA CC CTC CATTG | | |
| | | | | | |
| | | | ATACT GG GGG GTAAC | | |
| | | | _ C _ | | |
| GAM117 | LOC197131 | 3' | CAATGAGTGGATCATG 3419 | TCT | |
| | | | TATGATCC CTCATTG | | |
| | | | | | |
| | | | GTACTAGG GAGTAAC | | |
| | | | T__ | | |
| GAM117 | LOC219942 | 3' | CAACAAGCGGGGGGTCATA 3598 | _ CA | |
| | | | TATGATCCTCT CT TTG | | |
| | | | | | |
| | | | ATACTGGGGGG GA AAC | | |
| | | | C AC | | |
| GAM118 | B3GAT1 | 5' | CAGTTGGGCCGACTCTCC 1855 | ACTA | |
| | | | GGAGAGTT GGCCCAACTG | | |
| | | | | | |
| | | | CCTCTCAG CCGGGTTGAC | | |
| | | | G__ | | |
| GAM118 | B3GAT1 | 5' | CAGTTGGGCCGACTCTCC 2362 | ACTA | |
| | | | GGAGAGTT GGCCCAACTG | | |
| | | | | | |
| | | | CCTCTCAG CCGGGTTGAC | | |
| | | | G__ | | |
| GAM118 | GALNT7 | 3' | AGTTGAGAACTCTCCTG 2365 | A AGGCC | |
| | | | TAGGAGAGTT CT CAACT | | |
| | | | | | |
| | | | GTCCTCTCAA GA GTTGA | | |
| | | | A ____ | | |
| GAM118 | ZNF76 | 3' | CAGCTGGGCGCCCACTCTCCT 1019 | TACTAG A | |
| | | | AGGAGAGT GCCCA CTG | | |
| | | | | | |
| | | | TCCTCTCA CGGGT GAC | | |
| | | | CCCG__ C | | |
| GAM118 | DKFZp434M0331 | 5' | CAGTTGAGCCTCATGGCTCTCC 1727 | CT C | |
| | | | GGAGAGTTA AGGC CAACTG | | |
| | | | | | |
| | | | CCTCTCGGT TCCG GTTGAC | | |
| | | | AC A | | |
| GAM118 | FLJ20666 | 5' | CAGTCACCTGATGACTCTCC 1763 | C CCCA | |
| | | | GGAGAGTTA TAGG ACTG | | |
| | | | | | |

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|--------|-----------|----|-----------------------------|-------------|
| | | | CCTCTCAGT GTCC TGAC | |
| | | | A AC__ | |
| GAM118 | FYCO1 | 3' | CAGTCAGGCCCCAGGTTCTTCC 2064 | G TTA A_ CA |
| | | | GGA AG CT GGCC ACTG | |
| | | | | |
| | | | CCT TC GA CCGG TGAC | |
| | | | _ TTG CC AC | |
| GAM118 | ILF3 | 5' | CAGTTGAACCCAGCAGCCCGCC 1121 | AGA A A CC |
| | | | GG GTT CT GG CAACTG | |
| | | | | |
| | | | CC CGA GA CC GTTGAC | |
| | | | GCC C C AA | |
| GAM118 | KIAA0193 | 3' | CAGTTGGGCCTAATCCTGCCTC 1544 | A TAC__ |
| | | | GAG GT TAGGCCCACTG | |
| | | | | |
| | | | CTC CG ATCCGGGTTGAC | |
| | | | _ TCCTA | |
| GAM118 | KIAA1163 | 3' | CAGCTGGACCTAGCTGATTCTC 3121 | _ C A |
| | | | GAGAGTTA CTAGG CCA CTG | |
| | | | | |
| | | | CTCTTAGT GATCC GGT GAC | |
| | | | C A C | |
| GAM118 | KIAA1247 | 3' | GGCTCCCTAGCAACTCCCTA 2609 | A A C__ |
| | | | TAGG GAGTT CTAGG CC | |
| | | | | |
| | | | ATCC CTCAA GATCC GG | |
| | | | _ C CTC | |
| GAM118 | KIAA1870 | 5' | CAGCTGGGCCTGCAGTTCCTCC 2293 | A TT _ A |
| | C | | GG GAG ACT AGGCCCA CTG | |
| | | | | |
| | | | CC CTC TGA TCCGGGT GAC | |
| | | | _ CT CG C | |
| GAM118 | LOC146517 | 3' | CAGTTAAACCTAGATCCCTCCC 3095 | A TTA_ CCC |
| | T | | AGG GAG CTAGG AACTG | |
| | | | | |
| | | | TCC CTC GATCC TTGAC | |
| | | | _ CCTA AAA | |
| GAM118 | LOC162083 | 5' | CAGCTGGGCTCCATAGACCCTC 3242 | A ACTA_ A |
| | C | | GGAG GTT GGCCCA CTG | |
| | | | | |
| | | | CCTC CAG TCGGGT GAC | |
| | | | C ATACC C | |
| GAM118 | LOC220477 | 5' | CAGTTGGGCCCTGTACCATCCC 3041 | A GT_ TA |
| | | | GG GA TAC GGCCCAACTG | |
| | | | | |
| | | | CC CT ATG CCGGGTTGAC | |
| | | | _ ACC TC | |
| GAM118 | LOC222237 | 3' | AGCTGGGCCTAGTCAACT 3650 | _ A |
| | | | AGTT ACTAGGCCCA CT | |
| | | | | |

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|--------|-----------|----|----------------------------|--------|------|
| | | | TCAA TGATCCGGGT GA | | |
| | | | C C | | |
| GAM118 | LOC255096 | 5' | TGGGCCAGCAGATTCTCC 3745 | A_ | A |
| | | | GGAGAGTT CT GGCCCA | | |
| | | | | | |
| | | | CCTCTTAG GA CCGGGT | | |
| | | | AC _ | | |
| GAM118 | LOC92340 | 3' | CAGCCAGGCCCTCTTCTCCTG 2837 | TTACTA | CAA |
| | | | TAGGAGAG GGCC CTG | | |
| | | | | | |
| | | | GTCCTCTT CCGG GAC | | |
| | | | CTC__ ACC | | |
| GAM119 | ARG1 | 3' | TAAGTTGGCAAAGACTTA 700 | __ | |
| | | | TAAGTCTT CCAAGTTG | | |
| | | | | | |
| | | | ATTCAGAA GGTTCAAT | | |
| | | | AAC | | |
| GAM119 | BACH2 | 3' | TGATGCTGCAGTGGAAC 1964 | C | AGT |
| | | | GT TTCCA TGGCATCA | | |
| | | | | | |
| | | | CA AAGGT GTCGTAGT | | |
| | | | A GAC | | |
| GAM119 | CDR1 | 3' | TGATTTACTGGAAGACTTG 1083 | A | TGGC |
| | | | TAAGTCTTCCA GT ATCA | | |
| | | | | | |
| | | | G TTCAGAAGGT CA TAGT | | |
| | | | _ TT__ | | |
| GAM119 | CNTN3 | 3' | GCATTATTTGGAAGACTTA 2758 | TG_ | |
| | | | TAAGTCTTCCAAGT GC | | |
| | | | | | |
| | | | ATTCAGAAGGTTTA CG | | |
| | | | TTA | | |
| GAM119 | ESRRG | 3' | GATGTCGAAGAACTTA 2748 | C | CAAG |
| | | | TAAGT TTC TTGGCATC | | |
| | | | | | |
| | | | ATTCA AAG AGCTGTAG | | |
| | | | _ A__ | | |
| GAM119 | FSTL1 | 3' | GATGCCAGAGAGAACTTA 1357 | CT | CAAG |
| | | | TAAGT TC TTGGCATC | | |
| | | | | | |
| | | | ATTCA AG GACCGTAG | | |
| | | | AG A__ | | |
| GAM119 | GABRB2 | 3' | TGATGTAGGACTTGGAAC 1967 | C | G_ |
| | | | GT TTCCAAGTT GCATCA | | |
| | | | | | |
| | | | CA AAGGTTTCAG TGTAGT | | |
| | | | A GA | | |
| GAM119 | GABRB2 | 3' | TGATGTAGGACTTGGAAC 776 | C | G_ |
| | | | GT TTCCAAGTT GCATCA | | |
| | | | | | |

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|--------|-------|----|---------------------------|---------|
| | | | CA AAGGTTTCAG TGTAGT | |
| | | | A GA | |
| GAM119 | MCP | 3' | ATGCCAACTCTTAAGATT 925 | CCA |
| | | | AGTCTT AGTTGGCAT | |
| | | | | |
| | | | TTAGAA TCAACCGTA | |
| | | | TTC | |
| GAM119 | NRIP1 | 3' | ATGCCAACAAAGCTTA 2548 | T CCAA |
| | | | TAAG CTT GTTGGCAT | |
| | | | | |
| | | | ATTC GAA CAACCGTA | |
| | | | _ A _ | |
| GAM119 | OPHN1 | 3' | GATGCAAACATTGGAAGATT 936 | _ G |
| | | | AGTCTTCCAA GTT GCATC | |
| | | | | |
| | | | TTAGAAGGTT CAA CGTAG | |
| | | | A A | |
| GAM119 | PTPRO | 3' | GAAGCACCGGGAAGACTTA 964 | AA TG A |
| | | | TAAGTCTTCC GT GC TC | |
| | | | | |
| | | | ATTCAGAAGG CA CG AG | |
| | | | GC _ A | |
| GAM119 | PTPRO | 3' | GAAGCACCGGGAAGACTTA 2155 | AA TG A |
| | | | TAAGTCTTCC GT GC TC | |
| | | | | |
| | | | ATTCAGAAGG CA CG AG | |
| | | | GC _ A | |
| GAM119 | PTPRO | 3' | GAAGCACCGGGAAGACTTA 2156 | AA TG A |
| | | | TAAGTCTTCC GT GC TC | |
| | | | | |
| | | | ATTCAGAAGG CA CG AG | |
| | | | GC _ A | |
| GAM119 | PTPRO | 3' | GAAGCACCGGGAAGACTTA 2157 | AA TG A |
| | | | TAAGTCTTCC GT GC TC | |
| | | | | |
| | | | ATTCAGAAGG CA CG AG | |
| | | | GC _ A | |
| GAM119 | PTPRO | 3' | GAAGCACCGGGAAGACTTA 2158 | AA TG A |
| | | | TAAGTCTTCC GT GC TC | |
| | | | | |
| | | | ATTCAGAAGG CA CG AG | |
| | | | GC _ A | |
| GAM119 | RAD50 | 5' | TGATGTCAATGGAGAACTTA 2419 | CT AG |
| | | | TAAGT TCCA TTGGCATCA | |
| | | | | |
| | | | ATTCA AGGT AACTGTAGT | |
| | | | AG _ | |
| GAM119 | RORB | 3' | GTGTTTCATGAAGACTTA 1338 | CAA TG |
| | | | TAAGTCTTC GT GCAT | |
| | | | | |

ATTCAGAAG TA TGTG
 ____ CT
 GAM119 SORD 3' TAACTTCATGAAGACTTA 990 C__
 TAAGTCTTC AAGTTG
 ||||| |||||
 ATTCAGAAG TTCAAT
 TAC
 GAM119 SULT1C1 3' ATGCCACCCTTTTGAAGC 797 T T__
 G CTTCCAAG TGGCAT
 | ||||| |||||
 C GAAGGTTT ACCGTA
 _ TCCC
 GAM119 WRB 3' GTTCTTTGAAGACTTA 1137 C TT
 TAAGTCTTC AAG GGC
 ||||| ||| |||
 ATTCAGAAG TTC TTG
 T _
 GAM119 ANKRD5 5' TGATCGCCCGGAAGACT 1978 AAGTT _
 AGTCTTCC GGC ATCA
 ||||| ||| |||
 TCAGAAGG CCG TAGT
 C__ C
 GAM119 C7orf10 3' TGATACCACTAAGAAGAAGATT 2084 CA__ T C
 TA TAAGTCTTC AGT GG ATCA
 ||||| ||| |||
 ATTTAGAAG TCA CC TAGT
 AAGAA _ A
 GAM119 DKFZP727M111 5' TGATGCCAACTCAGAC 1633 TCCA
 GTCT AGTTGGCATCA
 ||| |||||
 CAGA TCAACCGTAGT
 C__
 GAM119 FLJ13262 3' TGATGCCAACTCCCCGCACTT 2113 CTTCCA_
 AAGT AGTTGGCATCA
 ||| |||||
 TTCA TCAACCGTAGT
 CGCCCCC
 GAM119 FLJ20425 5' TGACGGCTTTTGTACAAGACTT 1755 C_ TT A_
 A TAAGTCTT CAAG GGC TCA
 ||||| ||| ||| |||
 ATTCAGAA GTTT TCG AGT
 CA T_ GC
 GAM119 KIAA0953 3' TGGAAACTAGAAGACTTA 2763 CA GG
 TAAGTCTTC AGTT CA
 ||||| ||| |||
 ATTCAGAAG TCAA GT
 A_ AG
 GAM119 KIAA1450 3' TGATGCTTCATTGAAGACTTA 2732 C GTT
 TAAGTCTTC AA GGCATCA
 ||||| || |||||

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| | | ATTCAGAAG TT TCGTAGT | |
| | | _ ACT | |
| GAM119 | NEUROD6 5' | TGAAAAGATTTGGAAGAC 2000 | GGCA |
| | | GTCTTCCAAGTT TCA | |
| | | | |
| | | CAGAAGGTTTAG AGT | |
| | | AAA_ | |
| GAM119 | PRO0255 3' | GTTTCTTGAAAGACTTA 1475 | C TT |
| | | TAAGTCTT CAAG GGC | |
| | | | |
| | | ATTCAGAA GTTC TTG | |
| | | A T_ | |
| GAM119 | UBE3B 5' | TGATGCCGAGGAAAGACT 3069 | _ AAG |
| | | AGTCTT CC TTGGCATCA | |
| | | | |
| | | TCAGAA GG AGCCGTAGT | |
| | | A _ | |
| GAM119 | ZIM2 3' | ATGTCAGTAGGAGACTTA 1623 | CAAG |
| | | TAAGTCTTC TTGGCAT | |
| | | | |
| | | ATTCAGAGG GACTGTA | |
| | | AT_ | |
| GAM119 | LOC112868 3' | TGTAGACATGAAGACTTA 2962 | CAA G |
| | | TAAGTCTTC GTT GCA | |
| | | | |
| | | ATTCAGAAG CAG TGT | |
| | | TA_ A | |
| GAM119 | LOC116166 3' | TAAC TTCATGAAGACTTA 2545 | C_ |
| | | TAAGTCTTC AAGTTG | |
| | | | |
| | | ATTCAGAAG TTCAAT | |
| | | TAC | |
| GAM119 | LOC123855 3' | TGAGCACGCTTGGAATAC 3033 | C TG A |
| | | GT TTCCAAGT GC TCA | |
| | | | |
| | | CA AAGGTTTCG CG AGT | |
| | | T CA _ | |
| GAM119 | LOC146818 5' | GATGCCGAAGAAGGCT 3100 | CAAG |
| | | AGTCTTC TTGGCATC | |
| | | | |
| | | TCGGAAG AGCCGTAG | |
| | | A_ | |
| GAM119 | LOC152190 5' | TGACAACTGGAAGACTT 2864 | A G |
| | | AAGTCTTCCA GTTG CA | |
| | | | |
| | | TTCAGAAGGT CAAC GT | |
| | | _ A | |
| GAM119 | LOC153077 3' | TGATACCAACTTGAGATAACTT 3366 | CT _ C |
| | | AAGT TC CAAGTTGG ATCA | |
| | | | |

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| | TTCA AG GTTCAACC TAGT | |
| | AT A A | |
| GAM119 LOC158382 3' | TGATAGCTGATAAGACTTA 3388 | CCAA TG _ |
| | TAAGTCTT GT GC ATCA | |
| | | |
| | ATTCAGAA TA CG TAGT | |
| | ____ GT A | |
| GAM119 LOC158476 3' | TGATCTCGTCAGGAGACTTA 3391 | CAAGT ____ |
| | TAAGTCTTC TGGC ATCA | |
| | | |
| | ATTCAGAGG ACTG TAGT | |
| | ____ CTC | |
| GAM119 LOC164397 5' | ATGTCTTCTGAAGACTTA 3249 | CA TT |
| | TAAGTCTTC AG GGCAT | |
| | | |
| | ATTCAGAAG TC CTGTA | |
| | __ TT | |
| GAM119 LOC196510 3' | TGATCTGGCTTGGCAGACTTA 3416 | T TG C |
| | TAAGTCT CCAAGT G ATCA | |
| | | |
| | ATTCAGA GGTTCTG C TAGT | |
| | C GT _ | |
| GAM119 LOC200220 3' | TGATCTGGCTTGGCAGACTTA 3445 | T TG C |
| | TAAGTCT CCAAGT G ATCA | |
| | | |
| | ATTCAGA GGTTCTG C TAGT | |
| | C GT _ | |
| GAM119 LOC201477 5' | CAACTGAGGTCTGTAAGACTTA 3472 | ____ A_ |
| | TAAGTCTT CC AGTTG | |
| | | |
| | ATTCAGAA GG TCAAC | |
| | TGTCT AG | |
| GAM119 LOC201696 5' | TGATGCCATTGAAGACTT 2650 | CAAGT |
| | AAGTCTTC TGGCATCA | |
| | | |
| | TTCAGAAG ACCGTAGT | |
| | TT__ | |
| GAM119 LOC220469 3' | GATGGCCAGAAGATTTA 3049 | CAAGT _ |
| | TAAGTCTTC TGGC ATC | |
| | | |
| | ATTTAGAAG ACCG TAG | |
| | ____ G | |
| GAM119 LOC221272 3' | TGACACCAACTTTTGAGATTTA 3615 | CC CA |
| | TAAGTCTT AAGTTGG TCA | |
| | | |
| | ATTTAGAG TTCAACC AGT | |
| | TT AC | |
| GAM119 LOC222166 3' | TGAGGCCCCAGAGGACTTA 3636 | CAAGTT A |
| | TAAGTCTTC GGC TCA | |
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| | | ATTCAGGAG CCG AGT | | |
| | | ACC__ G | | |
| GAM119 | LOC253220 5' | TGAGCAGCTCCTGGAAGAC 3706 | __ | G A |
| | | GTCTTCCA AGTTG C TCA | | |
| | | | | |
| | | CAGAAGGT TCGAC G AGT | | |
| | | CC __ | | |
| GAM119 | LOC51275 5' | TGATGGAAGTGGAAGATT 1694 | AG | GG |
| | | AGTCTTCCA TT CATCA | | |
| | | | | |
| | | TTAGAAGGT AG GTAGT | | |
| | | GA __ | | |
| GAM119 | LOC54505 5' | GATTTCTGGAAGACTTA 2800 | AGTT | C |
| | | TAAGTCTTCCA GG ATC | | |
| | | | | |
| | | ATTCAGAAGGT CT TAG | | |
| | | ____ T | | |
| GAM119 | LOC90844 3' | TGATTGCATTGGAAGATCA 2682 | A | GTTG _ |
| | | A GTCTTCCAA GCA TCA | | |
| | | | | |
| | | A TAGAAGGTT CGT AGT | | |
| | | C A__ T | | |
| GAM119 | LOC92697 5' | GATGCCACCAGACTTA 2882 | TCCAA | T |
| | | TAAGTCT GT GGCATC | | |
| | | | | |
| | | ATTCAGA CA CCGTAG | | |
| | | C__ _ | | |
| GAM120 | KIF5C 3' | ACAAATTCTATTGAAGTATTT 1122 | AC | |
| | | GAATAT TCAATAGAATTTGT | | |
| | | | | |
| | | TTTATG AGTTATCTTAAACA | | |
| | | A_ | | |
| GAM120 | DKFZP564M182 3' | ACAATTGTCAAGTATATTCTG 3097 | CA | AAT |
| | | TAGAATATACT ATAG TTGT | | |
| | | | | |
| | | GTCTTATATGA TGTT AACA | | |
| | | AC __ | | |
| GAM120 | KIAA0852 5' | ACAAATTCGTAAGTATCCTCTA 1594 | AT | CAATA |
| | | TAGA ATACT GAATTTGT | | |
| | | | | |
| | | ATCT TATGA CTAAACA | | |
| | | CC ATG__ | | |
| GAM120 | PRO0097 5' | CTATTGAGTAGTATTCTA 1472 | _ | |
| | | TAGAATAT ACTCAATAG | | |
| | | | | |
| | | ATCTTATG TGAGTTATC | | |
| | | A | | |
| GAM120 | LOC222161 5' | TTGTATTAGTATATTCTA 3578 | C | G |
| | | TAGAATATACT AATA AA | | |
| | | | | |

ATCTTATATGA TTAT TT
 _ G
 GAM120 LOC255811 5' ACAAAGATGGCTATCGGTATAT 3662 CA AA____
 TCTA TAGAATATACT ATAG TTTGT
 ||||| ||| ||||
 ATCTTATATGG TATC AAACA
 C_ GG TAG
 GAM121 DPYD 3' TATTAAGTAAAATCCCCTTC 2569 TAT
 GA GGGATTTTACTTAATA
 || |||||
 CT CCCTAAAATGAATTAT
 TC_
 GAM121 KIAA1240 3' TATTAATGTTTAAATCCCATCT 2761 T T_ _
 C GA ATGGGATTT AC TTAATA
 || ||||| || |||||
 CT TACCCTAAA TG AATTAT
 C TT T
 GAM121 KIAA1843 3' TATTACAGAAAATCCCATATTC 2624 A A _
 A A GATATGGGATTTT CT TAATA
 | ||||| || |||||
 A TTATACCCTAAAA GA ATTAT
 C _ C
 GAM121 LOC122786 3' ATTAAGTAATCCACCATTCTT 2995 T GATT
 A TAAGA ATGG T TACTTAAT
 |||| ||| |||||
 ATTCT TACC AATGAATTA
 T ACCT
 GAM122 FGF12 3' AACTAACTGTATTGTTATT 1935 TAG
 AATAACAGT TAGTTTAGTT
 ||||| |||||
 TTATTGTTA GTCAAATCAA
 T_
 GAM122 FGG 3' AACTGCTAACTTCTATTGA 1965 AC
 TCAATA AGTTAGTAGTT
 |||| |||||
 AGTTAT TCAATCGTCAA
 CT
 GAM122 NEBL 3' AACTAACTGTCAACTGTTG 1295 AG T
 TAACAGTT TAGTT AGTT
 ||||| |||| |||
 GTTGTCAA GTCAA TCAA
 CT _
 GAM122 RPE 3' AACTAAATATTTATAACTGTTC 2623 AT GTA_
 TGA TCA AACAGTTA GTTTAGTT
 || ||||| |||||
 AGT TTGTCAAT TAAATCAA
 C_ ATTTA
 GAM122 TRHDE 3' AACTAAATTTCTCAACTGTTAT 1446 A _ T
 GA TCA TAACAGTT AG AGTTTAGTT
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AGT ATTGTCAA TC TTAAATCAA
_ C T
GAM122 BCMP1 3' AACTAAACATTCTCTGTTCTGA 2197 AT TT A
TCA AACAG AGT GTTTAGTT
||| |||| ||| |||||
AGT TTGTC TTA CAAATCAA
C_ TC _
GAM122 DKFZP434A0225 3' AACTAAACCTAATGCTGCTGTT 3624 T ____
A TAACAGT AGTA GTTTAGTT
||||| ||| |||||
ATTGTCG TCGT CAAATCAA
_ AATC
GAM122 FLJ12899 3' ACTAAAATACTGTTATTGG 2069 TAGTAG
TCAATAACAGT TTTAGT
||||||| ||||
GGTTATTGTCA AAATCA
TA____
GAM122 PREI3 3' AACTAAACTACTAAGTTA 2747 AG
TAAC TTAGTAGTTTAGTT
||| |||||
ATTG AATCATCAAATCAA
_
GAM122 PSIP2 3' AATTAAGCAACTGACATTGA 2323 AACA A
TCAAT GTTAGT GTTTAGTT
|||| ||||| |||||
AGTTA CAGTCA CGAATTAA
_ A
GAM122 LOC220963 3' AACTAAACTACTTGTGTGTTG 3526 A TT
A TCAATA CAG AGTAGTTTAGTT
||||| ||| |||||
AGTTGT GTT TCATCAAATCAA
_ GT
GAM123 LOC143098 5' CGATGATCTGGCCGAAGAGCTT 3051 A_ _ TT
AAGCT TCG TCA GATCATCG
|||| ||| ||| |||||
TTCGA AGC GGT CTAGTAGC
GA C _
GAM124 CALB2 3' AAAGAAGAGTTTACAGACAATA 853 ATTTA_
A TTATTGTCTG TTTCTTT
||||||| |||||
AATAACAGAC GAAGAAA
ATTGA
GAM124 TRAF5 3' AAAGAAATAGGTTCAACAGG 1133 A CT
A TCTT TTGT GATTTATTTCTTT
|||| ||| |||||
AGGA AACA TTGGATAAAGAAA
C C_
GAM124 C15orf5 3' AAAGAAAGGCACCATCAGACAA 2173 A TTA____
AAGA TCTT TTGTCTGAT TTTCTTT
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|--------|---------------|----|-----------------------------|---------|-----------|
| | | | AGAA AACAGACTA | AAAGAAA | |
| | | | — CCACGG | | |
| GAM124 | DKFZp761K1423 | 3' | AAAGAAATAAATCCAACAA | 1826 | CT |
| | | | TTGT GATTTATTTCTTT | | |
| | | | | | |
| | | | AACA CTAAATAAAGAAA | | |
| | | | AC | | |
| GAM124 | FLJ12892 | 5' | AAAGAAACATCATCTTCAGATA | 2801 | TTTA_____ |
| | | | ATAAGA CTTATTGTCTGA TTTCTTT | | |
| | | | | | |
| | | | GAATAATAGACT AAAGAAA | | |
| | | | TCTACTAC | | |
| GAM124 | MGC15437 | 3' | AAAGAAATAAATGACAAT | 2292 | TG |
| | | | ATTGTC ATTTATTTCTTT | | |
| | | | | | |
| | | | TAACAG TAAATAAAGAAA | | |
| | | | — | | |
| GAM124 | MGC27016 | 3' | AAAGAAATGATGAGACAAAAAG | 2503 | A G T |
| | | | A TCTT TTGTCT ATT ATTTCTTT | | |
| | | | | | |
| | | | AGAA AACAGA TAG TAAAGAAA | | |
| | | | A G _ | | |
| GAM124 | LOC154089 | 3' | AAGAAATATTACAATAAGG | 3187 | CTGATT |
| | | | TCTTATTGT TATTTCTT | | |
| | | | | | |
| | | | GGAATAACA ATAAAGAA | | |
| | | | TT_____ | | |
| GAM124 | LOC159053 | 3' | AAAGAAATAAACTTTTGGACAG | 3395 | TG_____ |
| | | | TTGTC A TTTATTTCTTT | | |
| | | | | | |
| | | | GACAG T AAATAAAGAAA | | |
| | | | GT TTC | | |
| GAM125 | XPR1 | 3' | CTGAGCATATCTCTCGTAACA | 1152 | AAATCA A |
| | | | TGTTACGA ATAT TTCAG | | |
| | | | | | |
| | | | ACAATGCT TATA GAGTC | | |
| | | | CTC_____ C | | |
| GAM126 | DFNA5 | 3' | TGCACGTAAAAAGTTGAC | 1109 | GC A |
| | | | GTCAAT TTAAACGT CA | | |
| | | | | | |
| | | | CAGTTG AAATTGCA GT | | |
| | | | A_ C | | |
| GAM126 | LRAT | 3' | TGTCTTTTAAAGCATTTACTAA | 2557 | C CGT |
| | | | TTAGT AATGCTTTAA ACA | | |
| | | | | | |
| | | | AATCA TTACGAAATT TGT | | |
| | | | T TTC | | |
| GAM126 | PKHD1 | 3' | TACACTATAGCACTTTGACTAA | 2449 | ___ T AC |
| | | | TTAGTCAA TGCT TA GTA | | |
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|--------|-----------|----|-----------------------|------------|-----------|--------|----|--|
| | | | AATCAGTT | ACGA | AT | CAT | | |
| | | | TC | T | CA | | | |
| GAM126 | HSPC055 | 5' | CGTTGAAGCACA | ACTAA | 1480 | CAA | | |
| | | | TTAGT | TGCTTTAACG | | | | |
| | | | | | | | | |
| | | | AATCA | ACGAAGTTGC | | | | |
| | | | AC_ | | | | | |
| GAM126 | PRO0386 | 5' | TACTTTGAGAAACATTGACTA | 1845 | C__ | C | | |
| | | | TAGTCAATG | TTTAA | GTA | | | |
| | | | | | | | | |
| | | | ATCAGTTAC | GAGTT | CAT | | | |
| | | | AAA | T | | | | |
| GAM126 | LOC121441 | 3' | TGTTTCTAAGCCATTGACTAA | 2992 | _ | TAACGT | | |
| | | | TTAGTCAATG | CTT | ACA | | | |
| | | | | | | | | |
| | | | AATCAGTTAC | GAA | TGT | | | |
| | | | C | TCTT__ | | | | |
| GAM127 | ADAMTS5 | 3' | ATTGGAAACTGAAATTCAGA | 1351 | CA | G | TG | |
| | | | TC | AATT | CAGTTTC | GT | | |
| | | | | | | | | |
| | | | AG | TTAA | GTCAAAG | TA | | |
| | | | AC | A | GT | | | |
| GAM127 | BHLHB3 | 3' | GATACCAGATAATCACAA | 2161 | CA | _ | | |
| | | | TTG | GTT | TCTGGTATC | | | |
| | | | | | | | | |
| | | | AAC | TAA | AGACCATAG | | | |
| | | | AC | T | | | | |
| GAM127 | CCR2 | 3' | GCTGAAAACCTGCAACTTG | 767 | A | CT | | |
| | | | CAA | TTGCAGTTT | GGT | | | |
| | | | | | | | | |
| | | | GTT | AACGTCAAA | TCG | | | |
| | | | C | AG | | | | |
| GAM127 | DCN | 3' | ACCTAACTGCAATGTGGA | 868 | A | TCT | | |
| | | | TCCA | ATTGCAGTT | GGT | | | |
| | | | | | | | | |
| | | | AGGT | TAACGTCAA | CCA | | | |
| | | | G | T__ | | | | |
| GAM127 | DCN | 3' | ACCTAACTGCAATGTGGA | 2421 | A | TCT | | |
| | | | TCCA | ATTGCAGTT | GGT | | | |
| | | | | | | | | |
| | | | AGGT | TAACGTCAA | CCA | | | |
| | | | G | T__ | | | | |
| GAM127 | DCN | 3' | ACCTAACTGCAATGTGGA | 2422 | A | TCT | | |
| | | | TCCA | ATTGCAGTT | GGT | | | |
| | | | | | | | | |
| | | | AGGT | TAACGTCAA | CCA | | | |
| | | | G | T__ | | | | |
| GAM127 | DCN | 3' | ACCTAACTGCAATGTGGA | 2423 | A | TCT | | |
| | | | TCCA | ATTGCAGTT | GGT | | | |
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|--------|-------|----|-----------------------------|-----|------|-----|
| | | | AGGT TAACGTCAA CCA | | | |
| | | | G T__ | | | |
| GAM127 | DCN | 3' | ACCTAACTGCAATGTGGA 2424 | A | TCT | |
| | | | TCCA ATTGCAGTT GGT | | | |
| | | | | | | |
| | | | AGGT TAACGTCAA CCA | | | |
| | | | G T__ | | | |
| GAM127 | DCN | 3' | ACCTAACTGCAATGTGGA 2425 | A | TCT | |
| | | | TCCA ATTGCAGTT GGT | | | |
| | | | | | | |
| | | | AGGT TAACGTCAA CCA | | | |
| | | | G T__ | | | |
| GAM127 | EXTL1 | 5' | GGACACGGCCCTGCATTCTGGA 1116 | AAT | TTT | GTA |
| | | | TCCA TGCAG CTG TCC | | | |
| | | | | | | |
| | | | AGGT ACGTC GGC AGG | | | |
| | | | CTT CC_ AC_ | | | |
| GAM127 | FASN | 3' | GGACACCAGAGCTGCCGACTTG 1088 | A _ | T | A |
| | GA | | TCCAA TTG CAGTT CTGGT TCC | | | |
| | | | | | | |
| | | | AGGTT AGC GTCGA GACCA AGG | | | |
| | | | C C _ C | | | |
| GAM127 | INHBB | 3' | GTCAGAAACTGCCATTTG 905 | T | | |
| | | | CAAAT GCAGTTTCTGGT | | | |
| | | | | | | |
| | | | GTTTA CGTCAAAGACTG | | | |
| | | | C | | | |
| GAM127 | NEDD4 | 3' | GATGGAAAACCTGAAATTTGGA 2875 | G | CTGG | |
| | | | TCCAAATT CAGTTT TATC | | | |
| | | | | | | |
| | | | AGGTTTAA GTCAAA GTAG | | | |
| | | | A AG__ | | | |
| GAM127 | NFYA | 3' | ACCAAAACTGCAATCAGGA 1955 | AA | C | |
| | | | TCC ATTGCAGTTT TGGT | | | |
| | | | | | | |
| | | | AGG TAACGTCAAA ACCA | | | |
| | | | AC _ | | | |
| GAM127 | NFYA | 3' | ACCAAAACTGCAATCAGGA 933 | AA | C | |
| | | | TCC ATTGCAGTTT TGGT | | | |
| | | | | | | |
| | | | AGG TAACGTCAAA ACCA | | | |
| | | | AC _ | | | |
| GAM127 | RAD17 | 5' | ACCTGCAACTGTAATTTG 967 | | TCT | |
| | | | CAAATTGCAGTT GGT | | | |
| | | | | | | |
| | | | GTTTAATGTCAA CCA | | | |
| | | | CGT | | | |
| GAM127 | RAD17 | 5' | ACCTGCAACTGTAATTTG 2410 | | TCT | |
| | | | CAAATTGCAGTT GGT | | | |
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|--------|---------------|----|-----------------------------|-----|-------|
| | | | GTTTAATGTCAA CCA | | |
| | | | CGT | | |
| GAM127 | RAD17 | 5' | ACCTGCAACTGTAATTTG 2411 | TCT | |
| | | | CAAATTGCAGTT GGT | | |
| | | | | | |
| | | | GTTTAATGTCAA CCA | | |
| | | | CGT | | |
| GAM127 | RAD17 | 5' | ACCTGCAACTGTAATTTG 2412 | TCT | |
| | | | CAAATTGCAGTT GGT | | |
| | | | | | |
| | | | GTTTAATGTCAA CCA | | |
| | | | CGT | | |
| GAM127 | RAD17 | 5' | ACCTGCAACTGTAATTTG 2413 | TCT | |
| | | | CAAATTGCAGTT GGT | | |
| | | | | | |
| | | | GTTTAATGTCAA CCA | | |
| | | | CGT | | |
| GAM127 | RAD17 | 5' | ACCTGCAACTGTAATTTG 2414 | TCT | |
| | | | CAAATTGCAGTT GGT | | |
| | | | | | |
| | | | GTTTAATGTCAA CCA | | |
| | | | CGT | | |
| GAM127 | ZNF146 | 3' | GGACACCAGAAAATTTGTA 1358 | — | A |
| | | | TGCAG TTTCTGGT TCC | | |
| | | | | | |
| | | | ATGTT AAAGACCA AGG | | |
| | | | TA C | | |
| GAM127 | CHST3 | 3' | GGACACCAGAAGACGATTCAGA 1096 | CA | CAG A |
| | | | TC AATTG TTTCTGGT TCC | | |
| | | | | | |
| | | | AG TTAGC GAAGACCA AGG | | |
| | | | AC A_ C | | |
| GAM127 | DKFZp762E1511 | 3' | ATGCTACTGAATTTGGA 2531 | G | TTCT |
| | | | TCCAAATT CAGT GGTAT | | |
| | | | | | |
| | | | AGGTTTAA GTCA TCGTA | | |
| | | | — ——— | | |
| GAM127 | EIF5 | 5' | GATACCAAAAAGTTGCAAT 878 | — | C |
| | | | ATTGCAG TTT TGGTATC | | |
| | | | | | |
| | | | TAACGTT AAA ACCATAG | | |
| | | | G A | | |
| GAM127 | LATS1 | 3' | GGATACCACAGCCAATT 2563 | CA | TC |
| | | | AATTG GTT TGGTATCC | | |
| | | | | | |
| | | | TTAAC CGA ACCATAGG | | |
| | | | — C_ | | |
| GAM127 | MGC27277 | 3' | CCAAAATTGCAATTCAGA 2505 | CA | C |
| | | | TC AATTGCAGTTT TGG | | |
| | | | | | |

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|--------|-----------|----|-----------------------------|--------|--------|
| | | | AG TTAACGTTAAA ACC | | |
| | | | AC _ | | |
| GAM127 | POLD3 | 3' | ACTAAACTGAATTTG 3538 | G | C |
| | | | CAAATT CAGTTT TGGT | | |
| | | | | | |
| | | | GTTTAA GTCAAA ATCA | | |
| | | | _ _ | | |
| GAM127 | TSLRP | 5' | GATACATCACTGAAATTTGGA 1435 | G | TTCTG |
| | | | TCCAAATT CAGT GTATC | | |
| | | | | | |
| | | | AGGTTTAA GTCA CATAG | | |
| | | | A CTA__ | | |
| GAM127 | LOC147463 | 3' | ATACCAGTGGCAAATTTGGA 3108 | _ | AGTTT |
| | | | TCCAAATT GC CTGGTAT | | |
| | | | | | |
| | | | AGGTTTAA CG GACCATA | | |
| | | | A GT__ | | |
| GAM127 | LOC161734 | 3' | GGATACCGTTTTCAACTTGGA 3400 | A | C TTTC |
| | | | TCCAA TTG AG TGGTATCC | | |
| | | | | | |
| | | | AGGTT AAC TT GCCATAGG | | |
| | | | C _ TT__ | | |
| GAM127 | LOC164173 | 3' | GATATTGAACTGCATCTGGA 3235 | AAT | CT |
| | | | TCCA TGCAGTTT GGTATC | | |
| | | | | | |
| | | | AGGT ACGTCAAG TTATAG | | |
| | | | CT_ _ | | |
| GAM127 | LOC199675 | 3' | GCCAAAGCCACA ACTTGGA 3429 | A | CA C |
| | | | TCCAA TTG GTTT TGGT | | |
| | | | | | |
| | | | AGGTT AAC CGAA ACCG | | |
| | | | C AC _ | | |
| GAM127 | LOC200150 | 5' | GCCAACTGCAGTTTG 3439 | TTC | |
| | | | CAAATTGCAGT TGGT | | |
| | | | | | |
| | | | GTTTGACGTCA ACCG | | |
| | | | _ | | |
| GAM127 | LOC51185 | 3' | ATACCAGAAACATCTACTTGGG 1679 | ATTGCA | |
| | | | TCCAA GTTTCTGGTAT | | |
| | | | | | |
| | | | GGGTT CAAAGACCATA | | |
| | | | CATCTA | | |
| GAM127 | LOC90459 | 3' | GCTGAAACTGCAATTGGA 2643 | A | T |
| | | | TCCAA TTGCAGTTTC GGT | | |
| | | | | | |
| | | | AGGTT AACGTCAAAG TCG | | |
| | | | _ _ | | |
| GAM127 | LOC91694 | 5' | ATACCAGAGGTCACTTCAG 2769 | C | _ |
| | | | TTG AGT TTCTGGTAT | | |
| | | | | | |

GAC TCA GAGACCATA
 T CTG
 GAM128 SCNN1G 3' ACCTGAACTATTAGCACGTC 793 ____ CA
 GA TGCTAATA TCAGGT
 || ||||| |||||
 CT ACGATTAT AGTCCA
 GC CA
 GAM128 YY1 3' ACCTGATGTGTACATC 1016 CTA
 GATG ATACATCAGGT
 ||| |||||
 CTAC TGTGTAGTCCA
 A____
 GAM128 FLJ21940 3' CCTGATGTGTACCTTA 2014 A TAAT
 TAAG TGC ACATCAGG
 ||| ||| |||||
 ATTC ATG TGTAGTCC
 C ____
 GAM128 PRO0159 5' ACCTGATGTATTGCTCT 1474 T T
 AGA GC AATACATCAGGT
 ||| || |||||
 TCT CG TTATGTAGTCCA
 - -
 GAM128 LOC200282 3' CCTGATGTAGGTCTTATT 3448 GCTAA
 AATAAGAT TACATCAGG
 ||||| |||||
 TTATTCTG ATGTAGTCC
 G____
 GAM129 PCDH9 5' ACATAGGGGATAGTAGCCAAC 3262 G C
 GTTGGCTACTATCTT TA GT
 ||||| ||||| || ||
 CAACCGATGATAGGG AT CA
 G A
 GAM129 ERO1L 3' GTACAATAACAACCTCA 1508 GC CTATC
 TGAGTTG TA TTGTAC
 ||||| || |||||
 ACTCAAC AT AACATG
 A____
 GAM129 LOC253287 5' AAGATAATGCCAACTCA 3740 TAC
 TGAGTTGGC TATCTT
 ||||| |||||
 ACTCAACCG ATAGAA
 TA____
 GAM129 LOC254268 5' ACAACTGACAGCAGCCAGCTCA 3674 A A ____
 TGAGTTGGCT CT TC TTGT
 ||||| || || |||||
 ACTCGACCGA GA AG AACA
 C C TC
 GAM130 AP1B1 3' AGCCACAGAAGCTGTGCC 802 A
 GGCATGGTTTCTGTG CT
 ||||| ||||| ||

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|--------|--------|----|--------------------------|--------|----|
| | | | CCGTGTCGAAGACAC GA | | |
| | | | C | | |
| GAM130 | BBS2 | 5' | AGCCACAGAAGGCGCCG 2214 | AT G | A |
| | | | CGGC G TTTCTGTG CT | | |
| | | | | | |
| | | | GCCG C GAAGACAC GA | | |
| | | | __ G C | | |
| GAM130 | FRK | 5' | AGCCACAGAAAGCAAGCCG 890 | A G | A |
| | | | CGGC TG TTTCTGTG CT | | |
| | | | | | |
| | | | GCCG AC AAAGACAC GA | | |
| | | | A G C | | |
| GAM130 | HSPD1 | 3' | TAGTCACAGAAATTCC 2560 | CAT | |
| | | | GG GGTTTCTGTGACTA | | |
| | | | | | |
| | | | CC TTAAAGACACTGAT | | |
| | | | _____ | | |
| GAM130 | IL20RA | 3' | TAGGAACTAACTATGCC 1501 | CT GA | |
| | | | GGCATGGTTT GT CTA | | |
| | | | | | |
| | | | CCGTATCAAA CA GAT | | |
| | | | T_ AG | | |
| GAM130 | LAMC3 | 3' | TAGTCACACTCCCTGCCG 1269 | T TTTC | |
| | | | CGGCA GG TGTGACTA | | |
| | | | | | |
| | | | GCCGT CC ACACTGAT | | |
| | | | C TC__ | | |
| GAM130 | MEST | 3' | TAGTCAAGTCACCATGCTG 2872 | TT G | |
| | | | CGGCATGGT CT TGACTA | | |
| | | | | | |
| | | | GTCGTACCA GA ACTGAT | | |
| | | | CT _ | | |
| GAM130 | MKI67 | 3' | AGCCACAGGAGATGTC 927 | GG | A |
| | | | GGCAT TTTCTGTG CT | | |
| | | | | | |
| | | | CTGTA GAGGACAC GA | | |
| | | | __ C | | |
| GAM130 | MMP19 | 3' | AGCCACAGAAACCACGTT 2011 | A | A |
| | | | GGC TGGTTTCTGTG CT | | |
| | | | | | |
| | | | TTG ACCAAAGACAC GA | | |
| | | | C C | | |
| GAM130 | MMP19 | 3' | AGCCACAGAAACCACGTT 2012 | A | A |
| | | | GGC TGGTTTCTGTG CT | | |
| | | | | | |
| | | | TTG ACCAAAGACAC GA | | |
| | | | C C | | |
| GAM130 | MS4A8B | 3' | AGTCTAGGAAACCATGCTG 2200 | | GT |
| | | | CGGCATGGTTTCT GACT | | |
| | | | | | |

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|--------|---------|----|---------------------------|--------|---|
| | | | GTCGTACCAAAGG CTGA | | |
| | | | AT | | |
| GAM130 | PSMD9 | 3' | TAGCCACAGACATGCTG 957 | GTT | A |
| | | | CGGCATG TCTGTG CTA | | |
| | | | | | |
| | | | GTCGTAC AGACAC GAT | | |
| | | | ____ C | | |
| GAM130 | SH3GL2 | 3' | TAGTCACAGAACTGCTG 984 | TGGT | |
| | | | CGGCA TTCTGTGACTA | | |
| | | | | | |
| | | | GTCGT AAGACACTGAT | | |
| | | | C____ | | |
| GAM130 | SPTAN1 | 3' | AGTCACAATCATCATGTC 994 | TTC | |
| | | | GGCATGGT TGTGACT | | |
| | | | | | |
| | | | CTGTACTA ACACTGA | | |
| | | | CTA | | |
| GAM130 | SYNGR1 | 3' | AGTCACAGACTGTCCTGCC 1146 | T TT__ | |
| | | | GGCA GG TCTGTGACT | | |
| | | | | | |
| | | | CCGT CC AGACACTGA | | |
| | | | _ TGTC | | |
| GAM130 | TRIM9 | 3' | AGTCACAGAACTGGGGGTC 2353 | AT__ T | |
| | | | GGC GGTT CTGTGACT | | |
| | | | | | |
| | | | CTG TCAA GACACTGA | | |
| | | | GGGG _ | | |
| GAM130 | TRPM2 | 5' | AGTTGCGAAACCATGTCTG 1011 | T TG | |
| | | | CGGCATGGTTTC G ACT | | |
| | | | | | |
| | | | GCTGTACCAAAG C TGA | | |
| | | | _ GT | | |
| GAM130 | ATPAF1 | 3' | AGTCACAGAGATGAGCC 2582 | ATG | |
| | | | GGC GTTTCTGTGACT | | |
| | | | | | |
| | | | CCG TAGAGACACTGA | | |
| | | | AG_ | | |
| GAM130 | CENTG2 | 3' | TAGTCACGCGGCACGCGCCG 1587 | A _ TC | |
| | | | CGGC TG GTT TGTGACTA | | |
| | | | | | |
| | | | GCCG GC CGG GCACTGAT | | |
| | | | C A C_ | | |
| GAM130 | COL12A1 | 3' | AGCCACAGAAGATGTC 2381 | GG | A |
| | | | GGCAT TTTCTGTG CT | | |
| | | | | | |
| | | | CTGTA GAAGACAC GA | | |
| | | | ____ C | | |
| GAM130 | COL12A1 | 3' | AGCCACAGAAGATGTC 1103 | GG | A |
| | | | GGCAT TTTCTGTG CT | | |
| | | | | | |

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|--------|------------------|----------------------|------|--------|
| | | CTGTA GAAGACAC GA | | |
| | | — C | | |
| GAM130 | DKFZp547I224 3' | AGCCGCTGCAAAATCATGCC | 1902 | CT__ A |
| | | GGCATGGTTT GTG CT | | |
| | | | | |
| | | CCGTACTAAA CGC GA | | |
| | | ACGT C | | |
| GAM130 | DKFZp566H0824 3' | AGTGAGCTGAGACCATGCC | 1721 | T G_ |
| | | GGCATGGTTTC GT ACT | | |
| | | | | |
| | | CCGTACCAGAG CG TGA | | |
| | | T AG | | |
| GAM130 | FLJ11726 3' | AGTGAGCCGAGACCATGCC | 2119 | T G_ |
| | | GGCATGGTTTC GT ACT | | |
| | | | | |
| | | CCGTACCAGAG CG TGA | | |
| | | C AG | | |
| GAM130 | FLJ12668 3' | TAGTCACTTGCCACCATGCC | 2124 | TTCT_ |
| | | GGCATGGT GTGACTA | | |
| | | | | |
| | | CCGTACCA CACTGAT | | |
| | | CCGTT | | |
| GAM130 | FLJ13385 3' | TAGTCACAAAGATAATACC | 2098 | C G C |
| | | GG AT GTTT TGTGACTA | | |
| | | | | |
| | | CC TA TAGA ACACTGAT | | |
| | | A A A | | |
| GAM130 | FLJ14936 3' | TAGTCACAGACACAGGAGCC | 2243 | ATG_ T |
| | | GGC GT TCTGTGACTA | | |
| | | | | |
| | | CCG CA AGACACTGAT | | |
| | | AGGA C | | |
| GAM130 | FLJ14957 3' | AGTCACAGCTGGGCTTCC | 2291 | CAT _ |
| | | GG GGTTT CTGTGACT | | |
| | | | | |
| | | CC TCGGG GACACTGA | | |
| | | T__ TC | | |
| GAM130 | HSU79275 3' | TAGTCACAAGATTTACCAT | 2746 | T__ _ |
| | | ATGGT TCT GTGACTA | | |
| | | | | |
| | | TACCA AGA CACTGAT | | |
| | | TTT A | | |
| GAM130 | KALI 3' | AGTGAGCCAAAATCATGCC | 2346 | CT G_ |
| | | GGCATGGTTT GT ACT | | |
| | | | | |
| | | CCGTACTAAA CG TGA | | |
| | | AC AG | | |
| GAM130 | KIAA0121 3' | TAGTCACAGAGTGGCTG | 2957 | ATGGT |
| | | CGGC TTCTGTGACTA | | |
| | | | | |

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|--------|----------|----|--------------------------|----------|--|
| | | | GTCG GAGACACTGAT | | |
| | | | GT__ | | |
| GAM130 | KIAA0254 | 3' | AGTCACAGGGAAGTGCTG 1540 | GG TT | |
| | | | CGGCAT T CTGTGACT | | |
| | | | I | | |
| | | | GTCGTG A GACACTGA | | |
| | | | A_ GG | | |
| GAM130 | KIAA0820 | 3' | AGCACAAACCATGTC 2838 | TC A | |
| | | | GGCATGGTT TGTG CT | | |
| | | | | | |
| | | | CTGTACCAA ACAC GA | | |
| | | | — — | | |
| GAM130 | KIAA0863 | 3' | AGTCATGGAGACCAGCC 3669 | A | |
| | | | GGC TGGTTTCTGTGACT | | |
| | | | | | |
| | | | CCG ACCAGAGGTACTGA | | |
| | | | — | | |
| GAM130 | KIAA1023 | 3' | AGCCACAGGAGATGTC 1728 | GG A | |
| | | | GGCAT TTTCTGTG CT | | |
| | | | | | |
| | | | CTGTA GAGGACAC GA | | |
| | | | — C | | |
| GAM130 | KIAA1161 | 5' | AGTCACAGAACATCTCC 3213 | CAT _ | |
| | | | GG GGT TTCTGTGACT | | |
| | | | | | |
| | | | CC CTA AAGACACTGA | | |
| | | | T__ C | | |
| GAM130 | KIAA1254 | 3' | TCACAGAAAGTAAAGCCG 2876 | A_ G | |
| | | | CGGC TG TTTCTGTGA | | |
| | | | | | |
| | | | GCCG AT AAAGACACT | | |
| | | | AA G | | |
| GAM130 | KIAA1805 | 3' | TAGCTTGTGAAACCATTC 3148 | C T TG _ | |
| | | | GG ATGGTTTC G A CTA | | |
| | | | I | | |
| | | | CC TACCAAAG T T GAT | | |
| | | | T _ GT C | | |
| GAM130 | KIAA1866 | 3' | TCACAGGACCGTCATGCTG 2587 | T__ | |
| | | | CGGCATGG TTCTGTGA | | |
| | | | | | |
| | | | GTCGTA CT AGGACACT | | |
| | | | GCC | | |
| GAM130 | KIAA1958 | 3' | AGTGAGCCGAGACCATGCC 3218 | T G_ | |
| | | | GGCATGGTTTC GT ACT | | |
| | | | | | |
| | | | CCGTACCAGAG CG TGA | | |
| | | | C AG | | |
| GAM130 | LIMK2 | 5' | AGTCACAGACGGATTTGC 1709 | T _ | |
| | | | GCA GGTT TCTGTGACT | | |
| | | | | | |

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|--------|-----------|----|--------------------|------|--------|
| | | | CGT TTAG AGACACTGA | | |
| | | | — GC | | |
| GAM130 | MGC12921 | 5' | AGTCACAGCAGCTGCC | 2666 | TG T |
| | | | GGCA GTT CTGTGACT | | |
| | | | | | |
| | | | CCGT CGA GACACTGA | | |
| | | | — C | | |
| GAM130 | MGC5149 | 3' | TAGCCACAGAAATGTC | 2939 | GGT A |
| | | | GGCAT TTCTGTG CTA | | |
| | | | | | |
| | | | CTGTA AAGACAC GAT | | |
| | | | — C | | |
| GAM130 | MOST2 | 5' | AGCCACCTGGCCATGCTG | 1909 | TCT A |
| | | | CGGCATGGTT GTG CT | | |
| | | | | | |
| | | | GTCGTACCGG CAC GA | | |
| | | | TC_ C | | |
| GAM130 | MRPL9 | 3' | AGTAGACCGAAACCATCC | 2195 | C T G_ |
| | | | GG ATGGTTTC GT ACT | | |
| | | | | | |
| | | | CC TACCAAAG CA TGA | | |
| | | | — C GA | | |
| GAM130 | NCBP2 | 3' | AGTCACAGAAGGTTCC | 1397 | C GG |
| | | | GG AT TTTCTGTGACT | | |
| | | | | | |
| | | | CC TG GAAGACACTGA | | |
| | | | T _ | | |
| GAM130 | PCYT1B | 3' | TAGTCACAGGAGCTGC | 1160 | TG |
| | | | GCA GTTTCTGTGACTA | | |
| | | | | | |
| | | | CGT CGAGGACACTGAT | | |
| | | | — | | |
| GAM130 | PIP3-E | 3' | AGTCACAAACAATGTC | 2764 | G TC |
| | | | GGCAT GTT TGTGACT | | |
| | | | | | |
| | | | CTGTA CAA ACACTGA | | |
| | | | A _ | | |
| GAM130 | PPP1R15B | 5' | AGTCGGAACCATCGCCG | 2288 | _ CTG |
| | | | CGGC ATGGTTT TGACT | | |
| | | | | | |
| | | | GCCG TACCAA GCTGA | | |
| | | | C AG_ | | |
| GAM130 | TFIP11 | 3' | TAGTCACAGTAATCCCC | 1410 | CAT T |
| | | | GG GGTT CTGTGACTA | | |
| | | | | | |
| | | | CC CTAA GACACTGAT | | |
| | | | C_ T | | |
| GAM130 | LOC132617 | 3' | AGTTTGAAATCATGCC | 3039 | TGT |
| | | | GGCATGGTTTC GACT | | |
| | | | | | |

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|--------|--------------|--------------------------|---------|---|
| | | CCGTACTAAAG TTGA | | |
| | | T__ | | |
| GAM130 | LOC147660 3' | AGTCACAGATCACGCC 3111 | A TT | |
| | | GGC TGG TCTGTGACT | | |
| | | | | |
| | | CCG ACT AGACACTGA | | |
| | | C _ | | |
| GAM130 | LOC149302 5' | AGTCACAGCAGCCGCC 3129 | AT T | |
| | | GGC GGTT CTGTGACT | | |
| | | | | |
| | | CCG CCGA GACACTGA | | |
| | | _ C | | |
| GAM130 | LOC151720 5' | AGTCACAAAAACCATGCTG 3160 | | C |
| | | CGGCATGGTTT TGTGACT | | |
| | | | | |
| | | GTCGTACCAA ACACTGA | | |
| | | A | | |
| GAM130 | LOC152215 3' | TAGTCACAAAGGGCTTACG 3167 | GCAT C_ | |
| | | CG GGTTT TGTGACTA | | |
| | | | | |
| | | GC TCGGG ACACTGAT | | |
| | | AT__ AA | | |
| GAM130 | LOC152426 3' | AGTCACAGGCAGGTGCC 3359 | G_ TT | |
| | | GGCAT GT CTGTGACT | | |
| | | | | |
| | | CCGTG CG GACACTGA | | |
| | | GA _ | | |
| GAM130 | LOC155179 3' | AGCCACAGGAGATGTC 3199 | GG A | |
| | | GGCAT TTTCTGTG CT | | |
| | | | | |
| | | CTGTA GAGGACAC GA | | |
| | | _ C | | |
| GAM130 | LOC157562 5' | TAGTCACATGGCCACACC 3381 | CA TC | |
| | | GG TGGTT TGTGACTA | | |
| | | | | |
| | | CC ACCGG ACACTGAT | | |
| | | AC T_ | | |
| GAM130 | LOC163115 3' | AGTCACAGATCCGATGTC 3244 | _ TT | |
| | | GGCAT GG TCTGTGACT | | |
| | | | | |
| | | CTGTA CC AGACACTGA | | |
| | | G T_ | | |
| GAM130 | LOC169026 3' | TAGTCACAAAATTTTACC 3260 | CAT C | |
| | | GG GGTTT TGTGACTA | | |
| | | | | |
| | | CC TTAAA ACACTGAT | | |
| | | ATT _ | | |
| GAM130 | LOC170106 5' | AGCCACAGGAAGTGTCC 3255 | C G A | |
| | | GG ATG TTTCTGTG CT | | |
| | | | | |

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|--------|--------------|--------------------------|-----|------|
| | | CC TGT AAGGACAC GA | | |
| | | _ G C | | |
| GAM130 | LOC170425 5' | TAGTCACAACCCAATGC 3048 | __ | TTC |
| | | GCAT GGT TGTGACTA | | |
| | | | | |
| | | CGTA CCA ACACTGAT | | |
| | | AC ____ | | |
| GAM130 | LOC197342 3' | AGTCACAGAAGGACTCGCC 3423 | AT | __ |
| | | GGC GGTT TCTGTGACT | | |
| | | | | |
| | | CCG TCAG AGACACTGA | | |
| | | C_ GA | | |
| GAM130 | LOC200488 5' | AGTCATGATCATGCCG 3477 | | TCT |
| | | CGGCATGGTT GTGACT | | |
| | | | | |
| | | GCCGTACTAG TACTGA | | |
| | | _____ | | |
| GAM130 | LOC219667 3' | TAGTCACAAATCAGAACTG 3517 | CA_ | TC |
| | | CGG TGGTT TGTGACTA | | |
| | | | | |
| | | GTC ACTAA ACACTGAT | | |
| | | AAG ____ | | |
| GAM130 | LOC220980 5' | AGCCACGTGAGCCATGCC 3592 | | C A |
| | | GGCATGGTTT TGTG CT | | |
| | | | | |
| | | CCGTACCGAG GCAC GA | | |
| | | T C | | |
| GAM130 | LOC253461 3' | AGCCACAGAAAATATACC 3700 | C G | A |
| | | GG ATG TTTCTGTG CT | | |
| | | | | |
| | | CC TAT AAAGACAC GA | | |
| | | A A C | | |
| GAM130 | LOC253502 3' | AGCCACAGAGGCCTGCC 3660 | T | A |
| | | GGCA GGTTTCTGTG CT | | |
| | | | | |
| | | CCGT CCGGAGACAC GA | | |
| | | _ C | | |
| GAM130 | LOC254211 5' | AGTCACAGAGAGGTGCC 3707 | | GG |
| | | GGCAT TTTCTGTGACT | | |
| | | | | |
| | | CCGTG AGAGACACTGA | | |
| | | G_ | | |
| GAM130 | LOC90785 3' | AGTGAGCCGAGACCATACC 2677 | C | T G_ |
| | | GG ATGGTTTC GT ACT | | |
| | | | | |
| | | CC TACCAGAG CG TGA | | |
| | | A C AG | | |
| GAM130 | LOC91050 3' | AGTCACAGAAATCATTCT 2701 | | C |
| | | GG ATGGTTTCTGTGACT | | |
| | | | | |

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|--------|-----------|----|---------------------------------|---------|--|
| | | | TC TACTAAAGACACTGA | | |
| | | | T | | |
| GAM130 | LOC91380 | 3' | AGTGAGCCGAGACCATGCC 2733 | T G_ | |
| | | | GGCATGGTTTC GT ACT | | |
| | | | | | |
| | | | CCGTACCAGAG CG TGA | | |
| | | | C AG | | |
| GAM131 | EIF2C1 | 3' | TTATTCCTCTCTGTCCACA 1414 A | T TACA | |
| | | | TG TGGACAGA GA AATAA | | |
| | | | | | |
| | | | AC ACCTGTCT CT TTATT | | |
| | | | _ _ CC_ | | |
| GAM131 | PCDHA9 | 3' | TATCTATATCTGTCTATCA 1461 | ___ | |
| | | | TGATGGACAGAT GATA | | |
| | | | | | |
| | | | ACTATCTGTCTA CTAT | | |
| | | | TAT | | |
| GAM131 | KIAA0923 | 3' | TATTTGTGTTGTCCATT 1463 | GATG | |
| | | | GATGGACA ATACAAATA | | |
| | | | | | |
| | | | TTACCTGT TGTGTTTAT | | |
| | | | ___ | | |
| GAM131 | UBF-fl | 3' | ATTTGTATATCTATCTACCA 2287 A C A | | |
| | | | TG TGGA AGATG TACAAAT | | |
| | | | | | |
| | | | AC ATCT TCTAT ATGTTTA | | |
| | | | C A _ | | |
| GAM131 | LOC119548 | 3' | CTTATCTGTTATGTGTTCATCA 2983 | G CAA | |
| | | | TGATGGACA ATGATA ATAAG | | |
| | | | | | |
| | | | ACTACTTGT TATTGT TATTC | | |
| | | | G C_ | | |
| GAM131 | LOC120400 | 5' | CTTATCCATCTCTGTCCATTA 3027 | T ACAA | |
| | | | TGATGGACAGA GAT ATAAG | | |
| | | | | | |
| | | | ATTACCTGTCT CTA TATTC | | |
| | | | _ CC_ | | |
| GAM132 | NARS | 3' | AAAGTTCGGGGAAAATACC 1125 | TA CAA | |
| | | | GGTATTTTT TGG ACTTT | | |
| | | | | | |
| | | | CCATAAAAG GCT TGAAA | | |
| | | | GG _ | | |
| GAM132 | BFAR | 3' | TGCACATAAAAAAATACCG 2581 | _ | |
| | | | CGGTATTTTTTATG GCA | | |
| | | | | | |
| | | | GCCATAAAAAATAC CGT | | |
| | | | A | | |
| GAM132 | HSNOV1 | 3' | AAAGTTCAAAAGTAGAAATACC 1720 | TATGGCA | |
| | | | GGTATTTTT AACTTT | | |
| | | | | | |

CCATAAAGA TTGAAA
 TGAAAAC
 GAM132 KIAA0628 3' AGGCTGCCATAACAAAATACC 1547 _ AA
 GGTATTTT TTATGGCA CT
 ||||| ||||| ||
 CCATAAAA AATACCGT GA
 C CG
 GAM132 KIAA1393 3' TAAAGTTTGATTGGAACATACC 2936 T TGG
 GGTAT TTTTA CAACTTTA
 ||||| ||||| |||||
 CCATA AAGGT GTTTGAAAT
 C TA_
 GAM132 LOC147054 5' TAAAGTTTACATGCTACAAAAA 3289 A ____
 ATAC GTATTTTTT TGGCA AACTTTA
 ||||| ||||| |||||
 CATAAAAAA ATCGT TTGAAAT
 C ACAT
 GAM133 TRIM 3' CAAATGTAAGGCCATGA 1684 AA GAC
 TCAT GCTT TACATTTG
 ||| ||| |||||
 AGTA CGGA ATGTAAAC
 C_ ____
 GAM133 MGC11296 3' CCAAATGTAAGTGCCATGA 2248 AA_ TGAC
 TCAT GCT TACATTTGG
 ||| ||| |||||
 AGTA TGA ATGTAAACC
 CCG ____
 GAM133 PRO2037 5' CAAATGCTGTTTATGATA 1853 TTGACTA
 TATCATAAGC CATTTG
 ||||| |||||
 ATAGTATTTG GTAAAC
 TC_____
 GAM134 PMX1 3' TCTATAGTGATGAAACATT 1996 A ACCGT
 AATG TTTCATCA TAGA
 ||| ||||| |||
 TTAC AAAGTAGT ATCT
 _ GAT_
 GAM134 FLJ22557 3' TCTGGCATGATAAAATCATGGA 2083 A C ACC
 TC ATGATTT ATCA GTTAGA
 || ||||| ||| |||||
 AG TACTAAA TAGT CGGTCT
 G A A_
 GAM134 KIAA0618 5' TCTAGTGGATGAGAATCA 1563 CA A
 TGATTT TCA CCGTTAGA
 ||||| ||| |||||
 ACTAAG AGT GGTGATCT
 _ A
 GAM134 LOC154215 3' AACGGTTGCCGCGCCATTG 3188 ATT AT
 CAATG TC CAACCGTT
 ||||| || |||||

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|--------|-----------|--------------------------------|-----------|
| | | GTTAC GG GTTGGCAA | |
| | | C__ CC | |
| GAM135 | GARP | 3' ATCAACAAATCTTCACTGAGC 1220 | C TTA_ |
| | | GCTC GT ATTTGTTGAT | |
| | | | |
| | | CGAG CA TAAACAATA | |
| | | T CTTC | |
| GAM135 | TEM8 | 3' AGGGAATTAAAGAAAGCCATG 1790 | CCG G |
| | | CATGGCT TTTAATTT TT | |
| | | | |
| | | GTACCGA AAATTAAG GA | |
| | | AAG G | |
| GAM135 | TRHR | 3' ATCAACAAAAGGGAGAACATG 1009 | G_ G AATT |
| | | CATG CTCC TTT TGTGAT | |
| | | | |
| | | GTAC GAGG AAA ACAACTA | |
| | | AA G ____ | |
| GAM135 | LGI2 | 3' ATCAACAAACAAATCAAAGCCA 1792 | CC_ AA |
| | | TGGCT GTTT TTTGTTGAT | |
| | | | |
| | | ACCGA TAAA AAACAATA | |
| | | AAC C_ | |
| GAM135 | MGC4638 | 3' TCAACAAATGTGAGTCAT 2212 | CGTTTA |
| | | ATGGCTC ATTTGTTGA | |
| | | | |
| | | TACTGAG TAAACAATA | |
| | | TG____ | |
| GAM135 | LOC139065 | 5' CAACAAACAAGAGCTATG 3035 | CGTTTAA |
| | | CATGGCTC TTTGTTG | |
| | | | |
| | | GTATCGAG AAACAAC | |
| | | AAC____ | |
| GAM135 | LOC154282 | 3' ATCAACAAAAAGGAGGACCA 3372 | C G AA |
| | | TGG TCC TTT TTTGTTGAT | |
| | | | |
| | | ACC AGG AGG AAACAATA | |
| | | _ _ AA | |
| GAM135 | LOC91516 | 5' CAACAAAAAGGAGCTAT 2745 | GTTTAA |
| | | ATGGCTCC TTTGTTG | |
| | | | |
| | | TATCGAGG AAACAAC | |
| | | AA____ | |
| GAM136 | C20orf28 | 3' CCACTCCGGAGATCCGGGT 1629 | G ATA_ |
| | | ACTCGGATCT CT TGG | |
| | | | |
| | | TGGGCCTAGA GG ACC | |
| | | _ CCTC | |
| GAM136 | MGC5139 | 5' CCAAAGAAGATCCGAGTT 2994 | G ATA |
| | | AACTCGGATCT CT TGG | |
| | | | |

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|--------|-----------|----|----------------------------|---------|--|
| | | | TTGAGCCTAGA GA ACC | | |
| | | | A A _ | | |
| GAM136 | PRO0899 | 3' | CCTGCAGCAGACCCGAGTTG 1847 | A A T | |
| | | | TAAGTCGG TCTGCT TA GG | | |
| | | | | | |
| | | | GTTGAGCC AGACGA GT CC | | |
| | | | C C _ | | |
| GAM136 | PRO1386 | 3' | CCACATAGCAAGGTCTGA 2187 | _ A | |
| | | | TCGGATCT GCTAT TGG | | |
| | | | | | |
| | | | AGTCTGGA CGATA ACC | | |
| | | | A C | | |
| GAM136 | PTPRT | 3' | CCATGTAAATCCGGGTTA 2399 | CTGC | |
| | | | TAAGTCGGAT TATATGG | | |
| | | | | | |
| | | | ATTGGGCCTA ATGTACC | | |
| | | | A _ | | |
| GAM136 | TCL6 | 3' | CCATTGCAGATTCGAGT 1919 | TAT | |
| | | | ACTCGGATCTGC ATGG | | |
| | | | | | |
| | | | TGAGCTTAGACG TACC | | |
| | | | T _ | | |
| GAM136 | TCL6 | 3' | CCATTGCAGATTCGAGT 1433 | TAT | |
| | | | ACTCGGATCTGC ATGG | | |
| | | | | | |
| | | | TGAGCTTAGACG TACC | | |
| | | | T _ | | |
| GAM136 | TEX27 | 3' | CCATATAGCAAGTTTAGT 1968 | C TC | |
| | | | ACT GGA TGCTATATGG | | |
| | | | | | |
| | | | TGA TTT ACGATATACC | | |
| | | | _ GA | | |
| GAM136 | LOC255759 | 5' | CCTGTCAGGATCCGAGT 3739 | GCT T | |
| | | | ACTCGGATCT ATA GG | | |
| | | | | | |
| | | | TGAGCCTAGG TGT CC | | |
| | | | AC _ _ | | |
| GAM137 | APXL | 3' | ACTTACTTATTTTATCTA 842 | CT C | |
| | | | TAGATAAA AT AGTAAGT | | |
| | | | | | |
| | | | ATCTATTT TA TCATTCA | | |
| | | | T _ T | | |
| GAM137 | CKN1 | 3' | ACTTCTGTATAGTTTATTTAGT 702 | _ T | |
| | CA | | TGACTAGATAAACTAT CAG AAGT | | |
| | | | | | |
| | | | ACTGATTTATTTGATA GTC TTCA | | |
| | | | T _ | | |
| GAM137 | HMGA2 | 3' | ACCTACTAATAGTTTGTGATC 1032 | CTA C A | |
| | | | GA GATAAACTAT AGTA GT | | |
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|--------|-----------|----|-----------------------------|------------|
| | | | CT TTGTTTGATA TCAT CA | |
| | | | AG_ A C | |
| GAM137 | ZNF36 | 3' | ACTTAAGGATCCTTCTAGTCA 3626 | TAAACT AG |
| | | | TGACTAGA ATC TAAGT | |
| | | | | |
| | | | ACTGATCT TAG ATTCA | |
| | | | TCC_ GA | |
| GAM137 | FLJ23191 | 3' | GTTGATAGCCCTCTAGTCA 2065 | TAAA |
| | | | TGACTAGA CTATCAGT | |
| | | | | |
| | | | ACTGATCT GATAGTTG | |
| | | | CCC_ | |
| GAM137 | KIAA0841 | 3' | ACTTACTGAAATTCCTCAGTCA 2918 | A_ TAAACTA |
| | | | TGACT GA TCAGTAAGT | |
| | | | | |
| | | | ACTGA CT AGTCATTCA | |
| | | | CC TAA_ | |
| GAM137 | KIAA1243 | 3' | ACCTATGGGCAGTTTATCTG 2977 | AT A A |
| | | | TAGATAAACT C GTA GT | |
| | | | | |
| | | | GTCTATTTGA G TAT CA | |
| | | | CG G C | |
| GAM137 | RNF20 | 3' | CTGTAGGACAGTTTATCAGTCA 1882 | A A AGTA |
| | | | TGACT GATAAACT TC AG | |
| | | | | |
| | | | ACTGA CTATTTGA AG TC | |
| | | | _ C GATG | |
| GAM137 | LOC118851 | 3' | ACTTTGGGAAATTCATCTGGTC 3025 | A CTA AGT |
| | A | | TGACTAGAT AA TC AAGT | |
| | | | | |
| | | | ACTGGTCTA TT AG TTCA | |
| | | | C AA_ GGT | |
| GAM137 | LOC150005 | 3' | ACTAGCTGCTTCTAGTCA 3322 | TAAACTAT A |
| | | | TGACTAGA CAGT AGT | |
| | | | | |
| | | | ACTGATCT GTCG TCA | |
| | | | TC_ A | |
| GAM137 | LOC221036 | 3' | ACTTACCGATAGTTTCAGT 3585 | A TA A |
| | | | ACT GA AACTATC GTAAGT | |
| | | | | |
| | | | TGA CT TTGATAG CATTCA | |
| | | | _ _ C | |
| GAM138 | COG7 | 3' | AAAAGAGTTGTAAATTAAAGAT 2795 | _ G |
| | G | | TATCTTTAA TA AACTCTTTT | |
| | | | | |
| | | | GTAGAAATT AT TTGAGAAAA | |
| | | | AA G | |
| GAM138 | DUSP5 | 3' | GAAAAGAGTTCTTCAGAT 1111 | TTAAT |
| | | | ATCT AGAACTCTTTTC | |
| | | | | |

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|--------|-----------|----|------------------------|--------------------|--------------|----------|---------|
| | | | | TAGA | TCTTGAGAAAAG | | |
| | | | | CT | _____ | | |
| GAM138 | C6orf29 | 3' | AAAAGATTTTATTAAGATA | 2278 | | C | |
| | | | TATCTTTAATAGAA | TCTTTT | | | |
| | | | | | | | |
| | | | ATAGAAATTATTTT | AGAAAA | | | |
| | | | | | | | |
| GAM138 | CGR19 | 3' | GAAAAGTACACTTTCTACTAAA | 1311 | | A | CT_____ |
| | | | GATG | TATCTTTA TAGAA | CTTTTC | | |
| | | | | | | | |
| | | | GTAGAAAT ATCTT | GAAAAG | | | |
| | | | C | TCACAT | | | |
| GAM138 | DSCR6 | 3' | GAAAAGAGTAACAGAAAGATAG | 1865 | | AATAGA | |
| | | | CTATCTTT | ACTCTTTTC | | | |
| | | | | | | | |
| | | | GATAGAAA | TGAGAAAAG | | | |
| | | | GACAA | _____ | | | |
| GAM138 | ETL | 3' | GAAATAGTTCTGTCAAAAATAG | 1982 | | C A | CT |
| | | | T | ACTAT TTT ATAGAACT | TTTC | | |
| | | | | | | | |
| | | | TGATA AAA TGTCTTGA | AAAG | | | |
| | | | A | C | T_ | | |
| GAM138 | FLJ21269 | 3' | GAGGCTTATTA AAAAATAGT | 2138 | | C | AA |
| | | | ACTAT TTTAATAG | CTC | | | |
| | | | | | | | |
| | | | TGATA AAATTATT | GAG | | | |
| | | | A | CG | | | |
| GAM138 | HNT | 3' | GAAAAGAGTTTTAAAAAAGA | 1692 | | AA | |
| | | | TCTTT | TAGAACTCTTTTC | | | |
| | | | | | | | |
| | | | AGAAA ATTTTGAGAAAAG | | | | |
| | | | AA | | | | |
| GAM138 | KCNB2 | 3' | AAAAGAGCTCTATTAGGA | 3690 | | T | A |
| | | | TCTT AATAGA | CTCTTTT | | | |
| | | | | | | | |
| | | | AGGA TTATCT | GAGAAAA | | | |
| | | | _____ | C | | | |
| GAM138 | KIAA0794 | 3' | GAAAAGAACAAGAAAGATAG | 3163 | | AATAGAAC | |
| | | | CTATCTTT | TCTTTTC | | | |
| | | | | | | | |
| | | | GATAGAAA | AGAAAAG | | | |
| | | | GAACA | _____ | | | |
| GAM138 | LOC123342 | 5' | GAAAAGAGTTCTAAACATGGT | 3031 | | C | TAA |
| | | | ACTAT TT | TAGAACTCTTTTC | | | |
| | | | | | | | |
| | | | TGGTA AA | ATCTTGAGAAAAG | | | |
| | | | C | _____ | | | |
| GAM138 | LOC144920 | 3' | AAAAGAGTTCTAAAGAAATAG | 3270 | | C | AA |
| | | | CTAT TTT | TAGAACTCTTTT | | | |
| | | | | | | | |

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|--------|-----------|----|------------------------------|-----|-------|
| | | | GATA AAG ATCTTGAGAAAA | | |
| | | | _ AA | | |
| GAM138 | LOC153688 | 3' | GAAAAGAGTTTCTGCAAGATA 3370 | TAA | _ |
| | | | TATCTT TAGAA CTCTTTTC | | |
| | | | | | |
| | | | ATAGAA GTCTT GAGAAAAG | | |
| | | | C_ T | | |
| GAM138 | LOC51336 | 5' | GAAAAGAATTCTGTTGAAATCA 1707 | ATC | C |
| | | | GT ACT TTTAATAGAA TCTTTTC | | |
| | | | | | |
| | | | TGA AAGTTGTCTT AGAAAAG | | |
| | | | CTA A | | |
| GAM139 | SCN1A | 3' | GAAAAACAAATTCTTAAATTTTC 3451 | TA_ | C |
| | | | A TGG TTAAGAATT GTTTTTC | | |
| | | | | | |
| | | | ACT AATTCTTAA CAAAAAG | | |
| | | | TTA A | | |
| GAM139 | FLJ13315 | 5' | GAAAAACGGAGGATTAACCA 2127 | A | GAA |
| | | | TGGT TTAA TTCGTTTTTC | | |
| | | | | | |
| | | | ACCA AATT AGGCAAAAAG | | |
| | | | A AGG | | |
| GAM139 | KIAA0940 | 3' | AAAATGGTATTATTAATACCAT 1584 | G | _ |
| | | | A TATGGTATTAA AAT TCGTTTT | | |
| | | | | | |
| | | | ATACCATAATT TTA GGTA AAA | | |
| | | | A T | | |
| GAM139 | SARM | 3' | GAAATATAATTCTTAATATCAT 1608 | C | T |
| | | | A TATGGTATTAAGAATT GT TTTC | | |
| | | | | | |
| | | | ATACTATAATTCTTAA TA AAAG | | |
| | | | _ T | | |
| GAM139 | LOC144231 | 5' | TGTAATTCTTAATACCAT 3266 | _ | |
| | | | ATGGTATTAAGAATT CG | | |
| | | | | | |
| | | | TACCATAATTCTTAA GT | | |
| | | | T | | |
| GAM139 | LOC148734 | 3' | GAAAATGGGGCCCTTAATAC 3124 | AA_ | |
| | | | GTATTAAG TTCGTTTTT | | |
| | | | | | |
| | | | CATAATTC GGGTAAAAG | | |
| | | | CCG | | |
| GAM140 | MBD1 | 3' | TTAAATATGCATCTGGCCCAGG 924 | C | TTTAA |
| | | | AA TTCCT GGCCA ATATTTAA | | |
| | | | | | |
| | | | AAGGA CCGGT TATAAATT | | |
| | | | C CTACG | | |
| GAM140 | MBD1 | 3' | TTAAATATGCATCTGGCCCAGG 1644 | C | TTTAA |
| | | | AA TTCCT GGCCA ATATTTAA | | |
| | | | | | |

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|--------|-----------|----|-----------------------------|---------|
| | | | AAGGA CCGGT TATAAATT | |
| | | | C CTACG | |
| GAM140 | MBD1 | 3' | TTAAATATGCATCTGGCCCAGG 1645 | C TTTTA |
| | AA | | TTCCT GGCCA ATATTTAA | |
| | | | | |
| | | | AAGGA CCGGT TATAAATT | |
| | | | C CTACG | |
| GAM140 | MBD1 | 3' | TTAAATATGCATCTGGCCCAGG 1646 | C TTTTA |
| | AA | | TTCCT GGCCA ATATTTAA | |
| | | | | |
| | | | AAGGA CCGGT TATAAATT | |
| | | | C CTACG | |
| GAM140 | LOC254734 | 3' | TTAAATATTCAGAACCGAGGA 3666 | CCA T |
| | | | TCCTCGG TTT AATATTTAA | |
| | | | | |
| | | | AGGAGCC AGA TTATAAATT | |
| | | | A__ C | |
| GAM140 | LOC51026 | 3' | AAGTATTAACCAAGGAA 1659 | C CCA |
| | | | TTCCT GG TTTTAATATTT | |
| | | | | |
| | | | AAGGA CC AAAATTATGAA | |
| | | | A ____ | |
| GAM141 | AICDA | 3' | TTGCAAGGAAATTGTGCTTTAT 1923 | C____ C |
| | C | | GATAAAGC TTCCT GCAA | |
| | | | | |
| | | | CTATTTCTG AAGGA CGTT | |
| | | | TGTTA A | |
| GAM141 | GCG | 3' | GGAATAAAGTTTTATCAAA 895 | C____ |
| | | | TTTGATAAAGC TTCC | |
| | | | | |
| | | | AAACTATTTTG AAGG | |
| | | | AAAT | |
| GAM141 | PTPN1 | 3' | TTGCATCAAGGGCTTTATCAAA 960 | CCTC |
| | | | TTTGATAAAGCCTT GCAA | |
| | | | | |
| | | | AAACTATTTCTGGGA CGTT | |
| | | | ACTA | |
| GAM141 | SCO2 | 5' | GCGAGGAGCATCAGA 1189 | AAA CT |
| | | | TTTGAT GC TCCTCGC | |
| | | | | |
| | | | AGACTA CG AGGAGCG | |
| | | | ____ _ | |
| GAM141 | UNG | 3' | TGTGAGCTTTATCAGA 2394 | CTTCC |
| | | | TTTGATAAAGC TCGCA | |
| | | | | |
| | | | AGACTATTTCTG AGTGT | |
| | | | ____ _ | |
| GAM141 | UNG | 3' | TGTGAGCTTTATCAGA 1013 | CTTCC |
| | | | TTTGATAAAGC TCGCA | |
| | | | | |

AGACTATTTTCG AGTGT

GAM141 BM046 3' TGCAAGAAAAAGGACTTATTAA 1831 AG C__ C
A TTTGATAA CCTT CT GCA
||||||| ||| || |||
AAATTATT GGAA GA CGT
CA AAA A

GAM141 DKFZP761G1913 3' TGCCAGGCTTTGCCAAA 2209 A TCCTC
TTTG TAAAGCCT GCA
||| ||||| |||
AAAC GTTTCGGA CGT
C C____

GAM141 KIAA0057 3' GTGAGGAAGACTTTACCAA 1422 A C
TTG TAAAG CTCCTCGC
||| ||||| |||||
AAC ATTTC GAAGGAGTG
C A

GAM141 RTCD1 3' TTGCTGAGAAGGCTTCATTAAA 1053 A C _
TTTGAT AAGCCTTC TC GCAA
||||| ||||| || |||
AAATTA TTCGGAAG AG CGTT
C _ T

GAM141 LOC127396 3' TGAGAAGGCCTTATTAAA 3005 A C
TTTGATAA GCCTTC TCG
||||||| ||||| |||
AAATTATT CGGAAG AGT
C _

GAM141 LOC130074 3' TGAGAGGCTTTATGAAA 3044 G TC
TTT ATAAAGCCT CTCG
||| ||||| |||
AAA TATTTTCGGA GAGT
G _

GAM141 LOC149134 5' TGCAGGAAAGTTTACCAAA 3308 ATA C C
TTTG AAGC TTCCT GCA
||| ||| ||||| |||
AAAC TTTG AAGGA CGT
CA_ A _

GAM141 LOC219818 3' TTGCAAGGAAGGCCTAATCA 3503 AAA C
TGAT GCCTTCCT GCAA
||| ||||| |||
ACTA CGGAAGGA CGTT
ATC A

GAM141 LOC256714 3' TGCTGGGCTTTAGCAAA 3702 A TCCTC
TTTG TAAAGCCT GCA
||| ||||| |||
AAAC ATTTTCGGG CGT
G T____

GAM141 LOC91149 5' TGCAAAGAAGGTTTCCAGA 2714 ATA CTC
TTTG AAGCCTTC GCA
||| ||||| |||

AGAC TTTGGAAG CGT
 C__ AAA
 GAM142 ACADSB 3' CCATCATTTGGAAAAATAAAGG 838 __ C TA
 C GCCTTTATT TCCA AT GATGG
 ||||| ||| || ||||
 CGGAAATAA AGGT TA CTACC
 AA T __
 GAM142 EDAR 3' CCATTTAAATGGGAATAAA 1985 CA
 TTTATTTCCA TTAGATGG
 ||||| |||||
 AAATAAGGGT AATTTACC
 A_
 GAM142 MAX 3' CCATTCCATGGAAATAAA 2515 CATTA
 TTTATTTCCA GATGG
 ||||| ||||
 AAATAAAGGT TTACC
 ACC__
 GAM142 MAX 3' CCATTCCATGGAAATAAA 923 CATTA
 TTTATTTCCA GATGG
 ||||| ||||
 AAATAAAGGT TTACC
 ACC__
 GAM142 MPO 3' AATGTTTATGATAATAAAGGC 722 _ C__
 GCCTTTATT TC ACATT
 ||||| || ||||
 CGGAAATAA AG TGTA
 T TATT
 GAM142 NEK4 3' TAATGTAGAGATAAAAGC 995 C C
 GC TTTATTTTC ACATTA
 || ||||| |||||
 CG AAATAGAG TGTAAT
 A A
 GAM142 C20orf170 3' CCAAATAATAATGAAAATAAA 2608 C C_ GA_
 GGC GCCTTTATTT CA ATTA TGG
 ||||| || ||| |||
 CGGAAATAAA GT TAAT ACC
 A AA AAA
 GAM142 FLJ20435 3' CCATCTGGAGGAAATAAA 1756 ACA
 TTTATTTCC TTAGATGG
 ||||| |||||
 AAATAAAGG GGTCTACC
 A_
 GAM142 FLJ23071 3' CCATCTAATGTTTTAAAAGGC 2143 ATTTCC
 GCCTTT ACATTAGATGG
 |||| |||||
 CGGAAA TGTAATCTACC
 ATTT__
 GAM142 KIAA0562 3' CCACTATAGCAAGAAATAAAGG 1525 CACAT_ A
 C GCCTTTATTT TAG TGG
 ||||| ||| |||

CGGAAATAAAG ATC ACC
AACGAT _

GAM142 LRRFIP1 3' CCACTTAATAAAAATAGAGGC 1151 CCAC A
GCCTTTATTT ATTAG TGG
||||||| |||||
CGGAGATAAA TAATT ACC
AA__ C

GAM142 P115 3' CCATCTAATGTGATTGCTAAG 1051 TATTTTC
CTT CACATTAGATGG
||| |||||
GAA GTGTAATCTACC
TCGTTA

GAM142 SDCCAG16 3' CATTTTAAAAATAAAGGC 1316 CCACATT
GCCTTTATTT AGATG
||||||| |||||
CGGAAATAAA TTTAC
AAT__

GAM142 TIAF1 3' GATGTATGGAAATAAAGGC 2370 _
GCCTTTATTTCC ACATT
||||||| |||||
CGGAAATAAAGG TGTAG
TA

GAM142 LOC149711 3' CCAAATAATAATGAAAATAAA 3314 C C_ GA_
GGC GCCTTTATTT CA ATTA TGG
||||||| || |||||
CGGAAATAAA GT TAAT ACC
A AA AAA

GAM142 LOC169933 5' CCAGTAGGTGAAGATAAAGGC 3251 C ATTAGA
GCCTTTATTT CAC TGG
||||||| ||| |||
CGGAAATAGA GTG ACC
A GATG__

GAM143 SNX9 3' ACAAATTGTAAAGAATATGT 1673 CCG
ACATAT TTACAATTTGT
||||| |||||
TGTATA AATGTAAACA
AGA

GAM143 TOX 5' AACAAACCACAAACGGATGTG 1533 ACAA_
CATATCCGTT TTTGTT
||||||| |||||
GTGTAGGCAA AAACAA
ACACC

GAM143 DKFZP434C212 3' AACAAATTGCATAGGAGTGT 2833 A GTTA
ACAT TCC CAATTTGTT
||| ||| |||||
TGTG AGG GTTAAACAA
_ ATAC

GAM143 LOC151438 5' AACAAACCAAAAACGGATATG 3345 ACAA_
CATATCCGTT TTTGTT
||||||| |||||

GTATAGGCAA AAACAA
 AAACC
 GAM143 LOC221663 3' AACAAATTGCATGGATTTGT 3619 T TA
 ACA ATCCGT CAATTTGTT
 ||| ||||| |||||
 TGT TAGGTA GTTAAACAA
 T C_
 GAM143 LOC257358 5' AACATGACTAACGGATATTC 3730 C CAATT
 A ATATCCGTTA TGTT
 | ||||| |||
 C TATAGGCAAT ACAA
 T CAGT_
 GAM143 LOC56832 3' AACAAATTGTGGATCATG 2703 _ GTT
 CAT ATCC ACAATTTGTT
 ||| ||| |||||
 GTA TAGG TGTTAAACAA
 C _
 GAM144 SOX9 3' ATGATCCTAAAAATAACCG 732 TG C_
 CG TGTTT AGGATCAT
 || ||||| |||||
 GC ATAAA TCCTAGTA
 CA AA
 GAM144 FLJ14356 3' ATGAATGCAAACACATG 2171 _ GGA
 CGTGTGTTT CA TCAT
 ||||| || |||
 GTACACAAA GT AGTA
 C A_
 GAM144 KIAA0982 3' ATGACCCTGAAATGACTG 1464 C G A
 CA GT TGTTCAGG TCAT
 || || ||||| |||
 GT CA GTAAAGTCC AGTA
 _ _ C
 GAM144 KIAA1028 3' ATGATCCTGAAGAAAAAGGTGA 3546 ACGTGTG
 TCACC TTTCAGGATCAT
 |||| | |||||
 AGTGG GAAGTCCTAGTA
 AAAAA_
 GAM144 PCQAP 3' CCTTAAACACACATGGGA 1649 A C C_
 TC CCA GTGTGTTT AGG
 || ||| ||||| |||
 AG GGT CACACAAA TCC
 _ A AT
 GAM144 PRKWINK2 3' GATCCTGAAATCAAGG 3488 ACG T
 CC TG GTTTCAGGATC
 || || |||||
 GG AC TAAAGTCCTAG
 A _ _
 GAM144 RCD-8 3' ATGACCCTGAGATCGTG 1491 TGT A
 CACG GTTTCAGG TCAT
 ||| ||||| |||

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|--------|-----------|----|-----------------------------|--------|--------|
| | | | GTGC TAGAGTCC AGTA | | |
| | | | _____ C | | |
| GAM144 | SMOC2 | 3' | ATGATCCTAAACTTTTTGG 2945 | CGTGT | C |
| | | | CCA GTTT AGGATCAT | | |
| | | | | | |
| | | | GGT CAAA TCCTAGTA | | |
| | | | TTTT_ _ | | |
| GAM144 | SYNJ2 | 3' | ATCCTGAGCCATGGTG 2605 | CG T T | |
| | | | CACCA TG GTT CAGGAT | | |
| | | | | | |
| | | | GTGGT AC CGA GTCCTA | | |
| | | | _____ - - - | | |
| GAM144 | TRABID | 3' | ATGACCCTAAAGTTAGTGTGGT 2823 | GTG | C A |
| | G | | CACCACGT TTT AGG TCAT | | |
| | | | | | |
| | | | GTGGTGTG GAA TCC AGTA | | |
| | | | ATT A C | | |
| GAM144 | TSGA14 | 3' | CTGTGGACACACAAGGTGA 1861 | AC | _ |
| | | | TCACC GTGTGTTT CAG | | |
| | | | | | |
| | | | AGTGG CACACAGG GTC | | |
| | | | AA T | | |
| GAM144 | LOC197201 | 3' | TCTGGAAAACAACACACGGTGA 3421 | AC | _____ |
| | | | TCACC GTGTGT TTCAGG | | |
| | | | | | |
| | | | AGTGG CACACA AGGTCT | | |
| | | | _____ ACAA | | |
| GAM144 | LOC219401 | 3' | ATGAAGCAAACACACGTAGG 3579 | _ | CAGGA |
| | | | CC ACGTGTGTTT TCAT | | |
| | | | | | |
| | | | GG TGCACACAAA AGTA | | |
| | | | A CGA_ | | |
| GAM145 | INHBA | 3' | ACTAGAACAACCCAAATAGCA 904 | C C | CCAG |
| | | | TGCTATTT GG TG AGT | | |
| | | | | | |
| | | | ACGATAAA CC AC TCA | | |
| | | | C A AAGA | | |
| GAM145 | TBXAS1 | 5' | ACACTCTGAGAAAGAGCA 2182 | A | GGCTGC |
| | | | TGCT TTTC CAGAGTGT | | |
| | | | | | |
| | | | ACGA AAAG GTCTCACA | | |
| | | | G A_ | | |
| GAM145 | TBXAS1 | 5' | ACACTCTGAGAAAGAGCA 798 | A | GGCTGC |
| | | | TGCT TTTC CAGAGTGT | | |
| | | | | | |
| | | | ACGA AAAG GTCTCACA | | |
| | | | G A_ | | |
| GAM145 | KIAA1056 | 5' | ACACTTCAGCCGCAGCCAAATA 1576 | C | CA_ |
| | GCA | | TGCTATTT GGCTGC GAGTGT | | |
| | | | | | |

ACGATAAA CCGACG TTCACA
 _ CCGAC
 GAM145 LOC197342 3' GACACCTGGCTGAGCCGGAACA 3424 A _ A
 GCA TGCT TTTCGGCT GCCAG GTGTC
 ||| ||||| ||| ||||
 ACGA AAGGCCGA CGGTC CACAG
 C GT _
 GAM145 LOC91752 5' GACACTCTAGATGAAA 2779 G GCC
 TTTCG CT AGAGTGTC
 |||| || |||||
 AAAGT GA TCTCACAG
 A _
 GAM146 FLJ11838 3' ATGAATAAACATATCTTG 2078
 TAAGATATGTTTATTCAT
 ||||| |||||
 GTTCTATACAAATAAGTA

 GAM147 ATP10C 3' AATACAGGAAACAAGAGGTAC 2062 T _
 GT CCTC GTTTCCTGTATT
 || ||| |||||
 CA GGAG CAAAGGACATAA
 T AA
 GAM147 CASP10 3' ACAGGGAACAAAGAAACA 2304 C C_
 TGTT CT GTTTCCTGT
 ||| || |||||
 ACAA GA CAAGGGACA
 A AA
 GAM147 ZNF36 3' GGAAACAGAAACATAGA 3627 C C
 TCTATGTT CT GTTTC
 ||||| || |||||
 AGATACAA GA CAAAGG
 A _
 GAM147 DORFIN 3' AATACAGGAAATAGATAAACAT 1630 CC _
 G TATGTT TC GTTTCCTGTATT
 |||| || |||||
 GTACAA AG TAAAGGACATAA
 AT A
 GAM147 FLJ21313 3' AATACAGGATGAAAAACACTGA 2037 TA CC TT
 TC TGTT TCG TCCTGTATT
 || ||| || |||||
 AG ACAA AGT AGGACATAA
 TC AA _
 GAM147 KIAA1819 5' AATACAGGAGATAGAACCAGA 2865 AT CTC
 TCT GTTC GTTTCCTGTATT
 || ||| |||||
 AGA CAAG TAGAGGACATAA
 C_ A_
 GAM147 P37NB 3' ATGGGAAAAAAAACATAGA 1254 CCTCG
 TCTATGTT TTTCCTGT
 ||||| |||||

| | | | | |
|--------|-----------|----|-----------------------------|----------|
| | | | AGATACAA AAAGGGTA | |
| | | | AAA__ | |
| GAM147 | RAP140 | 5' | ATACAGATAGAAACATAGA 1613 | CC GTTTC |
| | | | TCTATGTT TC CTGTAT | |
| | | | | |
| | | | AGATACAA AG GACATA | |
| | | | __ ATA__ | |
| GAM147 | LOC127002 | 3' | AATATAAAAACAGAAACATAGA 3002 | C C CC |
| | | | TCTATGTT CT GTTT TGTATT | |
| | | | | |
| | | | AGATACAA GA CAAA ATATAA | |
| | | | A _ A_ | |
| GAM147 | LOC132332 | 3' | AATACAGTTGCAGAGGAGCATA 3046 | _ TTC |
| | | | TATGTTCCCTC GT CTGTATT | |
| | | | | |
| | | | ATACGAGGAG CG GACATAA | |
| | | | A TT_ | |
| GAM147 | LOC145624 | 5' | ACTAGAAGAGGAACATA 3276 | GT CT |
| | | | TATGTTCCCTC TTC GT | |
| | | | | |
| | | | ATACAAGGAG AAG CA | |
| | | | _ AT | |
| GAM148 | NR4A2 | 3' | AATAGTATTTTCAGACACTATG 1277 | A CA |
| | | | TATAGT TCTGAAAT TATT | |
| | | | | |
| | | | GTATCA AGACTTTA ATAA | |
| | | | C TG | |
| GAM148 | PRKCN | 3' | ATGATTATTCCAGATACTGTA 1252 | A__ |
| | | | TATAGTATCTG AATCAT | |
| | | | | |
| | | | ATGTCATAGAC TTAGTA | |
| | | | CTTA | |
| GAM148 | BIVM | 3' | ATGGTGGGTGATTTTCAGATAT 1739 | AT_ |
| | | | GTATCTGAAATCAT TCAT | |
| | | | | |
| | | | TATAGACTTTAGTG GGTA | |
| | | | GGT | |
| GAM148 | DCLRE1A | 3' | ATGAAGATTGTTTCAGATACT 2843 | ATCATA |
| | | | AGTATCTGAA TTCAT | |
| | | | | |
| | | | TCATAGACTT AAGTA | |
| | | | GTTAG_ | |
| GAM148 | EBF2 | 3' | ATGAAGCCTTTTCAGATAC 1995 | TCATA |
| | | | GTATCTGAAA TTCAT | |
| | | | | |
| | | | CATAGACTTT AAGTA | |
| | | | CCG__ | |
| GAM148 | FLJ10852 | 3' | GAATATTTTCAGATACTATA 1873 | TC |
| | | | TATAGTATCTGAAA ATATTC | |
| | | | | |

ATATCATAGACTTT TATAAG

GAM148 FLJ20220 3' ATGAATAACATTTTCAGATAC 1742 CA
GTATCTGAAAT TATTCAT
||||||||| |||||
CATAGACTTTA ATAAGTA
CA

GAM148 FLJ21952 3' ATGATATTCTAGATACTATA 1992 _ _
TATAGTATCT GAA ATCAT
||||||||| ||| |||||
ATATCATAGA CTT TAGTA
T A

GAM148 MGC10724 3' ATGAAGACCCAGATACTA 2274 AAA ATA
TAGTATCTG TC TTCAT
||||||||| || |||||
ATCATAGAC AG AAGTA
CC_ _

GAM148 MGC4238 3' ATGGAAGGACTTCAGATAC 2247 A ATA
GTATCTGAA TC TTCAT
||||||||| || |||||
CATAGACTT AG AGGTA
C GA_

GAM148 Rab11-FIP2 3' ATGACAGTATCTGCAGATACTA 1581 AAATCATAT
TA TATAGTATCTG TCAT
||||||||| |||||
ATATCATAGAC AGTA
GTCTATGAC

GAM148 LOC90768 3' ATGAAGGTGTGTCCCAGATATT 2674 AAAT_ A
A TAGTATCTG CAT TTCAT
||||||||| ||| |||||
ATTATAGAC GTG AAGTA
CCTGT G

GAM149 ANPEP 3' CTAAATCTGAGGAATCAAC 805 CT TA
GTTGAT CTCA GATTTAG
||||| ||||| |||||
CAACTA GAGT CTAAATC
AG _

GAM149 NP 3' TCTAAATCACCAGAGACCAAAC 724 GA_ CATA
GTT TCTCT GATTTAGA
||| ||||| |||||
CAA AGAGA CTAAATCT
ACC CCA_

GAM149 TFAP2C 3' CTAGATCAACAGATCAAC 1000 CTCATA
GTTGATCT GATTTAG
||||||| |||||
CAACTAGA CTAGATC
CAA_

GAM149 ZNF83 5' CTAAATGTGAGATCAAGGA 1813 G T AGAT
TC TTGATCTC CAT TTAG
|| ||||| ||| |||||

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|--------|-----------|----|-----------------------------|-----------|
| | | | AG AACTAGAG GTA AATC | |
| | | | G T _____ | |
| GAM149 | MGC26766 | 3' | TTTACATCATGAGAGATCAA 2509 | A T |
| | | | TTGATCTCTCAT GAT TAGA | |
| | | | | |
| | | | AACTAGAGAGTA CTA ATTT | |
| | | | _ C | |
| GAM149 | SCYB10 | 3' | TCTAAATGTTGAAAGATCAA 836 | C TAG |
| | | | TTGATCT TCA ATTTAGA | |
| | | | | |
| | | | AACTAGA AGT TAAATCT | |
| | | | A TG_ | |
| GAM150 | EBAF | 3' | TACAGCTGAGCAATGCA 2721 | CG AAATA |
| | | | TGCAT GT TAGCTGTA | |
| | | | | |
| | | | ACGTA CG GTCGACAT | |
| | | | A_ A_____ | |
| GAM150 | F7 | 3' | ATACGCAAACACACCGATGCA 706 | AAATATA T |
| | | | TGCATCGGT GC GTAT | |
| | | | | |
| | | | ACGTAGCCA CG CATA | |
| | | | CACAAA_ _ | |
| GAM150 | F7 | 3' | ATACGCAAACACACCGATGCA 1885 | AAATATA T |
| | | | TGCATCGGT GC GTAT | |
| | | | | |
| | | | ACGTAGCCA CG CATA | |
| | | | CACAAA_ _ | |
| GAM150 | MGC3771 | 3' | TAGAACATTTACCGATGC 2178 | ATAG |
| | | | GCATCGGTAAAT CTG | |
| | | | | |
| | | | CGTAGCCATTTA GAT | |
| | | | CAA_ | |
| GAM150 | LOC146438 | 3' | TAGAACATTTACCGATGC 3091 | ATAG |
| | | | GCATCGGTAAAT CTG | |
| | | | | |
| | | | CGTAGCCATTTA GAT | |
| | | | CAA_ | |
| GAM151 | BPGM | 3' | TAAGAAGAAATGCAAAAG 852 | CG |
| | | | CTT GCATTTCTTTTA | |
| | | | | |
| | | | GAA CGTAAAGAAGAAT | |
| | | | AA | |
| GAM151 | HAS2 | 3' | AAATGAAATGCCAAAGGAA 1198 | C T |
| | | | TTCCTT GGCATTTT TTT | |
| | | | | |
| | | | AAGGAA CCGTAAAG AAA | |
| | | | A T | |
| GAM151 | HDAC2 | 3' | CATTAAAAAGAAAATATTGAAA 3507 | _ CA_ |
| | GGAA | | TTCCTT CGG TTTCTTTTAAATG | |
| | | | | |

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|--------|-----------|----|-----------------------------|---------|
| | | | AAGGAA GTT AAAGAAAAATTAC | |
| | | | A ATA | |
| GAM151 | XRCC2 | 3' | CATTAAAAAGTGGGCAAAGGA 1208 | CG ATTT |
| | | | TCCTT GC CTTTTTAATG | |
| | | | | |
| | | | AGGAA CG GAAAAATTAC | |
| | | | A_ GGT_ | |
| GAM151 | APACD | 3' | CATTAAAAAGAAACCAGGAA 1249 | TC CA |
| | | | TTCCT GG TTTCTTTTAAATG | |
| | | | | |
| | | | AAGGA CC AAAGAAAAATTAC | |
| | | | — — | |
| GAM151 | SCIN | 3' | CATTAAAATAACCTGAAGGAA 2313 | CATTCT |
| | | | TTCCTTCGG TTTAATG | |
| | | | | |
| | | | AAGGAAGTC AAAATTAC | |
| | | | CAAT_ | |
| GAM151 | USP16 | 3' | CATTAAATACATGCCAGAAG 1303 | _ TTCTT |
| | | | CTTC GGCAT TTTAATG | |
| | | | | |
| | | | GAAG CCGTA AAATTAC | |
| | | | A CAT_ | |
| GAM151 | LOC115004 | 3' | AAAAGAAATCCGAAAGAA 2970 | C C |
| | | | TTC TTCGG ATTTCTTT | |
| | | | | |
| | | | AAG AAGCC TAAAGAAAA | |
| | | | A _ | |
| GAM151 | LOC146520 | 5' | GAAGAGAAATGCCATAGGAA 3096 | TC |
| | | | TTCCT GGCATTTCTTTT | |
| | | | | |
| | | | AAGGA CCGTAAAGAGAAG | |
| | | | TA | |
| GAM151 | LOC219333 | 3' | CATTAAAAAAAACATGCCG 3607 | _ C |
| | | | CGGCAT TT TTTTAAATG | |
| | | | | |
| | | | GCCGTA AA AAAAATTAC | |
| | | | CA A | |
| GAM152 | EIF1A | 3' | CTTTGTGTTTTTGGTTTACCCT 3442 | A_ TCT |
| | | | AG TAACTAAA CGCAAAG | |
| | | | | |
| | | | TC ATTTGGTTT GTGTTTC | |
| | | | CC TT_ | |
| GAM152 | ENAM | 3' | TTTGTTTTTAGTTATCTTA 2217 | A TCTC |
| | | | TAAGATAA CTAAA GCAAA | |
| | | | | |
| | | | ATTCTATT GATTT TGTTT | |
| | | | _ T_ | |
| GAM152 | MYCL1 | 3' | TTTGTTGGTAGCTTATCTTA 1204 | A AATC |
| | | | TAAGATAA CTA TCGCAA | |
| | | | | |

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|--------|-----------|----|-----------------------------|------------|---|
| | | | ATTCTATT GAT GGTGTTT | | |
| | | | C ____ | | |
| GAM152 | ZNF42 | 5' | CTTTGATGTATTCTAGTTTATC 1018 | AATCT | _ |
| | T | | AGATAAACTA CG CAAAG | | |
| | | | | | |
| | | | TCTATTTGAT GT GTTTC | | |
| | | | CTTAT A | | |
| GAM152 | FLJ23604 | 3' | AGAATATAGTTTATCTTA 2134 | AA_ | |
| | | | TAAGATAAACTA TCT | | |
| | | | | | |
| | | | ATTCTATTTGAT AGA | | |
| | | | ATA | | |
| GAM152 | HEY2 | 3' | AGATCTAGTTTATCTTA 1419 | _ A | |
| | | | TAAGATAAA CTA ATCT | | |
| | | | | | |
| | | | ATTCTATTT GAT TAGA | | |
| | | | T C | | |
| GAM152 | TSC22 | 3' | TGGGACCTAGGCTATCTTA 1265 | AA AA | |
| | | | TAAGATA CTA TCTCG | | |
| | | | | | |
| | | | ATTCTAT GAT AGGGT | | |
| | | | CG CC | | |
| GAM153 | FLJ20296 | 3' | ACATTAATAAATTTATTGATTC 1748 | A CAA | |
| | CA | | TG AATC GGATTTATTAATGT | | |
| | | | | | |
| | | | AC TTAG TTAAATAATTACA | | |
| | | | C TTA | | |
| GAM153 | RAB22A | 3' | ACATTAATAAATTCTAAGTTTC 2546 | CCA | |
| | A | | TGAAAT AGGATTTATTAATGT | | |
| | | | | | |
| | | | ACTTTG TCTTAAATAATTACA | | |
| | | | AA_ | | |
| GAM153 | UPLC1 | 3' | ACATTTGTTCTCTTGGATCTCA 1740 | A _ TTTATT | |
| | | | TGA ATCCAAG GA AATGT | | |
| | | | | | |
| | | | ACT TAGGTTCT CT TTACA | | |
| | | | C T TGT__ | | |
| GAM153 | LOC122886 | 3' | ACACTGTGTTCCCTTGGACCTC 3028 | AA TT TAA | |
| | | | GA TCCAAGGA TAT TGT | | |
| | | | | | |
| | | | CT AGGTTCCCT GTG ACA | | |
| | | | CC T_ TC_ | | |
| GAM153 | LOC222194 | 3' | ACATCATCTGTTCTTGGACCTC 3637 | AA TTATTA | |
| | A | | TGA TCCAAGGAT ATGT | | |
| | | | | | |
| | | | ACT AGGTTCTTG TACA | | |
| | | | CC TCTAC_ | | |
| GAM154 | ITGB1 | 3' | AGTAAATGTCCTGCTA 909 | GA | |
| | | | TAGCAGGACATT TGCT | | |
| | | | | | |

ATCGTCCTGTAA ATGA

GAM154 RHO 3' TCTAGAGCATGGAGCCTCTA 754 C ACA G
TAG AGG TT ATGCTCTAGA
||| ||| || |||||
ATC TCC AG TACGAGATCT
_ G_ G

GAM154 XPNPEP2 3' CTGGGTCCACATCCTGCTA 1015 CAT AT T
TAGCAGGA TG GC CTAG
||||| || |||||
ATCGTCCT AC TG GGTC
AC_ C_ _

GAM154 FLJ12700 3' CTAGAACAGGATGTCCTGC 2110 GA C
GCAGGACATT TG TCTAG
||||| || |||||
CGTCCTGTAG AC AGATC
G_ A

GAM154 FLJ13291 3' GTCCAGAGTTAACTGCCCTGCT 2234 A TTGAT A
G TAGCAGG CA GCTCT GAC
||||| || |||||
GTCGTCC GT TGAGA CTG
C CAAT_ C

GAM154 FLJ20811 5' CTAGAGCACAAAGTCCTGCTA 2782 A A
TAGCAGGAC TTG TGCTCTAG
||||| ||| |||||
ATCGTCCTG AAC ACGAGATC

GAM154 KIAA1643 3' TCCAGAGCCTCTGTCCTGC 2693 TT T A
GCAGGACA GA GCTCT GA
||||| || |||||
CGTCCTGT CT CGAGA CT
_ C C

GAM154 KIAA1755 3' TCCAGAGCATTTATCTGC 2596 ACATT A
GCAGG GATGCTCT GA
|||| ||||| ||
CGTCT TTACGAGA CT
AT_ C

GAM154 KIAA1762 3' GTCTAGAGCACACACCGCT 2669 A ACAT A
AGC GG TG TGCTCTAGAC
||| || || |||||
TCG CC AC ACGAGATCTG
_ AC_ C

GAM154 MGC13033 5' TCCAGAGCATTCCTTCTA 2199 C CATTG A
TAG AGGA ATGCTCT GA
||| ||| ||||| ||
ATC TCCT TACGAGA CT
T _ C

GAM154 SLC7A3 5' TCTTCTTCAATTCCTGCTA 2281 C TGCTCT
TAGCAGGA ATTGA AGA
||||| ||||| |||

ATCGTCCT TAACT TCT
 _ TCT__
 GAM154 LOC112609 3' GTCTAGAGTGATCCATCC 2960 CATT _
 GGA GAT GCTCTAGAC
 ||| ||| |||||
 CCT CTA TGAGATCTG
 AC_ G
 GAM154 LOC157349 5' GTCCAAAAGTTTAACTGTCCTG 3201 _ T CTA_
 C GCAGGACA TTGA GCT GAC
 ||||| ||| ||| |||
 CGTCCTGT AATT TGA CTG
 C _ AAAC
 GAM154 LOC90625 3' TCCAGATGATGCTCCTGCTA 2662 _ ATGC A
 TAGCAGGA CATTG TCT GA
 ||||| |||| ||| ||
 ATCGTCCT GTAGT AGA CT
 C _ C
 GAM155 MGAT4B 5' CCGCTACAAGGACAGTG 2360 ATAT TC
 CACT GTT TGTAGCGG
 ||| ||| |||||
 GTGA CAG ACATCGCC
 _ GA
 GAM155 PRKAR2A 3' GCCACAGAACACATACAG 1091 A _ A
 CT TATGT TTCTGT GC
 || |||| ||||| ||
 GA ATACA AAGACA CG
 C C C
 GAM155 SCD 3' GCCACGGAAACATACAGAGGA 1177 A A A
 TCC CT TATGTTTCTGT GC
 ||| || ||||| ||
 AGG GA ATACAAAGGCA CG
 A C C
 GAM155 DKFZp761H079 3' GCCACCTGAAACATAAAATGGA 2506 CTA T_ A
 TCCA TATGTTTC GT GC
 ||| ||||| ||| ||
 AGGT ATACAAAG CA CG
 AAA TC C
 GAM155 KIAA0417 3' GCCATGATGGAACAGATAGTG 2910 A AGC
 CACTAT TGTTTCTGT GGC
 ||||| ||||| ||| ||
 GTGATA ACAAAGGTA CCG
 G GTA
 GAM155 LRBA 3' CCAATTATGGAACATACAGTG 1327 A C_
 GA TCCACT TATGTTTCTGTAG GG
 ||||| ||||| ||| ||
 AGGTGA ATACAAAGGTATT CC
 C AA
 GAM155 SYAP1 3' GCCACAGAAACATAAGT 2279 A A
 ACT TATGTTTCTGT GC
 ||| ||||| ||| ||

TGA ATACAAAGACA CG
 _ C
 GAM155 LOC143188 5' ACAGAAACTATAGCAGA 3264 CA T
 TC CTATA GTTTCTGT
 || |||| |||||
 AG GATAT CAAAGACA
 AC _
 GAM155 LOC157292 3' GCCTCAGAAACATAAGTG 3378 A TA
 CACT TATGTTTCTG GC
 ||| ||||| ||
 GTGA ATACAAAGAC CG
 _ TC
 GAM156 C18orf1 3' AGTCATTATTGTTGCAGGA 2561 _ T TT
 TCC GCA AT TAATGACT
 ||| ||| || |||||
 AGG CGT TG ATTACTGA
 A _ TT
 GAM156 CRYZ 3' AAGAGTCATCATAGTAGGAA 866 GCA TTTA
 TTCC TAT ATGACTCTT
 ||| ||| |||||
 AAGG ATA TACTGAGAA
 ATG C__
 GAM156 TRPC5 3' GAAGTGTCAAAATATGAGAA 1434 CG TAA T
 TTC CATATTT TGAC CTTC
 ||| ||||| ||| |||
 AAG GTATAAA ACTG GAAG
 A_ _ T
 GAM156 DAP13 3' GAAGAACAGTTGAAACATGC 1862 A GAC
 GCAT TTTTAAT TCTTC
 ||| ||||| |||
 CGTA AAAGTTG AGAAG
 C ACA
 GAM156 DKFZP564O0463 3' GAAGAGCCATTACATGC 1481 ATTT A
 GCAT TAATG CTCTTC
 ||| ||||| |||||
 CGTA ATTAC GAGAAG
 C_ C
 GAM156 GRID1 3' AAGAACCATTAGGAGTGGA 2822 ATA AC
 TTCCGC TTTTAATG TCTT
 ||||| ||||| |||
 AAGGTG AGGATTAC AGAA
 _ CA
 GAM156 MGC30052 3' AAGACTTTTTTGAAATATGCA 2499 C AAT_ C
 GAA TTC GCATATTTT GA TCTT
 ||| ||||| || |||
 AAG CGTATAAAA TT AGAA
 A GTTTT C
 GAM156 MGC32104 5' AAGAGTCATGCTGTGATGAA 2494 CG TTTTA
 TTC CATA ATGACTCTT
 ||| ||| |||||

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|--------|-----------|----|-----------------------------|-------|---------|
| | | | AAG GTGT TACTGAGAA | | |
| | | | TA CG__ | | |
| GAM156 | SCN9A | 5' | GAAGAGGAATTAATAATACAG 975 | GC_ | GA |
| | GA | | TCC ATATTTTAAT CTCTTC | | |
| | | | | | |
| | | | AGG TATAAAATTA GAGAAG | | |
| | | | ACA AG | | |
| GAM156 | STK17A | 3' | AGTCCAATTAATAATATGGAA 1154 | GC | __ |
| | | | TTCC ATATTTTAAT GACT | | |
| | | | | | |
| | | | AAGG TATAAAATTA CTGA | | |
| | | | __ AC | | |
| GAM156 | LOC148738 | 3' | AAGAATCATTAAAGGAAGC 2519 | ATA | C |
| | | | GC TTTTAATGA TCTT | | |
| | | | | | |
| | | | CG GAAATTACT AGAA | | |
| | | | AAG A | | |
| GAM157 | BLMH | 3' | GGTGGCCTAAGAGTTGAGCTC 734 | A | CT |
| | | | GAGCTCAAC CTTA CCGCC | | |
| | | | | | |
| | | | CTCGAGTTG GAAT GGTGG | | |
| | | | A CC | | |
| GAM157 | BLVRB | 3' | GGCAATAAATGTTGAGCC 768 | A | C CTCC |
| | | | G GCTCAACA TTA GCC | | |
| | | | | | |
| | | | C CGAGTTGT AAT CGG | | |
| | | | _ A AA__ | | |
| GAM157 | DHCR7 | 3' | GGTAGCGTGCACGGTGTTGAAC 821 | C | TACTC C |
| | T | | AG TCAACACT CGC ACC | | |
| | | | | | |
| | | | TC AGTTGTGG GCG TGG | | |
| | | | A CACGT A | | |
| GAM157 | FGFR1 | 3' | GGTGACAGAGTGAGTGAGACTC 2032 | _ AAC | __ |
| | | | GAG CTC ACTTACTC CGCC | | |
| | | | | | |
| | | | CTC GAG TGAGTGAG GTGG | | |
| | | | A __ ACA | | |
| GAM157 | FGFR1 | 3' | GGTGACAGAGTGAGTGAGACTC 2034 | _ AAC | __ |
| | | | GAG CTC ACTTACTC CGCC | | |
| | | | | | |
| | | | CTC GAG TGAGTGAG GTGG | | |
| | | | A __ ACA | | |
| GAM157 | HEM1 | 3' | GGTGACTTGAGCTTGAGCTC 1200 | CA | CTC |
| | | | GAGCTCAA CTTA CGCC | | |
| | | | | | |
| | | | CTCGAGTT GAGT GTGG | | |
| | | | C_ TCA | | |
| GAM157 | NT5C3 | 5' | GGTGGCGGGGGTGGTGCTGGCT 1689 | T A | TA |
| | C | | GAGC CA CACT CTCCGCCACC | | |
| | | | | | |

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| | | | CTCG GT GTGG GGGGCGGTGG | | |
| | | | _ C TG | | |
| GAM157 | OTOR | 3' | GCGGGGAAATGTTGAGCTC 1894 | C A | |
| | | | GAGCTCAACA TT CTCCGC | | |
| | | | | | |
| | | | CTCGAGTTGT AA GGGGCG | | |
| | | | A _ | | |
| GAM157 | PRPSAP2 | 5' | GCAATCAGTAAACATTGAGCT 954 | CAC_ CC_ | |
| | C | | GAGCTCAA TTACT GC | | |
| | | | | | |
| | | | CTCGAGTT AATGA CG | | |
| | | | ACAA CTAA | | |
| GAM157 | C14orf4 | 5' | GGTGGCGGAGGCCCGCAGCTC 2788 | CAACACTTA | |
| | | | GAGCT CTCCGCCACC | | |
| | | | | | |
| | | | CTCGA GAGGCGGTGG | | |
| | | | CCCCCG_ | | |
| GAM157 | CG012 | 3' | GGCGACAGAGTGAGTGAGACTC 3272 | _ AAC _ | |
| | | | GAG CTC ACTTACTC CGCC | | |
| | | | | | |
| | | | CTC GAG TGAGTGAG GCGG | | |
| | | | A _ ACA | | |
| GAM157 | DKFZP434K2235 | 5' | GGTGGCGGGTAACGCCGGAAGCTC 3278 | C AACAC T | |
| | | | GAG TC TTAC CCGCCACC | | |
| | | | | | |
| | | | CTC AG AATG GGCGGTGG | | |
| | | | _ GCCGC _ | | |
| GAM157 | FLJ20699 | 3' | GGTGCAAGGATTGAGCTC 1766 | CA ACTC | |
| | | | GAGCTCAA CTT CGCC | | |
| | | | | | |
| | | | CTCGAGTT GAA GTGG | | |
| | | | AG C_ | | |
| GAM157 | FLJ23129 | 3' | GGCAACAGGAGAATGTCAAGCC 2088 | A CA C A _ | |
| | | | G GCT ACA TT CTCC GCC | | |
| | | | | | |
| | | | C CGA TGT AA GAGG CGG | | |
| | | | _ AC _ _ ACAA | | |
| GAM157 | HSPC065 | 3' | GTGACGGAGTAGAAGCTT 1482 | CAACAC C | |
| | | | GAGCT TTACTCCG CAC | | |
| | | | | | |
| | | | TTCGA GATGAGGC GTG | | |
| | | | A_ A | | |
| GAM157 | KIAA0960 | 3' | GGTAATTTAAGTGTGAAGT 3572 | _ CTCC | |
| | | | GCT CAACACTTA GCC | | |
| | | | | | |
| | | | TGA GTTGTGAAT TGG | | |
| | | | A TTAA | | |
| GAM157 | MGC12466 | 3' | GGTAAAGGAGTGTGAAGCTC 3127 | C A CC | |
| | | | GAG TCAACACTT CT GCC | | |
| | | | | | |

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|--------|-----------|----|-----------------------------|-------|------|
| | | | CTC AGTTGTGAG GA TGG | | |
| | | | A _ AA | | |
| GAM157 | MGC12904 | 3' | GCAGTGAGTGCTGAGCTC 2184 | A | CC |
| | | | GAGCTCA CACTTACT GC | | |
| | | | | | |
| | | | CTCGAGT GTGAGTGA CG | | |
| | | | C _ | | |
| GAM157 | MSTP028 | 3' | GGCAGTAAGTGTCCAGCTC 2224 | CA | CC |
| | | | GAGCT ACACTTACT GCC | | |
| | | | | | |
| | | | CTCGA TGTGAATGA CGG | | |
| | | | CC _ | | |
| GAM157 | RAB24 | 5' | TGACGGAGTAGCGAGCT 2397 | AACAC | C |
| | | | AGCTC TTACTCCG CA | | |
| | | | | | |
| | | | TCGAG GATGAGGC GT | | |
| | | | C_ A | | |
| GAM157 | LOC113828 | 5' | TGAGGAGACGTTGAGCTC 2439 | ACTTA | GC |
| | | | GAGCTCAAC CTCC CA | | |
| | | | | | |
| | | | CTCGAGTTG GAGG GT | | |
| | | | CA_ A_ | | |
| GAM157 | LOC152300 | 5' | GTGGACAGCATTGAGCTC 3169 | CA | TAC |
| | | | GAGCTCAA CT TCCGC | | |
| | | | | | |
| | | | CTCGAGTT GA AGGTG | | |
| | | | AC C_ | | |
| GAM157 | LOC197125 | 3' | GGCAGGTAACATTGAGCTC 3420 | CAC | CC |
| | | | GAGCTCAA TTACT GCC | | |
| | | | | | |
| | | | CTCGAGTT AATGG CGG | | |
| | | | AC_ A_ | | |
| GAM157 | LOC219848 | 3' | GGTGACAGAGTAGGTGCTC 3528 | TCAAC | _ |
| | | | GAGC ACTTACTC CGCC | | |
| | | | | | |
| | | | CTCG TGGATGAG GTGG | | |
| | | | _ ACA | | |
| GAM157 | LOC51157 | 5' | GGTGGCGGGGTTTTGCAGAGCT 1671 | AA | CTT |
| | C | | GAGCTC CA ACTCCGCCACC | | |
| | | | | | |
| | | | CTCGAG GT TGGGGCGGTGG | | |
| | | | AC TT_ | | |
| GAM157 | LOC92270 | 5' | GGTGACAGAGTGAGTGAGACTC 2828 | _ AAC | _ |
| | | | GAG CTC ACTTACTC CGCC | | |
| | | | | | |
| | | | CTC GAG TGAGTGAG GTGG | | |
| | | | A _ ACA | | |
| GAM158 | B3GALT3 | 3' | GCTGGTGTAACAAACCTACTA 1057 | A | C G_ |
| | CA | | TGTGGTAG TTTGTT TATA AGC | | |
| | | | | | |

ACATCATC AAACAA ATGT TCG
 C _ GG
 GAM158 KIAA1985 5' GCTCTGTATTAACAAATCCA 2066 A C____
 CCA TGGT GATTTGTT TATAGAGC
 |||| ||||| |||||
 ACCA CTAAACAA ATGTCTCG
 C AATT
 GAM158 MCM10 3' CTATGCAAATTACCACA 1835 A TCT
 TGTGGT GATTTGT ATAG
 ||||| ||||| |||
 ACACCA TTAAACG TATC

 GAM158 LOC149707 5' CTCCACAACATCTACCA 3137 _ TCTATA
 TGGTAGAT TTGT GAG
 ||||| ||| |||
 ACCATCTA AACA CTC
 C C____
 GAM158 LOC200227 5' CTCCACAACATCTACCA 3446 _ TCTATA
 TGGTAGAT TTGT GAG
 ||||| ||| |||
 ACCATCTA AACA CTC
 C C____
 GAM158 LOC255718 5' GCTCTATAGAACATGTCTAC 3741 T
 GTAGAT TGTTCTATAGAGC
 ||||| |||||
 CATCTG ACAAGATATCTCG
 T
 GAM159 DSG3 3' TTAAATGTTTGGGTTTCATAC 873 C_
 GTAT ATTTAAACATTTAA
 ||| |||||
 CATA TGGGTTTGTAATT
 CT
 GAM159 LPIN1 3' AAATGATAATGATACTG 2791 TAAA
 CAGTATCATT CATTT
 ||||| |||||
 GTCATAGTAA GTAAA
 TA_
 GAM159 TRPM1 3' AAATGAAAGTGATGATACTGT 928 TAAA_
 ACAGTATCATT CATTT
 ||||| |||||
 TGTCATAGTAG GTAAA
 TGAAA
 GAM159 DEPP 3' GTTAAATGTTTTCTGTCTTCTG 1347 TAT_ TTT
 TT AACAG CA AAACATTTAAC
 |||| || |||||
 TTGTC GT TTTGTAAATTG
 TTCT CT_
 GAM159 FLJ20668 3' TTAAATGGACCATGATACT 1764 TTAAA
 AGTATCAT CATTTAA
 ||||| |||||

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|--------|-----------|----|------------------------|--------------|--------|--|
| | | | TCATAGTA | GTAAATT | | |
| | | | CCAG_ | | | |
| GAM159 | KIAA1524 | 5' | TAAATGTTTAGAACCTACTGT | 2975 | TCA | |
| | | | ACAGTA | TTTAAACATTTA | | |
| | | | | | | |
| | | | TGTCAT | AGATTTGTAAAT | | |
| | | | CCA | | | |
| GAM159 | PRO1617 | 5' | AAATCAGTGAATGGTACTG | 1850 | AAC | |
| | | | CAGTATCATTTA | ATTT | | |
| | | | | | | |
| | | | GTCATGGTAAGT | TAAA | | |
| | | | GAC | | | |
| GAM159 | SDF1 | 3' | GTAAATGTGATGAATACTGT | 3502 | _ TAA | |
| | | | ACAGTAT CATT | ACATTTAAC | | |
| | | | | | | |
| | | | TGTCATA GTAG | TGTAAATTG | | |
| | | | A | _ | | |
| GAM159 | LOC130074 | 3' | GTTAGGTGTCAATTGATACT | 3043 | TTTAA | |
| | | | AGTATCA | ACATTTAAC | | |
| | | | | | | |
| | | | TCATAGT | TGTGGATTG | | |
| | | | TAAC_ | | | |
| GAM159 | LOC146952 | 5' | TAAATGTAATTTTATGTACTGT | 3287 | T TT _ | |
| | | T | AACAGTA CAT AA | ACATTTA | | |
| | | | | | | |
| | | | TTGTCAT GTA TT | TGTAAAT | | |
| | | | _ TT AA | | | |
| GAM159 | LOC157983 | 3' | TTGCATGTAAATGATACT | 3208 | A T | |
| | | | AGTATCATTTAA CAT TAA | | | |
| | | | | | | |
| | | | TCATAGTAAATT GTA GTT | | | |
| | | | _ C | | | |
| GAM159 | LOC203289 | 3' | TTGCATGTAAATGATACT | 3463 | A T | |
| | | | AGTATCATTTAA CAT TAA | | | |
| | | | | | | |
| | | | TCATAGTAAATT GTA GTT | | | |
| | | | _ C | | | |
| GAM159 | LOC256544 | 3' | TTGCATGTAAATGATACT | 3695 | A T | |
| | | | AGTATCATTTAA CAT TAA | | | |
| | | | | | | |
| | | | TCATAGTAAATT GTA GTT | | | |
| | | | _ C | | | |
| GAM160 | APPL | 3' | AGAACAGAGATTTTACAGT | 1405 | A CA | |
| | | | ATTG TAAATCTC | TTCT | | |
| | | | | | | |
| | | | TGAC ATTTTAGAG | AAGA | | |
| | | | _ AC | | | |
| GAM160 | F8 | 3' | AATGGAGAGAATACAATA | 708 | A AAA | |
| | | | TATTG TA | TCTCCATT | | |
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|--------|----------|----|-----------------------------|----------|
| | | | ATAAC AT AGAGGTAA | |
| | | | _ AAG | |
| GAM160 | RAB6A | 3' | AGAATGGAAATAAACTCAATA 966 | TAAA_ C |
| | TTA | | TAATATTGA AT TCCATTCT | |
| | | | | |
| | | | ATTATAACT TA AGGTAAGA | |
| | | | CAAAA A | |
| GAM160 | RNF14 | 3' | AGAATGGAAATTTATAATAT 1097 | ATA C |
| | | | ATATTG AAAT TCCATTCT | |
| | | | | |
| | | | TATAAT TTTA AGGTAAGA | |
| | | | A_ A | |
| GAM160 | SART2 | 3' | AGAATTGGGTTTTATTAATATT 1443 | CC |
| | A | | TAATATTGATAAAATCT ATTCT | |
| | | | | |
| | | | ATTATAATTATTTTGGG TAAGA | |
| | | | T_ | |
| GAM160 | EEA1 | 3' | AATGGTTTTTGTTTTAACAATA 1035 | A CT__ |
| | TTA | | TAATATTG TAAAAT CCATT | |
| | | | | |
| | | | ATTATAAC ATTTTG GGTA | |
| | | | A TTTTT | |
| GAM160 | FLJ10980 | 3' | AGAATGGAGTGTACCAAATTA 2697 | A A AAAT |
| | | | TAAT TTG TA CTCCATTCT | |
| | | | | |
| | | | ATTA AAC AT GAGGTAAGA | |
| | | | _ C GT__ | |
| GAM160 | FLJ22794 | 3' | AATGGTCATCTTATCAATA 3532 | A CT |
| | | | TATTGATAA AT CCATT | |
| | | | | |
| | | | ATAACTATT TA GGTA | |
| | | | C CT | |
| GAM160 | KIAA1328 | 3' | AGAATGGAGCCCACTAATATTA 2601 | ATAAAAT |
| | | | TAATATTG CTCCATTCT | |
| | | | | |
| | | | ATTATAAT GAGGTAAGA | |
| | | | CACCC__ | |
| GAM160 | PRO0902 | 3' | AATGGAGATCAATTTTA 2357 | T TAAAA |
| | | | TAA ATTGA TCTCCATT | |
| | | | | |
| | | | ATT TAACT AGAGGTAA | |
| | | | T _____ | |
| GAM160 | RASGRP4 | 3' | AGAACAGGGATTCTATCAATG 2348 | _ CA |
| | T | | ATATTGATA AAATCTC TTCT | |
| | | | | |
| | | | TGTAACAT TTTAGGG AAGA | |
| | | | C AC | |
| GAM160 | WBP4 | 3' | AGAATGGAGACTTATACA 1363 | _ AA |
| | | | TG ATAA TCTCCATTCT | |
| | | | | |

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|--------|--------------|-----------------------------|------------|
| | | AC TATT AGAGGTAAGA | |
| | | A C_ | |
| GAM160 | LOC116150 3' | AGAATGGAGCAGTTTAATA 2443 | TAAAAT |
| | | TATTGA CTCCATTCT | |
| | | | |
| | | ATAATT GAGGTAAGA | |
| | | TGAC_ | |
| GAM160 | LOC164200 5' | AATGAGGTTGTTATCAATA 3248 | _ C |
| | | TATTGATAA AATCTC ATT | |
| | | | |
| | | ATAACTATT TTGGAG TAA | |
| | | G _ | |
| GAM160 | LOC51320 3' | AGAATGATAAATTATCAATAT 1702 | AATCTC |
| | | ATATTGATAA CATTCT | |
| | | | |
| | | TATAACTATT GTAAGA | |
| | | AAATA_ | |
| GAM161 | SELPLG 3' | CCAAACAGGAAGTGGACATTCT 2539 | A CG C |
| | | AGAAT TCCAT TTTG TTGG | |
| | | | |
| | | TCTTA AGGTG GGAC AACC | |
| | | C AA A | |
| GAM161 | FLJ21144 3' | CCAAAACATAAACAATAAATAT 2007 | CC C C_ |
| | TCTCA | TGAGAATAT AT GTTTG TTGG | |
| | | | |
| | | ACTCTTATA TA CAAAT AACC | |
| | | AA A ACAA | |
| GAM161 | KIAA0676 3' | CAAAGTGATGGAACCCTCA 1603 | AATA _ |
| | | TGAG TCCATCG TTTG | |
| | | | |
| | | ACTC AGGTAGT AAAC | |
| | | CCA_ G | |
| GAM161 | KIAA1393 3' | CAAGTGATGAATATGCTCA 2935 | A C GTTT |
| | | TGAG ATAT CATC GCTTG | |
| | | | |
| | | ACTC TATA GTAG TGAAC | |
| | | G A _ | |
| GAM161 | UBN1 3' | CCAAGTCACAGATAGACATTCC 1716 | A A C GTTT |
| | A | TG GAAT TC ATC GCTTGG | |
| | | | |
| | | AC CTTA AG TAG TGAACC | |
| | | _ C A ACAC | |
| GAM162 | CELSR3 3' | AGAACTGAAGACTTTAA 824 | TAT |
| | | TTAAAGTCTTC TTCT | |
| | | | |
| | | AATTCAGAAG AAGA | |
| | | TC_ | |
| GAM162 | GPR85 3' | TAGAAGTTTGAAGACTTTAA 1868 | T_ |
| | | TTAAAGTCTTC ATTTCTA | |
| | | | |

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|--------|---------|----|----------------------------|------|--|
| | | | AATTCAGAAG TGAAGAT | | |
| | | | TT | | |
| GAM162 | ITGAV | 3' | TAGAAATGGAGAGTTTAATA 908 | G T | |
| | | | TATTAAA TCT CTATTTCTA | | |
| | | | | | |
| | | | ATAATTT AGA GGTAAGAT | | |
| | | | G _ | | |
| GAM162 | MAPRE2 | 3' | TAGAAGTGAAGACCTTA 1487 | A T | |
| | | | TAA GTCTTC ATTTCTA | | |
| | | | | | |
| | | | ATT CAGAAG TGAAGAT | | |
| | | | C _ | | |
| GAM162 | PAX6 | 5' | AGGGGGAAGACTTTAA 837 | AT | |
| | | | TTAAAGTCTTCT TTCT | | |
| | | | | | |
| | | | AATTCAGAAGG GGGA | | |
| | | | — | | |
| GAM162 | PAX6 | 5' | AGGGGGAAGACTTTAA 726 | AT | |
| | | | TTAAAGTCTTCT TTCT | | |
| | | | | | |
| | | | AATTCAGAAGG GGGA | | |
| | | | — | | |
| GAM162 | SLC24A1 | 3' | TAGAAATAGAACAGCTTAATA 1150 | A C_ | |
| | | | TATTAA GT TTCTATTTCTA | | |
| | | | | | |
| | | | ATAATT CG AAGATAAAGAT | | |
| | | | _ AC | | |
| GAM162 | SLC31A1 | 3' | TAGAAATAGATATTTTAA 864 | TCT | |
| | | | TTAAAG TCTATTTCTA | | |
| | | | | | |
| | | | AATTTT AGATAAAGAT | | |
| | | | TAT | | |
| GAM162 | SLC4A7 | 3' | TAGAACAATAGAACTTTAATA 1043 | C _ | |
| | | | TATTAAAGT TTCTATT TCTA | | |
| | | | | | |
| | | | ATAATTTCA AAGATAA AGAT | | |
| | | | _ CA | | |
| GAM162 | ZNF22 | 3' | TAGAAATAGAGATGCTTTA 3527 | C_ | |
| | | | TAAAGT TTCTATTTCTA | | |
| | | | | | |
| | | | ATTTCTG GAGATAAAGAT | | |
| | | | TA | | |
| GAM162 | ARGBP2 | 5' | GGAAAAGTGAAGACTTTAATA 1041 | TA_ | |
| | | | TATTAAAGTCTTC TTTCT | | |
| | | | | | |
| | | | ATAATTCAGAAG AAAGG | | |
| | | | TCA | | |
| GAM162 | C20orf7 | 3' | AGAAATGGATAGCTTTAA 2056 | CT | |
| | | | TTAAAGT TCTATTTCT | | |
| | | | | | |

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| | | AATTTTCG AGGTAAAGA | |
| | | AT | |
| GAM162 | FLJ12704 3' | AGAACGCTGGACTTTAATG 2125 | TCTAT |
| | | TATTAAAGTCT TTCT | |
| | | | |
| | | GTAATTTTCAGG AAGA | |
| | | TCGC_ | |
| GAM162 | FLJ13194 3' | TAGAAATGTTCTCAGACTTTAA 2141 | TC__ |
| | | TTAAAGTCT TATTTCTA | |
| | | | |
| | | AATTTTCAGA GTAAAGAT | |
| | | CTCTT | |
| GAM162 | FLJ20005 3' | AGAAAAAGACTTTAA 1731 | CTA |
| | | TTAAAGTCTT TTTCT | |
| | | | |
| | | AATTTTCAGAA AAAGA | |
| | | — | |
| GAM162 | FLJ20417 5' | TAGAAATAAACAAGGCTTTA 1754 | C__ |
| | | TAAAGTCTT TATTTCTA | |
| | | | |
| | | ATTTTCGGAA ATAAAGAT | |
| | | CAA | |
| GAM162 | KIAA0712 3' | AGAAATTAAGACTTTAA 1529 | CT |
| | | TTAAAGTCTT ATTTCT | |
| | | | |
| | | AATTTTCAGAA TAAAGA | |
| | | T_ | |
| GAM162 | KIAA0750 5' | AGAAAGAGAAGACTTTAA 1510 | A |
| | | TTAAAGTCTTCT TTTCT | |
| | | | |
| | | AATTTTCAGAAGA AAAGA | |
| | | G | |
| GAM162 | KIAA1128 3' | TAGAGTATTCAGACTTTGATA 2821 | TCTAT |
| | | TATTAAAGTCT TTCTA | |
| | | | |
| | | ATAGTTTCAGA GAGAT | |
| | | CTTAT | |
| GAM162 | KIAA1281 3' | TAGAAGAGAGAGACTTTAA 3461 | _ A |
| | | TTAAAGTCT TCT TTTCTA | |
| | | | |
| | | AATTTTCAGA AGA GAAGAT | |
| | | G _ | |
| GAM162 | KIAA1841 3' | AGAGAACAGACTTTAATA 3151 | TCTA |
| | | TATTAAAGTCT TTTCT | |
| | | | |
| | | ATAATTTTCAGA AGAGA | |
| | | CA__ | |
| GAM162 | Rab11-FIP2 3' | AGATGTAGAACTTTAATA 1580 | CT T |
| | | TATTAAAGT TCTAT TCT | |
| | | | |

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|--------|-----------|----|-----------------------------|------|
| | | | ATAATTTCA AGATG AGA | |
| | | | — T | |
| GAM162 | RABEX5 | 3' | TAGTCGATGGAAGACTTTAA 1504 | T_ |
| | | | TTAAAGTCTTCTATT CTA | |
| | | | | |
| | | | AATTCAGAAGGTAG GAT | |
| | | | CT | |
| GAM162 | SGKL | 3' | TAGAGGTAAGACTTTAATA 1438 | TC |
| | | | TATTAAAGTCT TATTCTA | |
| | | | | |
| | | | ATAATTCAGA ATGGAGAT | |
| | | | — | |
| GAM162 | SYTL3 | 3' | TAGAAAATGGCCAGATTTTAAT 3183 | T_ _ |
| | A | | TATTAAAGTCT CTATTT CTA | |
| | | | | |
| | | | ATAATTTTAGA GGTAAGAT | |
| | | | CC A | |
| GAM162 | TTY7 | 3' | GAAAAAGACTTTTGATA 2220 | CTA |
| | | | TATTAAAGTCTT TTTC | |
| | | | | |
| | | | ATAGTTTCAGAA AAAG | |
| | | | — | |
| GAM162 | LOC113612 | 3' | TAGAAATAGTTGACTTAATA 2968 | A TT |
| | | | TATTAA GTC CTATTTCTA | |
| | | | | |
| | | | ATAATT CAG GATAAAGAT | |
| | | | _ TT | |
| GAM162 | LOC121457 | 3' | TAGAAATAGTTCTTTAA 2993 | TCTT |
| | | | TTAAAG CTATTTCTA | |
| | | | | |
| | | | AATTC GATAAAGAT | |
| | | | TT_ | |
| GAM162 | LOC133491 | 3' | TAGAATTGGGACTTTAGTA 3015 | TT T |
| | | | TATTAAAGTC CTA TTCTA | |
| | | | | |
| | | | ATGATTTCAG GGT AAGAT | |
| | | | — T | |
| GAM162 | LOC143282 | 3' | AGAAATAGGCGTACTTTAA 3054 | CT_ |
| | | | TTAAAGT TCTATTTCT | |
| | | | | |
| | | | AATTCAGATAAAGA | |
| | | | TGC | |
| GAM162 | LOC143524 | 3' | TAGAGAAGGGAAAGACTTTA 3059 | _ A_ |
| | | | TAAAGTCTT CT TTTCTA | |
| | | | | |
| | | | ATTCAGAA GG AGAGAT | |
| | | | A GA | |
| GAM162 | LOC144559 | 5' | TAGAGAAGGGAAAGACTTTA 3066 | _ A_ |
| | | | TAAAGTCTT CT TTTCTA | |
| | | | | |

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|--------|--------------|-----------------------------|-------------|---|
| | | ATTTCAGAA GG AGAGAT | | |
| | | A GA | | |
| GAM162 | LOC153222 3' | TAGAAATGGTTGTA | CTT_ | |
| | | CTTTAATG 3180 | | |
| | | TATTAAGT CTATTTCTA | | |
| | | | | |
| | | GTAATTTCA GGTAAGAT | | |
| | | TGTT | | |
| GAM162 | LOC219623 5' | AGAAAAGAAGACTTCAAT 3525 | A | A |
| | | ATT AAGTCTTCT TTTCT | | |
| | | | | |
| | | TAA TTCAGAAGA AAAGA | | |
| | | C _ | | |
| GAM162 | LOC219918 5' | TAGAGAAGGGAAAGACTTTA 3530 | _ A_ | |
| | | TAAAGTCTT CT TTTCTA | | |
| | | | | |
| | | ATTTCAGAA GG AGAGAT | | |
| | | A GA | | |
| GAM162 | LOC220071 5' | TAGAGAAGGGAAAGACTTTA 3602 | _ A_ | |
| | | TAAAGTCTT CT TTTCTA | | |
| | | | | |
| | | ATTTCAGAA GG AGAGAT | | |
| | | A GA | | |
| GAM162 | LOC254431 3' | AGGTAAAGACTTTAGTA 3717 | C | |
| | | TATTAAGTCTT TATTT | | |
| | | | | |
| | | ATGATTCAGAA ATGGA | | |
| | | _ | | |
| GAM162 | LOC255515 3' | TAGAGAAGGGAAAGACTTTA 3688 | _ A_ | |
| | | TAAAGTCTT CT TTTCTA | | |
| | | | | |
| | | ATTTCAGAA GG AGAGAT | | |
| | | A GA | | |
| GAM162 | LOC56959 5' | ATAGAAACAGAGGACGTGACTT 3219 | _____ A III | |
| | | TGATA TAAAGTC TTCT TTTCTA T | | |
| | | | | |
| | | GTTTCAG GAGA AAAGAT A | | |
| | | TGCAG C III | | |
| GAM162 | LOC90906 3' | TAGAGAAGGGAAAGACTTTA 2685 | _ A_ | |
| | | TAAAGTCTT CT TTTCTA | | |
| | | | | |
| | | ATTTCAGAA GG AGAGAT | | |
| | | A GA | | |
| GAM163 | ENAM 5' | TATAGACCATTAAGAATA 2216 | TC C C | |
| | | TATTCTTA ATG GTC ATA | | |
| | | | | |
| | | ATAAGAAT TAC CAG TAT | | |
| | | _ _ A | | |
| GAM163 | EFNA5 3' | CTATGGACAAGGAAGAATAGT 876 | ATCATGC | |
| | | ATTATTCTT GTCCATAG | | |
| | | | | |

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|--------|-----------|----|------------------------|----------|----------|
| | | | TGATAAGAA | CAGGTATC | |
| | | | GGAA__ | | |
| GAM163 | LOC159199 | 5' | CTATGGACAAGCCAAGAA | 3236 | ATCAT __ |
| | | | TTCTT GC GTCCATAG | | |
| | | | | | |
| | | | AAGAA CG CAGGTATC | | |
| | | | C__ AA | | |
| GAM163 | LOC90321 | 3' | ATGGAGGTGGACAGAGAATAA | 2630 | ATCA G |
| | | | TTATTCTT TGC TCCAT | | |
| | | | | | |
| | | | AATAAGAG GTG AGGTA | | |
| | | | ACAG G | | |
| GAM164 | KRAS2 | 3' | AATATTATATTTTTTCTATAAA | 1166 | GAT |
| | AA | | TTTTTA AAAAAATATAATATT | | |
| | | | | | |
| | | | AAAAAT TTTTTTATATTATAA | | |
| | | | ATC | | |
| GAM164 | KRAS2 | 3' | AATATTATATTTTTTCTATAAA | 2331 | GAT |
| | AA | | TTTTTA AAAAAATATAATATT | | |
| | | | | | |
| | | | AAAAAT TTTTTTATATTATAA | | |
| | | | ATC | | |
| GAM165 | APXL | 3' | AGGACTTTCTCTTCTACAC | 843 | TATA |
| | | | GTGTGGGA AAAGTCCT | | |
| | | | | | |
| | | | CACATCTT TTTCAGGA | | |
| | | | CTC_ | | |
| GAM165 | ASTN | 3' | AGGTGCTTATATCCCACCAAC | 2852 | __ AA _ |
| | | | GT GTGGGATATA AGT CCT | | |
| | | | | | |
| | | | CA CACCCTATAT TCG GGA | | |
| | | | AC _ T | | |
| GAM165 | GALK2 | 3' | AGGACTTTCTGTGCCACA | 891 | G TA |
| | | | TGTGG ATA AAAGTCCT | | |
| | | | | | |
| | | | ACACC TGT TTTCAGGA | | |
| | | | G C_ | | |
| GAM165 | MCL1 | 3' | AGGACTTTTATACCTGT | 1970 | TG A |
| | | | G GG TATAAAAGTCCT | | |
| | | | | | |
| | | | T CC ATATTTTCAGGA | | |
| | | | GT _ | | |
| GAM165 | PACE4 | 5' | AGGACTTTTACTACCATGGTA | 2434 | TG ATA |
| | | | TACCGTG GG TAAAAGTCCT | | |
| | | | | | |
| | | | ATGGTAC TC ATTTTCAGGA | | |
| | | | CA _ | | |
| GAM165 | PODXL | 3' | AGGACTTTTATGGGCTCGGC | 1206 | G A_ |
| | | | GT TGGG TATAAAAGTCCT | | |
| | | | | | |

CG GCTC GTATTTTCAGGA
 _ GG
 GAM165 TNFSF8 3' GGA CTCTCTCACACAGG 811 _ TATAAA
 CC GTGTGGGA AGTCC
 || ||||| ||||
 GG CACACTCT TCAGG
 A C____

GAM165 ATP1B4 3' GACCTCTATATCCTGGTG 1401 GTGT AAA
 TACC GGGATATA GTC
 ||| ||||| ||
 GTGG TCCTATAT CAG
 _____ CTC

GAM165 CDC14A 3' AGGACCCTTATAGGTACTCACA 1047 A__ AA
 TGTGGG TATAA GTCCT
 ||||| ||||| |||||
 ACACTC ATATT CAGGA
 ATGG CC

GAM165 DKFZP434C171 3' GGACTCTTATGTCACTGCA 1641 TG_ A
 TG G GATATAA AGTCC
 || | ||||| |||||
 AC C CTGTATT TCAGG
 GT A C

GAM165 EMR2 3' AGGACTTTTCATACCGACAAC 1453 _ G A A
 GT GT GG TAT AAAGTCCT
 || ||| ||| |||||
 CA CA CC ATA TTTCAGGA
 A G _ C

GAM165 FYCO1 3' AGGACTTTTGTGGGGCCACAAG 2063 CG GA_
 TA TAC TGTGG TATAAAAGTCCT
 ||| ||||| |||||
 ATG ACACC GTGTTTTCAGGA
 A_ GGG

GAM165 GGA2 3' AGGACTTTCCCGTCCACACAC 2448 _ ATA
 GTGTG GGAT AAAGTCCT
 ||||| ||||| |||||
 CACAC CCTG TTTCAGGA
 A CCC

GAM165 GGA2 3' AGGACTTTCCCGTCCACACAC 1604 _ ATA
 GTGTG GGAT AAAGTCCT
 ||||| ||||| |||||
 CACAC CCTG TTTCAGGA
 A CCC

GAM165 ICT1 3' AGGACTTTCACACCATAAGG 834 G GATATA
 CC TGTGG AAAGTCCT
 || ||||| |||||
 GG ATACC TTTCAGGA
 A ACAC__

GAM165 ZFP100 3' AGGACTCCCTATCCCACA 2877 TAAA
 TGTGGGATA AGTCCT
 ||||| |||||

ACACCCTAT TCAGGA
 CCC_
 GAM165 LOC64744 3' GACTTTATGAAGATCCACAC 2607 ATA____
 GTGTGGGAT AAAGTC
 ||||| ||||
 CACACCCTA TTTCAG
 GAAGTA
 GAM166 MEF-2 3' TGCTATTAAATAGTAAAC 2688 T ATAAC
 GTTTACTATTTA TG GCA
 ||||| || ||
 CAAATGATAAAT AT CGT
 T ____
 GAM166 LOC146184 5' TATCAATAAATAGCAAAC 3281 A
 GTTT CTATTTATTGATA
 ||| |||||
 CAAA GATAAATAACTAT
 C
 GAM167 CDH5 3' CAGTGATGACTATTCTCAAATG 858 G A ATTC
 CAT TGA AATAGTCAT CTG
 ||| ||||| ||
 GTA ACT TTATCAGTA GAC
 A C GT_
 GAM167 LNK 3' CAGAGAACACTATTTTACAT 1216 CATA _
 ATGTGAAAATAGT TTC CTG
 ||||| || ||
 TACATTTTATCA AAG GAC
 C__ A
 GAM167 NPR2 3' CAGAAATGGACATTTTCATATG 786 A A C
 CATGTGAAAAT GTC TATT CTG
 ||||| || || ||
 GTATACTTTTA CAG GTAA GAC
 _ _ A
 GAM167 CLLD8 3' GCAGGAACACAATTAGGATATT 2219 G A _____ |||
 TTCATA AAATA TC TA TTCCTG C
 |||| || |||| |
 TTTAT AG AT AAGGAC G
 _ G TAACAC |||
 GAM167 FLJ22301 3' CAGGTGAGGACCATTTCAC 2094 A ATATT
 GTGAAAAT GTC CCTG
 ||||| || ||
 CACTTTTA CAG GGAC
 C GAGT_
 GAM167 FLJ22833 3' AGGGAACACCAGTTTTCACATG 2016 AGTCATA
 CATGTGAAAAT TTCCT
 ||||| ||||
 GTACACTTTTG AGGGA
 ACCACA_
 GAM167 KIAA0125 3' GAAATGACATTTCACATG 1548 AATA A
 CATGTGAA GTCAT TTC
 ||||| |||| ||

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|--------|----------|----|-----------------------------|---------|--------|
| | | | GTACACTT CAGTA AAG | | |
| | | | A__ _ | | |
| GAM167 | KIAA0125 | 3' | GAAATGACATTCACATG 1549 | AATA | A |
| | | | CATGTGAA GTCAT TTC | | |
| | | | | | |
| | | | GTACACTT CAGTA AAG | | |
| | | | A__ _ | | |
| GAM167 | KIAA0125 | 3' | GAAATGACATTCACATG 1550 | AATA | A |
| | | | CATGTGAA GTCAT TTC | | |
| | | | | | |
| | | | GTACACTT CAGTA AAG | | |
| | | | A__ _ | | |
| GAM167 | KIAA0125 | 3' | GAAATGACATTCACATG 1551 | AATA | A |
| | | | CATGTGAA GTCAT TTC | | |
| | | | | | |
| | | | GTACACTT CAGTA AAG | | |
| | | | A__ _ | | |
| GAM167 | KIAA0125 | 3' | GAAATGACATTCACATG 1552 | AATA | A |
| | | | CATGTGAA GTCAT TTC | | |
| | | | | | |
| | | | GTACACTT CAGTA AAG | | |
| | | | A__ _ | | |
| GAM167 | KIAA1199 | 3' | CAGAAATCTGCTGCATTTTCA 2951 | A_ | T T C |
| | | | TG CATGTGAAA TAG CA ATT CTG | | |
| | | | | | |
| | | | GTACACTTT GTC GT TAA GAC | | |
| | | | AC _ C A | | |
| GAM167 | LANCL2 | 3' | ATATGACTTCTTCACAT 1860 | AAT | |
| | | | ATGTGAA AGTCATAT | | |
| | | | | | |
| | | | TACACTT TCAGTATA | | |
| | | | CT_ | | |
| GAM167 | SEZ6 | 3' | CAGGAGTACCTTTCTCCACATG 2997 | AAAAT | TCA |
| | | | CATGTG AG TATTCCTG | | |
| | | | | | |
| | | | GTACAC TC ATGAGGAC | | |
| | | | CTCTT C__ | | |
| GAM167 | SNX10 | 3' | AGGAAGATATTTTCAGAT 1442 | G | GTCATA |
| | | | AT TGAAAATA TTCCT | | |
| | | | | | |
| | | | TA ACTTTTAT AAGGA | | |
| | | | G AG__ | | |
| GAM167 | TNFRSF21 | 3' | AGTGTGACTTTTCCCACA 1502 | AA | T |
| | | | TGTG AA AGTCATATT | | |
| | | | | | |
| | | | ACAC TT TCAGTGTGA | | |
| | | | CC T | | |
| GAM167 | TTY11 | 5' | CAGGAATAGTCAGCATTTTCA 2221 | ATAGTCA | |
| | | | T ATGTGAAA TATTCCTG | | |
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|--------|--------------|------------------------------|----------|
| | | TACACTTT ATAAGGAC | |
| | | ACGACTG | |
| GAM167 | LOC143879 3' | GAATACTTAGTATTTTCACATG 3063 | GTCA_ |
| | | CATGTGAAAATA TATTC | |
| | | | |
| | | GTACACTTTTAT ATAAG | |
| | | GATTC | |
| GAM167 | LOC145439 5' | CAGGAATACAGAGATTTTCGCAT 3078 | ATAGTCA |
| | G | CATGTGAAA TATTCCTG | |
| | | | |
| | | GTACGCTTT ATAAGGAC | |
| | | AGAGAC_ | |
| GAM167 | LOC147353 3' | CAGGAATAGAACTTGCACATG 3293 | AAAAT CA |
| | | CATGTG AGT TATTCCTG | |
| | | | |
| | | GTACAC TCA ATAAGGAC | |
| | | GT__ AG | |
| GAM167 | LOC221584 5' | GAATATGGGCTACTTCATATG 3620 | AA _ |
| | | CATGTGAA TAGTC ATATTC | |
| | | | |
| | | GTATACTT ATCGG TATAAG | |
| | | C_ G | |
| GAM167 | LOC257054 3' | CAGGAATGTGTCATTTCCCACA 3682 | A_ AGT |
| | | TGTG AAAT CATATTCCTG | |
| | | | |
| | | ACAC TTTA GTGTAAGGAC | |
| | | CC CT_ | |
| GAM167 | LOC91145 5' | CAGGAATGTACACTTTACAT 2713 | AATA C |
| | | ATGTGAA GT ATATTCCTG | |
| | | | |
| | | TACATTT CA TGTAAGGAC | |
| | | CA__ _ | |
| GAM167 | LOC93297 3' | GAATATGTTTGTGTATGTTTAC 2929 | A____ T |
| | ATG | CATGTGAA ATAG CATATTC | |
| | | | |
| | | GTACACTT TGTT GTATAAG | |
| | | GTATG T | |
| GAM168 | BACH2 3' | AAGCTGTTTCGTTGTATCA 1961 | A _ |
| | | TGA TACAACGAATA CTT | |
| | | | |
| | | ACT ATGTTGCTTGT GAA | |
| | | _ C | |
| GAM168 | GAN 3' | TGAAGTATAGGGATGTATTTA 1974 | ACGA_ |
| | | TGAATACA ATACTTCA | |
| | | | |
| | | ATTTATGT TATGAAGT | |
| | | AGGGA | |
| GAM168 | MHC2TA 3' | TGAAGCATTTACTTTGTGTTCA 720 | C__ A |
| | | TGAATACAA GAAT CTTCA | |
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|--------|----------|----|-----------------------------|--------|--|
| | | | ACTTGTGTT TTTA GAAGT | | |
| | | | TCA C | | |
| GAM168 | MTM1 | 3' | TGAAGTATTGTGTTTA 723 | ACGA | |
| | | | TGAATACA ATACTTCA | | |
| | | | | | |
| | | | ATTTGTGT TATGAAGT | | |
| | | | _____ | | |
| GAM168 | AWP1 | 3' | TGAAGTAATTGTGCTGTATTTA 1872 | ___ A | |
| | | | TGAATACA ACGA TACTTCA | | |
| | | | | | |
| | | | ATTTATGT TGTT ATGAAGT | | |
| | | | CG A | | |
| GAM168 | BLCAP | 3' | TGAAGTATGGTGTGTTCA 1324 | ACGA | |
| | | | TGAATACA ATACTTCA | | |
| | | | | | |
| | | | ACTTGTGT TATGAAGT | | |
| | | | GG__ | | |
| GAM168 | C5orf3 | 3' | TGAAGTATTCAGGTTCTCA 1859 | AT AAC | |
| | | | TGA AC GAATACTTCA | | |
| | | | | | |
| | | | ACT TG CTTATGAAGT | | |
| | | | CT GA_ | | |
| GAM168 | CRK7 | 3' | AAGCTGTCCGTTGTATTC 1690 | A _ | |
| | | | GAATACAACG ATA CTT | | |
| | | | | | |
| | | | CTTATGTTGC TGT GAA | | |
| | | | C C | | |
| GAM168 | FLJ11101 | 3' | TGAAGTTTTGATTGTATTTA 1814 | _ T | |
| | | | TGAATACAA CGAA ACTTCA | | |
| | | | | | |
| | | | ATTTATGTT GTTT TGAAGT | | |
| | | | A _ | | |
| GAM168 | FLJ12876 | 3' | TGAAGTGTAGATCATTGTATTC 2004 | C ____ | |
| | A | | TGAATACAA GA ATACTTCA | | |
| | | | | | |
| | | | ACTTATGTT CT TGTGAAGT | | |
| | | | A AGA | | |
| GAM168 | KLF12 | 3' | TGAAGTGTAGATTTGTATTTA 1374 | CGA_ | |
| | | | TGAATACAA ATACTTCA | | |
| | | | | | |
| | | | ATTTATGTT TGTGAAGT | | |
| | | | TAGA | | |
| GAM168 | MGC4734 | 3' | AAGTGTTCTGTATTCA 2513 | AC | |
| | | | TGAATACA GAATACTT | | |
| | | | | | |
| | | | ACTTATGT CTTGTGAA | | |
| | | | _____ | | |
| GAM168 | PRO2000 | 3' | GAGTATTCTTTATATTCA 1469 | C C | |
| | | | TGAATA AA GAATACTT | | |
| | | | | | |

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|--------|-----------|----|-----------------------------|------------|--|
| | | | ACTTAT TT CTTATGAG | | |
| | | | A T | | |
| GAM168 | RAB33B | 3' | TGAAGTGTTCACATTCA 2191 | ACAAC | |
| | | | TGAAT GAATACTTCA | | |
| | | | | | |
| | | | ACTTA CTTGTGAAGT | | |
| | | | CA__ | | |
| GAM168 | RGS12 | 3' | TGAAGCCCGCTGTGTTC 972 | A AATA | |
| | | | TGAATACA CG CTTCA | | |
| | | | | | |
| | | | ACTTGTGT GC GAAGT | | |
| | | | C CC__ | | |
| GAM168 | ZNF387 | 3' | TGAAGTATGTTTGTATTTA 1522 | CGA | |
| | | | TGAATACAA ATACTTCA | | |
| | | | | | |
| | | | ATTTATGTT TATGAAGT | | |
| | | | TG_ | | |
| GAM168 | LOC158381 | 3' | TGAAGTAATTGTGCTGTATTTA 2905 | __ A | |
| | | | TGAATACA ACGA TACTTCA | | |
| | | | | | |
| | | | ATTTATGT TGTT ATGAAGT | | |
| | | | CG A | | |
| GAM168 | LOC196411 | 3' | AAGTTTCTTTGTGTTC 3412 | C T | |
| | | | TGAATACAA GAA ACTT | | |
| | | | | | |
| | | | ACTTGTGTT CTT TGAA | | |
| | | | T _ | | |
| GAM168 | LOC51186 | 5' | GAAGTCATTGTATTCA 1680 | C ATA | |
| | | | TGAATACAA GA CTTC | | |
| | | | | | |
| | | | ACTTATGTT CT GAAG | | |
| | | | A __ | | |
| GAM169 | RDX | 3' | TAGAGATTAAACCAATTA 971 | G | |
| | | | TAATTGGTTTAATC TTTA | | |
| | | | | | |
| | | | ATTAACCAAATTAG AGAT | | |
| | | | - | | |
| GAM169 | TRPC3 | 3' | AATAAATGTTGAAACCAACTGA 1010 | A AAT | |
| | | | TTA TTGGTTT CGTTTATT | | |
| | | | | | |
| | | | AGT AACCAAA GTAAATAA | | |
| | | | C GTT | | |
| GAM169 | LOC131000 | 3' | TAATAACGATTTAATGAA 3038 | G T | |
| | | | TT GTT AATCGTTTATTA | | |
| | | | | | |
| | | | AA TAA TTAGCAAATAAT | | |
| | | | G T | | |
| GAM170 | ACTA2 | 3' | TGTGAATGTCCTGTGGAA 839 | AG CTAAT _ | |
| | | | TTCCACAG CA TTC CA | | |
| | | | | | |

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|--------|--------|----|-----------------------------|-------|--------|
| | | | AAGGTGTC GT AAG GT | | |
| | | | CT _____ T | | |
| GAM170 | ASPH | 3' | GAAATAATTGCTCTGTTGAA 2251 | C | CTA |
| | | | TTC ACAGAGCA ATTTT | | |
| | | | | | |
| | | | AAG TGTCTCGT TAAAG | | |
| | | | T TAA | | |
| GAM170 | ASPH | 3' | GAAATAATTGCTCTGTTGAA 2253 | C | CTA |
| | | | TTC ACAGAGCA ATTTT | | |
| | | | | | |
| | | | AAG TGTCTCGT TAAAG | | |
| | | | T TAA | | |
| GAM170 | BRCA1 | 3' | TGGAAGTTAGCACTCTAGGGAA 1392 | AC | CA |
| | | | TTCC AGAG CTAATTTCCA | | |
| | | | | | |
| | | | AAGG TCTC GATTGAAGGT | | |
| | | | GA AC | | |
| GAM170 | CDC42 | 3' | GAAGACAGACATCTGTGGAA 856 | | GCA AA |
| | | | TTCCACAGA CT TTTC | | |
| | | | | | |
| | | | AAGGTGTCT GA GAAG | | |
| | | | ACA CA | | |
| GAM170 | CLASP1 | 3' | TTGGAAATAAAGAAGTGCTCTG 2718 | | A_____ |
| | | | CAGAGCACT ATTTCCAA | | |
| | | | | | |
| | | | GTCTCGTGA TAAAGGTT | | |
| | | | AGAAA | | |
| GAM170 | CPNE3 | 3' | GAAATTAGTGTGGGGAA 1069 | ACAGA | |
| | | | TTCC GCACTAATTTT | | |
| | | | | | |
| | | | AAGG TGTGATTAAAG | | |
| | | | GG_____ | | |
| GAM170 | DACH | 3' | TTGGAAATTTTCTATGG 2388 | C | CACT |
| | | | CCA AGAG AATTTCCAA | | |
| | | | | | |
| | | | GGT TCTT TTAAAGGTT | | |
| | | | A T_____ | | |
| GAM170 | ECM2 | 5' | GAAATTGGCTGGTGGAA 823 | AG | AC |
| | | | TTCCAC AGC TAATTTT | | |
| | | | | | |
| | | | AAGGTG TCG GTTAAAG | | |
| | | | G_ _ | | |
| GAM170 | EDNRA | 3' | TAGACTGTCTCTGTGGAA 2681 | | _ _ |
| | | | TTCCACAGAG CA CTA | | |
| | | | | | |
| | | | AAGGTGTCTC GT GAT | | |
| | | | T CA | | |
| GAM170 | ENC1 | 3' | TTGGAAATCAGTTGTG 1045 | GAGC | A |
| | | | CACA ACT ATTTCCAA | | |
| | | | | | |

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|--------|---------|----|----------------------------|---------|------|
| | | | GTGT TGA TAAAGGTT | | |
| | | | _____ C | | |
| GAM170 | FANCF | 3' | TTGGTGGCTGCCCTGTGGAA 1999 | A _ | ATTT |
| | | | TTCCACAG GCA CTA CCAA | | |
| | | | | | |
| | | | AAGGTGTC CGT GGT GGTT | | |
| | | | C C _____ | | |
| GAM170 | FCAR | 3' | GAAAACTTAGTCTGTGGAG 2405 | GCA _ | |
| | | | TTCCACAGA CTAA TTTC | | |
| | | | | | |
| | | | GAGGTGTCT GATT AAAG | | |
| | | | _____ CA | | |
| GAM170 | FCAR | 3' | GAAAACTTAGTCTGTGGAG 2407 | GCA _ | |
| | | | TTCCACAGA CTAA TTTC | | |
| | | | | | |
| | | | GAGGTGTCT GATT AAAG | | |
| | | | _____ CA | | |
| GAM170 | GAS7 | 3' | TTGGAAATATACAGCTCTGTG 1259 | ACTA_ | |
| | | | CACAGAGC ATTTCCAA | | |
| | | | | | |
| | | | GTGTCTCG TAAAGGTT | | |
| | | | ACATA | | |
| GAM170 | KCNJ5 | 5' | GAAATTAATCTCTGGGGAA 784 | A CAC | |
| | | | TTCC CAGAG TAATTTC | | |
| | | | | | |
| | | | AAGG GTCTC ATTAAAG | | |
| | | | G TA_ | | |
| GAM170 | MEF2A | 3' | GAGAAAATGCTTTGTAGAA 1228 | C CTAA | |
| | | | TTC ACAGAGCA TTTC | | |
| | | | | | |
| | | | AAG TGTTCGT AGAG | | |
| | | | A AAA_ | | |
| GAM170 | MIR16 | 3' | GGAAACTAACTCTGTGGAA 1704 | CAC A | |
| | | | TTCCACAGAG TA TTTCC | | |
| | | | | | |
| | | | AAGGTGTCTC AT AAAGG | | |
| | | | AA_ C | | |
| GAM170 | P4HB | 3' | TTGAAAATTCCGTCTGTGGGA 787 | G ACT C | |
| | | | TTCCACAGA C AATTT CAA | | |
| | | | | | |
| | | | AGGGTGTCT G TTAAA GTT | | |
| | | | _CC_ A | | |
| GAM170 | RAF1 | 3' | TTGGAATCAGCTTCTGGAGGA 3168 | A_ CA A | |
| | A | | TTCC CAGAG CT ATTTCCAA | | |
| | | | | | |
| | | | AAGG GTCTT GA TAAAGGTT | | |
| | | | AG C_ C | | |
| GAM170 | RPS6KA5 | 3' | TTGGAATTTTTCTGTTGAA 1153 | C CACT | |
| | | | TTC ACAGAG AATTTCCAA | | |
| | | | | | |

AAG TGTCTT TTAAAGGTT
 T T__
 GAM170 TBL1X 3' GAAATGGCCTGTGGAA 1233 A ACTA
 TTCCACAG GC ATTC
 ||||| || ||||
 AAGGTGTC CG TAAAG
 _ G__
 GAM170 ARHGAP10 5' GGAGCCTGCTTGTGGAA 1926 G CTAAT
 TTCCACA AGCA TTCC
 ||||| ||| ||||
 AAGGTGT TCGT GAGG
 _ CC__
 GAM170 ATP9A 3' TTGGAAATCAGTCTGT 2619 GCA A
 ACAGA CT ATTTCCAA
 |||| || |||||
 TGTCT GA TAAAGGTT
 _ C
 GAM170 Di-Ras2 3' TTGGAAATATGTTCCCTGGAA 1725 CA CTA
 TTCCA GAGCA ATTTCCAA
 |||| |||| |||||
 AAGGT CTTGT TAAAGGTT
 C_ A__
 GAM170 FHOD2 3' GAGAACGATGCTCTGTGAGA 2981 _ CTAA
 TC CACAGAGCA TTTC
 || ||||| ||||
 AG GTGTCTCGT AGAG
 A AGCA
 GAM170 FLJ10704 3' TTGGAAATTAGTGTTATCTGGA 1795 CAG
 A TTCCA AGCACTAATTTCCAA
 |||| |||||
 AAGGT TTGTGATTAAAGGTT
 CTA
 GAM170 FLJ12085 3' TTGGAAATTATGCACTTTG 2006 C A C
 CA AG GCA TAATTTCCAA
 || || || |||||
 GT TC CGT ATTAAGGTT
 T A _
 GAM170 FLJ20209 3' AGATTGGTTGCTCTGGAA 3351 CA _
 TTCCA GAGCA CTAATT
 |||| |||| |||||
 AAGGT CTCGT GGTTAGA
 _ T
 GAM170 FLJ22174 5' TTGGAAATTGAAGCTGTAGAG 1969 C AGCAC
 TTC ACAG TAATTTCCAA
 || ||| |||||
 GAG TGTC GTTAAAGGTT
 A GAA__
 GAM170 HSPC129 3' TTGGAAATTAAAGGTGGA 1685 AGAGCAC
 TCCAC TAATTTCCAA
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|--------|----------|----|------------------------|------------------|-------|--------|
| | | | AGGTG | ATTAAGGTT | | |
| | | | GAA_____ | | | |
| GAM170 | KIAA0632 | 3' | GGCCCCCAGTGCTCTGTGGGA | 1634 | | AATTT |
| | | | TTCCACAGAGCACT | CC | | |
| | | | | | | |
| | | | AGGGTGTCTCGTGA | GG | | |
| | | | CCCCC | | | |
| GAM170 | KIAA1184 | 3' | TTGGAAATCAGAAGTCTGTGAG | 1994 | _ | GCA A |
| | A | | TC CACAGA | CT ATTTCCAA | | |
| | | | | | | |
| | | | AG GTGTCT | GA TAAAGGTT | | |
| | | | A | GAA C | | |
| GAM170 | KIAA1671 | 3' | GAAATCAGTGTGTGGAG | 2725 | GA | A |
| | | | TTCCACA | GCACT ATTTC | | |
| | | | | | | |
| | | | GAGGTGT | TGTGA TAAAG | | |
| | | | _ | C | | |
| GAM170 | KIAA1728 | 3' | TGGTAGTGCTCCTGGAA | 2818 | CA | ATTT |
| | | | TTCCA | GAGCACTA CCA | | |
| | | | | | | |
| | | | AAGGT | CTCGTGAT GGT | | |
| | | | C_ | _____ | | |
| GAM170 | KIAA1737 | 3' | TTGGAAAAACCTCTGTGGAG | 2789 | | CACTAA |
| | | | TTCCACAGAG | TTTCCAA | | |
| | | | | | | |
| | | | GAGGTGTCTC | AAAGGTT | | |
| | | | CCAA_ | | | |
| GAM170 | KIAA1750 | 3' | ATTGGAAATTGTTGCTGTGTTC | 2811 | _____ | |
| | TGTG | | CAGAGCAC | TAATTTCCAA | T | |
| | | | | | I | |
| | | | GTCTTGTG | GTTAAAGGTT | A | |
| | | | TCGTT | | | |
| GAM170 | KIAA1900 | 3' | TGGAACATGTTGTGGAA | 2972 | GA | CTAA |
| | | | TTCCACA | GCA TTTCCA | | |
| | | | | | | |
| | | | AAGGTGT | TGT AAAGGT | | |
| | | | _ | AC_ | | |
| GAM170 | KIAA1946 | 3' | AAGTTAGTGCTCTGCTGAA | 3246 | CA | |
| | | | TTC | CAGAGCACTAATTT | | |
| | | | | | | |
| | | | AAG | GTCTCGTGATTGAA | | |
| | | | TC | | | |
| GAM170 | LALP1 | 3' | AAATGAATGGTCTGTGGAA | 1915 | G | CTA |
| | | | TTCCACAGA | CA ATTT | | |
| | | | | | | |
| | | | AAGGTGTCT | GT TAAA | | |
| | | | G | AAG | | |
| GAM170 | LRRFIP2 | 3' | TTGGAAATCTGCCTGCAGA | 1743 | CA | A CTA |
| | | | TC | CAG GCA ATTTCCAA | | |
| | | | | | | |

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|--------|---------|----|----------------------------|----------|-------|
| | | | AG GTC CGT TAAAGGTT | | |
| | | | AC _ C__ | | |
| GAM170 | MGC1842 | 3' | TGGCAGCAGTGCTCTGGGAA 2724 | A | AATTT |
| | | | TTCC CAGAGCACT CCA | | |
| | | | | | |
| | | | AAGG GTCTCGTGA GGT | | |
| | | | _ CGAC_ | | |
| GAM170 | MGC9753 | 5' | TGGCCTGGTGCCTGTGGAA 2333 | A | ATTT |
| | | | TTCCACAG GCACTA CCA | | |
| | | | | | |
| | | | AAGGTGTC CGTGGT GGT | | |
| | | | _ CC_ | | |
| GAM170 | PEG10 | 3' | GAATTGGTCTGTGGAA 1606 | GCA | |
| | | | TTCCACAGA CTAATTT | | |
| | | | | | |
| | | | AAGGTGTCT GGTAAAG | | |
| | | | _____ | | |
| GAM170 | PGRMC2 | 3' | TTGGAAATTAGGAGAAGGAA 1287 | ACAGAGCA | |
| | | | TTCC CTAATTTCCAA | | |
| | | | | | |
| | | | AAGG GATTAAAGGTT | | |
| | | | AAGAG__ | | |
| GAM170 | PPP4R1L | 5' | GGAAAGCCCTGTGGAA 3139 | A | ACTAA |
| | | | TTCCACAG GC TTTCC | | |
| | | | | | |
| | | | AAGGTGTC CG AAAGG | | |
| | | | C _____ | | |
| GAM170 | PRO0386 | 5' | GAAC TAATGTTCTGTGGAA 1843 | C | A |
| | | | TTCCACAGAGCA TA TTT | | |
| | | | | | |
| | | | AAGGTGTCTTGT AT AAG | | |
| | | | A C | | |
| GAM170 | PRO0456 | 3' | TGGAATTCATACTCTGTGGAA 1476 | CACTAAT | |
| | | | TTCCACAGAG TTCCA | | |
| | | | | | |
| | | | AAGGTGTCTC AAGGT | | |
| | | | ATACTT_ | | |
| GAM170 | SLC26A8 | 5' | AGTCAGTATCTGTGGAA 2455 | GC | A |
| | | | TTCCACAGA ACT ATT | | |
| | | | | | |
| | | | AAGGTGTCT TGA TGA | | |
| | | | A_ C | | |
| GAM170 | SNTG1 | 5' | TTGGAAATAGCTTTGTG 1867 | ACTA | |
| | | | CACAGAGC ATTTCCAA | | |
| | | | | | |
| | | | GTGTTTCG TAAAGGTT | | |
| | | | A__ | | |
| GAM170 | ZNF396 | 3' | TTGGAAATAAGTCAATGGAA 3034 | CA | GCA A |
| | | | TTCCA GA CT ATTTCCAA | | |
| | | | | | |

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|--------|--------------|-----------------------------|------------|--|
| | | AAGGT CT GA TAAAGGTT | | |
| | | AA ____ A | | |
| GAM170 | LOC145098 5' | TTGGAAATATCTTCTGTG 3074 | CACTA | |
| | | CACAGAG ATTTCCAA | | |
| | | | | |
| | | GTGTCTT TAAAGGTT | | |
| | | CTA__ | | |
| GAM170 | LOC146136 5' | GAAAAGGCCTCTGTGGAG 2964 | CA AA | |
| | | TTCCACAGAG CT TTTC | | |
| | | | | |
| | | GAGGTGTCTC GA AAAG | | |
| | | CG ____ | | |
| GAM170 | LOC148195 3' | GGAAGGCATCCTGTGGAA 3298 | A__ A AATT | |
| | | TTCCACAG GC CT TCC | | |
| | | | | |
| | | AAGGTGTC CG GA AGG | | |
| | | CTA _ ____ | | |
| GAM170 | LOC149086 5' | TGGAGATGATCCGTGGAA 3306 | A GCACTA | |
| | | TTCCAC GA ATTTCCA | | |
| | | | | |
| | | AAGGTG CT TAGAGGT | | |
| | | C AG ____ | | |
| GAM170 | LOC149420 3' | TTGGAAATTAGAGGTGGAA 3133 | AGAGCA | |
| | | TTCCAC CTAATTTCCAA | | |
| | | | | |
| | | AAGGTG GATTAAAGGTT | | |
| | | GA ____ | | |
| GAM170 | LOC149912 5' | TGGAAAGTGCTCTGTGG 3317 | AAT | |
| | | CCACAGAGCACT TTCCA | | |
| | | | | |
| | | GGTGTCTCGTGA AAGGT | | |
| | | ____ | | |
| GAM170 | LOC151816 5' | GGAGTGTGCTCTGGGAA 3350 | A TAAT | |
| | | TTCC CAGAGCAC TTCC | | |
| | | | | |
| | | AAGG GTCTCGTG GAGG | | |
| | | _ T ____ | | |
| GAM170 | LOC152991 5' | GAAATGGGTCATACTCTGTGGA 3365 | C__ A | |
| | | TCCACAGAG ACT ATTTT | | |
| | | | | |
| | | AGGTGTCTC TGG TAAAG | | |
| | | ATAC G | | |
| GAM170 | LOC157556 3' | TGGAGGGGTGCTCTGTGGAA 3382 | AA | |
| | | TTCCACAGAGCACT TTTCCA | | |
| | | | | |
| | | AAGGTGTCTCGTGG GGAGGT | | |
| | | ____ | | |
| GAM170 | LOC157697 5' | AAATCTTGTGCTCTGCGAA 3204 | CA TA_ | |
| | | TTC CAGAGCAC ATTT | | |
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|--------|--------------|-----------------------------|--------|----------|
| | | AAG GTCTCGTG TAAA | | |
| | | C_ TTC | | |
| GAM170 | LOC158431 3' | TGGAAATTGTTTCTGTAGAA 3390 | C | C T |
| | | TTC ACAGAG AC AATTCCA | | |
| | | | | |
| | | AAG TGTCTT TG TTAAAGGT | | |
| | | A _ _ | | |
| GAM170 | LOC200488 5' | GAAATGAGTCTGTGGGA 3478 | GCA | A |
| | | TTCCACAGA CT ATTTC | | |
| | | | | |
| | | AGGGTGTCT GA TAAAG | | |
| | | ___ G | | |
| GAM170 | LOC220565 3' | GAAAAGGCCTCTGTGGAG 3494 | CA | AA |
| | | TTCCACAGAG CT TTTC | | |
| | | | | |
| | | GAGGTGTCTC GA AAAG | | |
| | | CG _ | | |
| GAM170 | LOC221751 5' | TTGGAAATTGAAGCTGTAGAG 3552 | C | AGCAC |
| | | TTC ACAG TAATTTCCAA | | |
| | | | | |
| | | GAG TGTC GTTAAAGGTT | | |
| | | A GAA__ | | |
| GAM170 | LOC253978 5' | TTGGAATCTGTGCTTTGCAGAA 3743 | CA | TAAT |
| | | TTC CAGAGCAC TTCCAA | | |
| | | | | |
| | | AAG GTTTCGTG AAGGTT | | |
| | | AC TCT_ | | |
| GAM170 | LOC257319 3' | GAAATTAATCCTTTGTGG 3683 | CAC | |
| | | CCACAGAG TAATTTC | | |
| | | | | |
| | | GGTGTTC ATTAAAG | | |
| | | CTA | | |
| GAM170 | LOC92162 5' | GGAGGCGCCTGTGGAA 2816 | A A | AATT |
| | | TTCCACAG GC CT TCC | | |
| | | | | |
| | | AAGGTGTC CG GG AGG | | |
| | | _ C _ | | |
| GAM170 | LOC92391 3' | GGAACAGCTCTGTGGAA 2842 | ACTAAT | |
| | | TTCCACAGAGC TTCC | | |
| | | | | |
| | | AAGGTGTCTCG AAGG | | |
| | | AC__ | | |
| GAM171 | BACH2 3' | CCGTGTTGGCCCCAGCCACG 1963 | CA | ACAA AA_ |
| | | CG GC TG CCAACACGG | | |
| | | | | |
| | | GC CG AC GGTTGTGCC | | |
| | | AC _ CCC | | |
| GAM171 | NCL 3' | CGTGTGTTGTTTGGACTG 2552 | _ | CAAT |
| | | CAG CA GAACCAACACG | | |
| | | | | |

GTC GT TTTGGTTGTGC
 A ____
 GAM171 NEO1 3' CGTGTCTTTGTGCTGTG 932 T ACCAA
 CGCAGCACAA GA CACG
 ||||| || |||
 GTGTCGTGTT CT GTGC
 T ____
 GAM171 SLC21A3 3' CTGTTGGTGTGCTGC 1183 AATGA C
 GCAGCAC ACCAACA G
 ||||| ||||| |
 CGTCGTG TGGTTGT C
 ____ A
 GAM171 UGCG 5' CCGTGTTGGCGGCCGCAGCGG 1012 A ACAA AA
 CCGC GC TG CCAACACGG
 ||| || || |||||
 GGCG CG GC GGTGTGCGC
 A CCG_ _
 GAM171 MGC3101 3' CCGCGTTTTCTGTGCTGC 2047 AT CC A
 GCAGCACA GAA AAC CGG
 ||||| ||| ||| |||
 CGTCGTGT CTT TTG GCC
 C_ _ C
 GAM171 MGC3413 3' CCATGTTAGTGCTACATTGTGC 2269 A_ _ C C
 GCACAATG AC AACA GG
 ||||| || ||| ||
 CGTGTTAC TG TTGT CC
 ATCG A A
 GAM171 LOC151568 5' CCGTGTTGGCCTTGGCTAGG 2444 GC A TGAA
 CC AGC CAA CCAACACGG
 || ||| ||| |||||
 GG TCG GTT GGTGTGCGC
 A_ _ CC_
 GAM171 LOC152765 5' GTGTGTCTTGTGCTGC 3175 T ACCA
 GCAGCACAA GA ACAC
 ||||| || |||
 CGTCGTGTT CT TGTG
 _ G_
 GAM171 LOC158314 5' CCACCCTTCACTGTGCTGCGG 3387 A CCAACAC
 CCGCAGCACA TGAA GG
 ||||| ||| ||| ||
 GGCGTCGTGT ACTT CC
 C CCCA_
 GAM171 LOC57086 3' CTGTTGGTGTGCTGC 1914 AATGA C
 GCAGCAC ACCAACA G
 ||||| ||||| |
 CGTCGTG TGGTTGT C
 ____ A
 GAM172 ABCE1 3' TTGACATTTGATAAATAAACAT 2533 A A CATC
 CA C ATGT TATTTATC GTCAA
 | ||| ||||| |||||

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|--------|-----------|----|-----------------------------|-------|--------|
| | | | A TACA ATAAATAG CAGTT | | |
| | | | C A TTTA | | |
| GAM172 | DMC1 | 3' | TGATTTATGATAACTATACATT 1356 | T | CATC |
| | G | | CAATGTATA TTATC GTCA | | |
| | | | | | |
| | | | GTTACATAT AATAG TAGT | | |
| | | | C TATT | | |
| GAM172 | PHEMX | 3' | GTGGTCAAATATACATCA 2467 | A | AT |
| | | | C ATGTATATTT CCAT | | |
| | | | | | |
| | | | A TACATATAAA GGTG | | |
| | | | C CT | | |
| GAM172 | PHEMX | 3' | GTGGTCAAATATACATCA 2468 | A | AT |
| | | | C ATGTATATTT CCAT | | |
| | | | | | |
| | | | A TACATATAAA GGTG | | |
| | | | C CT | | |
| GAM172 | PHEMX | 3' | GTGGTCAAATATACATCA 2469 | A | AT |
| | | | C ATGTATATTT CCAT | | |
| | | | | | |
| | | | A TACATATAAA GGTG | | |
| | | | C CT | | |
| GAM172 | PHEMX | 3' | GTGGTCAAATATACATCA 1237 | A | AT |
| | | | C ATGTATATTT CCAT | | |
| | | | | | |
| | | | A TACATATAAA GGTG | | |
| | | | C CT | | |
| GAM172 | H-L(3)MBT | 3' | ACGATGGGGATACATT 1632 | ATTTA | |
| | | | AATGTAT TCCATCGT | | |
| | | | | | |
| | | | TTACATA GGGTAGCA | | |
| | | | G____ | | |
| GAM172 | KIAA0979 | 3' | GGTGGGATCAACATACATTG 1602 | A T _ | |
| | | | CAATGTAT TT ATCC ATC | | |
| | | | | | |
| | | | GTTACATA AA TAGG TGG | | |
| | | | C C G | | |
| GAM172 | LOC220672 | 3' | TTGACATTTGATAAATAACAT 2566 | A A | CATC |
| | CA | | C ATGT TATTTATC GTCAA | | |
| | | | | | |
| | | | A TACA ATAAATAG CAGTT | | |
| | | | C A TTTA | | |
| GAM172 | LOC257336 | 5' | TTGAAAAAATAAATGTACATT 3694 | | CCATCG |
| | | | AATGTATATTTAT TCAA | | |
| | | | | | |
| | | | TTACATGTAAATA AGTT | | |
| | | | AAAAA_ | | |
| GAM173 | MGC16169 | 3' | AGCACCAACAGCACAGTTCTTC 2312 | C__ _ | TAACAA |
| | A | | TGAAGAGC GC GTT TGCT | | |
| | | | | | |

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|--------|---------------|-----------------------------|------------|
| | | ACTTCTTG CG CAA ACGA | |
| | | ACA A CC_____ | |
| GAM173 | LOC151414 3' | AGCATTA AAAACGAGCTCT 3156 | C ____ AAC |
| | | TCA TGAAGAGC GC GTTT AATGCT | |
| | | | |
| | | ACTTCTCG CG CAAA TTACGA | |
| | | A AC AA_ | |
| GAM173 | LOC153817 5' | AGCATTGTAAAGTCTCTCTTC 2591 | CC G |
| | | A TGAAGAG GC TTTAACAATGCT | |
| | | | |
| | | ACTTCTC TG AAATTGTTACGA | |
| | | TC _ | |
| GAM173 | LOC51145 3' | AGCTGCAAAAACGAGCTCTTCA 1665 | CG AACAAT |
| | | TGAAGAGC CGTTT GCT | |
| | | | |
| | | ACTTCTCG GCAAA CGA | |
| | | A_ AACGT_ | |
| GAM174 | ENAM 5' | CAAAGGCAAGCTAACAAAGTTC 2215 | ACTAAT C |
| | | AA TTGAATTT CTTGCC TTG | |
| | | | |
| | | AACTTGAA GAACGG AAC | |
| | | ACAATC A | |
| GAM174 | DOCK3 3' | CAAGGACAAGGAGAATGAATTC 2750 | CTAA C |
| | | AA TTGAATTTA TCTTG CCTTG | |
| | | | |
| | | AACTTAAGT GGAAC GGAAC | |
| | | AAGA A | |
| GAM174 | GAPCENA 3' | AAGGGATCAGAAATTCAA 1412 | A AATCTTG |
| | | TTGAATTT CT CCCTT | |
| | | | |
| | | AACTTAAA GA GGGAA | |
| | | _ CTA_____ | |
| GAM175 | HNRPA2B1 3' | ATTTTGTGAATGGATTGGA 902 | G AGC |
| | | TCCAATC CAT TATAAAAT | |
| | | | |
| | | AGGTTAG GTA GTGTTTTA | |
| | | _ A_ | |
| GAM175 | HNRPA2B1 3' | ATTTTGTGAATGGATTGGA 2186 | G AGC |
| | | TCCAATC CAT TATAAAAT | |
| | | | |
| | | AGGTTAG GTA GTGTTTTA | |
| | | _ A_ | |
| GAM175 | bA430M15.1 3' | TATTTTATTACAGATTGGA 3073 | GCATAGCT |
| | | TCCAATC ATAAAAATA | |
| | | | |
| | | AGGTTAG TATTTTAT | |
| | | ACAT_____ | |
| GAM175 | LOC146481 3' | CTATTTTATAGCCACCCAGGTA 3092 | A GCATA_ |
| | | GG CC ATC GCTATAAAATAG | |
| | | | |

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|--------|-----------|----|----------------------------|--------|------|
| | | | GG TGG CGATATTTTATC | | |
| | | | A ACCCAC | | |
| GAM176 | LOC146229 | 3' | ACAGCAATCAAAACATCAA 3087 | GC | T |
| | | | TTGATGTTTTG TGCT GT | | |
| | | | | | |
| | | | AACTACAAAAC ACGA CA | | |
| | | | TA _ | | |
| GAM177 | FLJ20413 | 3' | ATAGACGAAAATCAACT 1753 | AT | |
| | | | AGTT ATTTTCGTCTAT | | |
| | | | | | |
| | | | TCAA TAAAAGCAGATA | | |
| | | | C_ | | |
| GAM178 | CRP | 3' | AGAAAATAACACCCAGAAAGG 2920 | GAA_ | ATAC |
| | AG | | CTCT TGG TAGTTTTCT | | |
| | | | | | |
| | | | GAGG ACC ATCAAAAGA | | |
| | | | AAAG CACA | | |
| GAM178 | DBY | 3' | AAAACAGCAGCCCTATTCAGA 1140 | ATA__ | A |
| | | | TCTGAATGG CT GTTTT | | |
| | | | | | |
| | | | AGACTTATC GA CAAAA | | |
| | | | CCGAC _ | | |
| GAM178 | ERBB2 | 3' | AAAGCGACCCATTTCAGAGA 1115 | ATACTA | |
| | | | TCTCTGAATGG GTTTT | | |
| | | | | | |
| | | | AGAGACTTACC CGAAA | | |
| | | | CAG__ | | |
| GAM178 | ITGA1 | 3' | AGAACATGTATTCATCCAGA 2660 | A | TA |
| | | | TCTG ATGGATAC GTTTT | | |
| | | | | | |
| | | | AGAC TACTTATG CAAGA | | |
| | | | C TA | | |
| GAM178 | MS4A1 | 3' | AGAAAATAAGTATCCATCAGAG 710 | A | A |
| | A | | TCTCTGA TGGATACT GTTTTCT | | |
| | | | | | |
| | | | AGAGACT ACCTATGA TAAAAGA | | |
| | | | _ A | | |
| GAM178 | ARSDR1 | 3' | AAAACAATTCTTCATTCAGA 1656 | TACTA | |
| | | | TCTGAATGGA GTTTT | | |
| | | | | | |
| | | | AGACTTACTT CAAAA | | |
| | | | CTTAA | | |
| GAM178 | ATP1B4 | 3' | AAACTAGTATGTGGAAAG 1400 | GAA | G |
| | | | CT TG ATACTAGTTTT | | |
| | | | | | |
| | | | GA GT TATGATCAAAA | | |
| | | | AAG G | | |
| GAM178 | FLJ00024 | 3' | AGAAAACCGTCCATTTAGA 2665 | ACTA | |
| | | | TCTGAATGGAT GTTTTCT | | |
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AGATTTACCTG CAAAAGA
      C__
GAM178 FLJ10493 3' AAAGCATATCCGTTCA 1782 CTA
      TGAATGGATA GTTTT
      ||||| |||
      ACTTGCCTAT CGAAA
      A__
GAM178 FLJ11175 3' AGACTAACATCCATTCTGA 1816 T AC
      TC GAATGGAT TAGTTT
      || ||||| |||||
      AG CTTACCTA ATCAGA
      T CA
GAM178 KIAA0977 3' AGAAAACTAGTGATACCA 1578 A__
      TGG TACTAGTTTTCT
      ||| |||||
      ACC GTGATCAAAAGA
      ATA
GAM178 TRIP3 3' AGAAAACTTGACATTCAGATGA 3102 _ GATACT
      TC TCTGAATG AGTTTTCT
      || ||||| |||||
      AG AGACTTAC TCAAAAGA
      T AGT__
GAM178 LOC149117 3' AAAACTTTATCCATTGAGA 3307 G CT
      TCT AATGGATA AGTTTT
      ||| ||||| |||||
      AGA TTACCTAT TCAAAA
      G T_
GAM178 LOC196993 5' AGAAAACTTTCCATTC 3471 TACT
      GAATGGA AGTTTTCT
      ||||| |||||
      CTTACCT TCAAAAGA
      T__
GAM178 LOC56965 5' AGAACTCTGTATCCATCAGAGA 1900 A T TT
      TCTCTGA TGGATAC AG TTCT
      ||||| ||||| || |||
      AGAGACT ACCTATG TC AAGA
      _ _ TC
GAM179 NUMA1 3' AGTCACTTCTCCATCACA 3604 A A
      TGTGATGGA AA TGA CT
      ||||| || |||||
      ACACTACCT TT ACTGA
      C C
GAM179 SLC15A1 3' ATTGGTCATCTTCCCTATCACA 1182 A_ A
      TGTGATGG AA ATGACTAAT
      ||||| || |||||
      ACACTATC TT TACTGGTTA
      CC C
GAM179 CNOT3 5' AAAATTCAGTTCCTCCATTACA 1505 AAAAT _
      TGTGATGGA GACT AATTTT
      ||||| ||| |||||

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ACATTACCT TTGA TTAAAA
CC__ C
GAM179 FLJ10898 5' AGTCATTTCTCCATCACA 2527 A
TGTGATGGA AAATGACT
||||||| |||||||
ACACTACCT TTTACTGA
C
GAM179 FLJ14686 3' AAAATTAGTTGTTACCTCCTCA 2286 T AA_ TG
CA TGTGA GGA AA ACTAATTTT
||||| || || |||||||
ACACT CCT TT TGATTAAAA
_ CCA GT
GAM179 HDAC9-PENDING 3' AAAATTGTATATTTTTTCCATC 1526 T TG__ T
TCA TG GATGGAAAAA AC AATTTT
|| ||||||| || |||||
AC CTACCTTTTT TG TTAAAA
T TATA _
GAM179 ZAK 3' GGTCACCTTCCCATCACA 2427 A A
TGTGATGG AAA TGA CT
||||||| || |||||
ACATTACC TTT ACTGG
C C
GAM179 LOC119548 5' TGGGCCATTTTTCCACAACA 2984 GA A_
TGT TGGAAAAATG CTA
||| ||||||| |||
ACA ACCTTTTTTAC GGT
AC CG
GAM179 LOC153937 5' AAAATGCAGTTTTTCTTCACA 3185 T GACTA
TGTGA GGAAAAAT ATTTT
||||| ||||||| |||||
ACACT CCTTTTTG TAAAA
T ACG__
GAM179 LOC221895 3' GGTACTTTTCTCATCACA 3568 _ ATG
TGTGATG GAAAA ACT
||||||| ||||| |||
ACACTAC CTTTT TGG
T CA_
GAM180 BLNK 5' GACGTGACCACTGGACAGTTAT 1441 ATTTTTAA
T GATAACTGT TCACGTC
||||||| |||||||
TTATTGACA AGTGCAG
GGTCACC_
GAM180 FLJ20152 3' GACAGGAAGAAAAATACAGTTA 1870 AA AC
TAACTGTATTTTT TC GTC
||||||||| || |||
ATTGACATAAAAA AG CAG
GA GA
GAM181 BTG2 3' GAAAAGACAAAGGTTAC 1330 AA C
GTGA CTTTGTC TTTC
||| ||||||| |||||

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|--------|---------|----|-----------------------------|-----------|--|
| | | | CATT GAAACAG AAAG | | |
| | | | G_ A | | |
| GAM181 | CELSR2 | 3' | GGAAAGGACAAAGCCACA 826 | AAA | |
| | | | TGTG CTTTGTCTTTCC | | |
| | | | | | |
| | | | ACAC GAAACAGGAAAGG | | |
| | | | C_ | | |
| GAM181 | GAB2 | 3' | AAAGGACAAGGACATGAG 1424 | GAAA | |
| | | | TTCATGT CTTTGTCTTT | | |
| | | | | | |
| | | | GAGTACA GGAACAGGAAA | | |
| | | | _____ | | |
| GAM181 | GAB2 | 3' | AAAGGACAAGGACATGAG 2375 | GAAA | |
| | | | TTCATGT CTTTGTCTTT | | |
| | | | | | |
| | | | GAGTACA GGAACAGGAAA | | |
| | | | _____ | | |
| GAM181 | GOLGA4 | 5' | AGAGTTTGAAATCTTCACATGA 2553 | AC_ TC | |
| | A | | TTCATGTGAA TTTG CTTT | | |
| | | | | | |
| | | | AAGTACACTT AAGT GAGA | | |
| | | | CTA TT | | |
| GAM181 | MEF2D | 3' | GAAAAGACAAAGTCCTCG 3721 | A_ C | |
| | | | TGA ACTTTGTC TTTC | | |
| | | | | | |
| | | | GCT TGAAACAG AAAG | | |
| | | | CC A | | |
| GAM181 | NEBL | 5' | AAAGGACGCCACATGAG 1294 | AAACTT | |
| | | | TTCATGTG TGTCCTTT | | |
| | | | | | |
| | | | GAGTACAC GCAGGAAA | | |
| | | | C_ | | |
| GAM181 | PCSK1 | 3' | GAAAATATGATGTTTCACAT 743 | T TG CC | |
| | | | ATGTGAAAC T T TTTC | | |
| | | | | | |
| | | | TACACTTTG A A AAAG | | |
| | | | T GT TA | | |
| GAM181 | PRKAR2B | 3' | GGAAAAGAGAGCTCTCTACATG 951 | AAACT G C | |
| | AA | | TTCATGTG TT TC TTTC | | |
| | | | | | |
| | | | AAGTACAT GA AG AAAGG | | |
| | | | CTCTC G A | | |
| GAM181 | SCGB3A2 | 3' | AAAGGACAAATAAGCAATGAA 2361 | _ GAAAC | |
| | | | TTCAT GT TTTGTCTTT | | |
| | | | | | |
| | | | AAGTA CG AAACAGGAAA | | |
| | | | A AAAT_ | | |
| GAM181 | SMP1 | 3' | AGAGGAAACTTTTCACATGAA 1490 | CTTTG | |
| | | | TTCATGTGAAA TCCTTT | | |
| | | | | | |

| | | | | | |
|--------|----------|----|-----------------------------|-----------|------|
| | | | AAGTACACTTT AGGAGA | | |
| | | | CAA__ | | |
| GAM181 | SYNGR1 | 3' | GGAAAAAAGGTTTCACAT 1147 | G__ | |
| | | | ATGTGAAACTTT TCC | | |
| | | | | | |
| | | | TACACTTTGGAA AGG | | |
| | | | AAA | | |
| GAM181 | TGFA | 3' | GGAAACTGTTTAATATCACATG 1001 | _____ | TTTG |
| | AA | | TTCATGTGA AAC TCC | | |
| | | | | | |
| | | | AAGTACACT TTG AGG | | |
| | | | ATAAT TCAA | | |
| GAM181 | ACAA2 | 5' | GGCAAAGTCTCACCTGAA 3540 | T A | |
| | | | TTCA GTGA ACTTTGTC | | |
| | | | | | |
| | | | AAGT CACT TGAAACGG | | |
| | | | C C | | |
| GAM181 | C1orf34 | 3' | AAAGGACAAAGCCTCAGGGAA 2576 | ATG AA | |
| | | | TTC TGA CTTTGTCTTT | | |
| | | | | | |
| | | | AAG ACT GAAACAGGAAA | | |
| | | | GG_ CC | | |
| GAM181 | CAMKK2 | 3' | GGAAAGGACCTGCCCCACATGA 1310 | AAACTTT | |
| | A | | TTCATGTG GTCCTTTCC | | |
| | | | | | |
| | | | AAGTACAC CAGGAAAGG | | |
| | | | CCCGTC_ | | |
| GAM181 | FLJ10849 | 3' | GAAAGGATAACATTTCTCATGA 1803 | T CT | |
| | A | | TTCATG GAAA TTGTCCTTTC | | |
| | | | | | |
| | | | AAGTAC CTTT AATAGGAAAG | | |
| | | | T AC | | |
| GAM181 | FLJ13262 | 3' | GGAATAAATTTACATGAA 2112 | C _ | |
| | | | TTCATGTGAAA TTTGT CC | | |
| | | | | | |
| | | | AAGTACACTTT AAATA GG | | |
| | | | _ A | | |
| GAM181 | FLJ21977 | 5' | GGACAAAGCTCACATGAA 2237 | AA | |
| | | | TTCATGTGA CTTTGTCC | | |
| | | | | | |
| | | | AAGTACACT GAAACAGG | | |
| | | | C_ | | |
| GAM181 | FLJ22301 | 3' | GAAAGCTCACTTCCATGAA 2095 | T ACTT TC | |
| | | | TTCATG GAA TG CTTTC | | |
| | | | | | |
| | | | AAGTAC CTT AC GAAAG | | |
| | | | _ C__ TC | | |
| GAM181 | HERC1 | 3' | GAAAGGACAGTTTTACATGAA 1071 | TT | |
| | | | TTCATGTGAAACT GTCCTTTC | | |
| | | | | | |

AAGTACATTTTGA CAGGAAAG

GAM181 KIAA0280 3' AAAGGAATCACATGAA 3536 AACTTTG
TTCATGTGA TCCTTT
||||||| |||||
AAGTACACT AGGAAA

A_____

GAM181 KIAA0391 3' GAAAAGATAATTACTTACATGA 1517 AACT C
A TTCATGTGA TTGTC TTTC
||||||| ||||| |||||
AAGTACATT AATAG AAAG

CATT A

GAM181 PRO1386 3' GAAAAAACAAAGTTCTGCATGA 2188 GA CC
G TTCATGT AACTTTGT TTTC
||||||| ||||| |||||
GAGTACG TTGAAACA AAAG

TC AA

GAM181 RBMS1 3' GAAAGGTGTTCTTACATGAA 1711 _ TTTGT
TTCATGTGA AAC CCTTTC
||||||| ||||| |||||
AAGTACATT TTG GGAAAG

C T_____

GAM181 RBMS1 3' GAAAGGTGTTCTTACATGAA 1712 _ TTTGT
TTCATGTGA AAC CCTTTC
||||||| ||||| |||||
AAGTACATT TTG GGAAAG

C T_____

GAM181 RBMS1 3' GAAAGGTGTTCTTACATGAA 1713 _ TTTGT
TTCATGTGA AAC CCTTTC
||||||| ||||| |||||
AAGTACATT TTG GGAAAG

C T_____

GAM181 RBMS1 3' GAAAGGTGTTCTTACATGAA 970 _ TTTGT
TTCATGTGA AAC CCTTTC
||||||| ||||| |||||
AAGTACATT TTG GGAAAG

C T_____

GAM181 ROBO2 5' AAAAGACAAAGTTCGAATTGA 2635 TG_ A C
TCA TGAA CTTTGTCT TTT
||| ||| ||||| |||||
AGT GCTT GAAACAG AAA

TAA _ A

GAM181 SGP28 3' AAAGAACAATATAATTTTCACA 1270 CT_____ C
TGAA TTCATGTGAAA TTGT CTTT
||||||| ||||| |||||
AAGTACACTTT AACAA GAAA

TAATAT A

GAM181 ST7L 3' AAAGGACAACACTGTAGATGAA 1746 G AAAC
TTCAT TG TTGTCCTTT
||||| ||||| |||||

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|--------|-----------|----|-----------------------------|-----------|
| | | | AAGTA AT AACAGGAAA | |
| | | | G GTC__ | |
| GAM181 | ST7L | 3' | AAAGGACAACACTGTAGATGAA 2456 | G AAAC |
| | | | TTCAT TG TTGTCCTTT | |
| | | | | |
| | | | AAGTA AT AACAGGAAA | |
| | | | G GTC__ | |
| GAM181 | ST7L | 3' | AAAGGACAACACTGTAGATGAA 2475 | G AAAC |
| | | | TTCAT TG TTGTCCTTT | |
| | | | | |
| | | | AAGTA AT AACAGGAAA | |
| | | | G GTC__ | |
| GAM181 | LOC152263 | 3' | GAAAGGACAAAATAAACACA 3356 | AAAC_ |
| | | | TGTG TTTGTCCTTTC | |
| | | | | |
| | | | ACAC AAACAGGAAAG | |
| | | | AAATA | |
| GAM181 | LOC157507 | 5' | ACAAAGCTATCACATGAA 3202 | AA_ |
| | | | TTCATGTGA CTTTGT | |
| | | | | |
| | | | AAGTACACT GAAACA | |
| | | | ATC | |
| GAM181 | LOC158158 | 3' | GAAAGGACATCTACACCGAA 3211 | AT AAAC |
| | | | TTC GTG TGTCCTTTC | |
| | | | | |
| | | | AAG CAC ACAGGAAAG | |
| | | | C_ ATCT__ | |
| GAM181 | LOC219730 | 3' | GGAAAGGACAAAATGGAGAGTG 3588 | GTGAAAC |
| | A | | TCAT TTTGTCCTTTCC | |
| | | | | |
| | | | AGTG AAACAGGAAAGG | |
| | | | AGAGGTA | |
| GAM181 | LOC255158 | 3' | GAAAAACAAAAAGTTATATAT 3693 | A _ CC |
| | GAA | | TTCATGTG AACTT TGT TTTC | |
| | | | | |
| | | | AAGTATAT TTGAA ACA AAAG | |
| | | | A AA AA | |
| GAM182 | PTPRM | 3' | ATGCAAACTCAACGATC 963 | G _ C |
| | | | GAT CGT GAGT TTGCAT | |
| | | | | |
| | | | CTA GCA CTCA AACGTA | |
| | | | _ A A | |
| GAM182 | HCA4 | 3' | AATGCAAGAAGGAACACATAAG 2450 | CG C GAG_ |
| | TA | | TACT ATG GT TCTTGCATT | |
| | | | | |
| | | | ATGA TAC CA AGAACGTAA | |
| | | | A_ A AGGA | |
| GAM182 | HCA4 | 3' | AATGCAAGAAGGAACACATAAG 3086 | CG C GAG_ |
| | TA | | TACT ATG GT TCTTGCATT | |
| | | | | |

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|--------|------------------|-----------------------------|-----|-----------|
| | | ATGA TAC CA AGAACGTAA | | |
| | | A_ A AGGA | | |
| GAM183 | FLJ13154 3' | ACCAGAAATCTCCACTGTAGT 2070 | ___ | A |
| | | ACTGCA GAGATTCT GT | | |
| | | | | |
| | | TGATGT CTCTAAGA CA | | |
| | | CAC C | | |
| GAM183 | HDAC9-PENDING 3' | ACTAGAATCTCTTAAGTAT 1527 | | GC |
| | | ATACT AGAGATTCTAGT | | |
| | | | | |
| | | TATGA TCTCTAAGATCA | | |
| | | AT | | |
| GAM183 | KIAA0232 3' | TTACTAGCATTGCAGTGTC 2958 | | AGATT |
| | | GATACTGCAG CTAGTAA | | |
| | | | | |
| | | CTGTGACGTT GATCATT | | |
| | | AC___ | | |
| GAM183 | KIAA1010 3' | ACTAGAATCTCTAGAATTTGA 2933 | | TACTGC |
| | | TCGA AGAGATTCTAGT | | |
| | | | | |
| | | AGTT TCTCTAAGATCA | | |
| | | TAAGA_ | | |
| GAM183 | LOC219894 3' | TGCTGTCTCTGCAGTACTGA 3596 | A | TCT |
| | | TCG TACTGCAGAGAT AGTA | | |
| | | | | |
| | | AGT ATGACGTCTCTG TCGT | | |
| | | C ___ | | |
| GAM184 | PABPC4 3' | AATAAAGAAAAAAATCTCCA 1064 | A | AG |
| | | TGGAGA TTTTTTTC TTGTT | | |
| | | | | |
| | | ACCTCT AAAAAAAG AATAA | | |
| | | A A_ | | |
| GAM184 | SH3GL2 3' | GACTGAAAAGAAATTCTCCA 983 | _ | |
| | | TGGAGAATTTTTTT CAGTT | | |
| | | | | |
| | | ACCTCTTAAAGAAA GTCAG | | |
| | | A | | |
| GAM184 | IMP-2 3' | CAAACAAAGAAAAAATTCCACA 1309 | GA | CAG |
| | | TG GAATTTTTTT TTGTTTG | | |
| | | | | |
| | | AC CTAAAAAAG AACAAAC | | |
| | | AC A_ | | |
| GAM184 | KIAA0872 3' | CAAAAGAAAAAAATTCTCC 1593 | _ | AG |
| | | GGAGAATTTTTTT C TTG | | |
| | | | | |
| | | CCTCTTAAAAAAA G AAC | | |
| | | A AA | | |
| GAM184 | MGC19570 5' | CAAACAACCGACTCCTTTCCA 2514 | | ATTTTTT A |
| | | TGGAGA TC GTTGTGTTG | | |
| | | | | |

ACCTTT AG CAACAAAC
 CCTC__ C
 GAM184 PTPN4 3' CAAACAAGGCTCAAAATTCTC 961 TTTCAG
 GAGAATTTT TTGTTTG
 ||||| |||||
 CTCTTAAAA AACAAAC
 CTCGG_
 GAM184 TIX1 5' CAAACAAGTGAAGCTGCA 2604 G AAT
 TG AG TTTTTCAGTTGTTTG
 || || |||||
 AC TC GAAAAAGTCAACAAAC
 G __
 GAM185 PSG5 3' AAAAAACTCCATGTTATTGGAC 955 TC_ AC
 TAA TTAGTTCA ATATGGA TTTT
 ||||| ||||| |||||
 AATCAGGT TGTACCT AAAAA
 TAT CA
 GAM185 FAPP2 3' AAAAAGCTGGTGGTGAAC 2267 ATGGAA
 GTTCATCAT CTTTT
 ||||| |||||
 CAAGTGGTG GAAAAA
 GTC__
 GAM185 LOC145820 3' AAGTGCCACAAAATGAACTAA 3084 CATA A
 TTAGTTCAT TGG ACTT
 ||||| |||||
 AATCAAGTA ACC TGAA
 AAAC G
 GAM185 LOC83690 3' AAAAAGTTGAACAAAGATGAAC 2202 ATATGG_
 TAA TTAGTTCATC AACTTTTT
 ||||| |||||
 AATCAAGTAG TTGAAAAA
 AAACAAG
 GAM186 IGF1 3' TATACTACAGCAGAATGACT 762 A ACG C
 AGTTATTC TG GTAG ATA
 ||||| || |||||
 TCAGTAAG AC CATC TAT
 _ GA_ A
 GAM186 FLJ20035 3' ATGTTCTGTCATGAATACT 1733 T T
 AGT ATTCATGACGG AGCAT
 || ||||| |||||
 TCA TAAGTACTGTC TTGTA
 - -
 GAM186 FXYD3 3' TATGCTACCCTTAATAAC 1966 TCA C
 GTTAT TGA GGTAGCATA
 |||| || |||||
 CAATA ATT CCATCGTAT
 __ C
 GAM186 FXYD3 3' TATGCTACCCTTAATAAC 1263 TCA C
 GTTAT TGA GGTAGCATA
 |||| || |||||

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|--------|--------|----|-----------------------------|---------|--|
| | | | CAATA ATT CCATCGTAT | | |
| | | | ___ C | | |
| GAM186 | GMFB | 3' | TATTGAGCCATGAATAATTTA 1090 | A___ | |
| | | | TAAGTTATTCATG CGGTA | | |
| | | | | | |
| | | | ATTTAATAAGTAC GTTAT | | |
| | | | CGA | | |
| GAM187 | ADCY2 | 3' | ATGTTGAATGTATCTAGTG 2710 | TT G | |
| | | | CACTAG TA ATTCAACAT | | |
| | | | | | |
| | | | GTGATC AT TAAGTTGTA | | |
| | | | T_ G | | |
| GAM187 | CCNA1 | 3' | GTTGGATCAACTAATG 1070 | C TA | |
| | | | CA TAGTT GATTCAAC | | |
| | | | | | |
| | | | GT ATCAA CTAGGTTG | | |
| | | | A _ | | |
| GAM187 | COG6 | 3' | ATGTTGACCTGAGCTAGT 2961 | AT | |
| | | | ACTAGTTTAG TCAACAT | | |
| | | | | | |
| | | | TGATCGAGTC AGTTGTA | | |
| | | | C_ | | |
| GAM187 | DACH | 3' | GTATATTGAACCCTAGGCTAGT 2387 | A_ C | |
| | G | | CACTAGTTTAG TTCAA ATAC | | |
| | | | | | |
| | | | GTGATCGGATC AAGTT TATG | | |
| | | | CC A | | |
| GAM187 | FKBP1A | 3' | GTGTGTTTACCTAAACTA 775 | ATTC | |
| | | | TAGTTTAG AACATAC | | |
| | | | | | |
| | | | ATCAAATC TTGTGTG | | |
| | | | CAT_ | | |
| GAM187 | HSPD1 | 3' | ATGTTCTAACTCCTAGACTAGT 2559 | ATTC___ | |
| | G | | CACTAGTTTAG AACAT | | |
| | | | | | |
| | | | GTGATCAGATC TTGTA | | |
| | | | CTCAATC | | |
| GAM187 | JJAZ1 | 3' | TATGTTGAATTGATCTAG 1622 | TTTA | |
| | | | CTAG GATTCAACATA | | |
| | | | | | |
| | | | GATC TTAAGTTGTAT | | |
| | | | TAG_ | | |
| GAM187 | MAN1A1 | 3' | GTATGTCAAAGAATAAATTAGT 3543 | GA_ CA | |
| | | | ACTAGTTTA TT ACATAC | | |
| | | | | | |
| | | | TGATTAAAT AA TGTATG | | |
| | | | AAG AC | | |
| GAM187 | PKIB | 3' | ATGTTGAAAGACTTAGTG 2254 | _ AGA | |
| | | | CACTA GTTT TTCAACAT | | |
| | | | | | |

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|--------|--------------|----|---------------------------|--------|
| | | | GTGAT CAGA AAGTTGTA | |
| | | | T _ | |
| GAM187 | RRM2B | 3' | GTATGTTGAAATAAACTA 2799 | GA |
| | | | TAGTTTA TTCAACATAC | |
| | | | | |
| | | | ATCAAAT AAGTTGTATG | |
| | | | A_ | |
| GAM187 | SWAP70 | 3' | GTATGTGCTGTAAACTAG 2917 | ATTCA |
| | | | CTAGTTTAG ACATAC | |
| | | | | |
| | | | GATCAAATT TGTATG | |
| | | | GTCG_ | |
| GAM187 | ABHD3 | 3' | GTTTTAATTTAACTAGT 2436 | C_ |
| | | | ACTAGTTTAGATT AAC | |
| | | | | |
| | | | TGATCAAATTTAA TTG | |
| | | | TT | |
| GAM187 | ATIP1 | 3' | ATGTTCTTTTAAATTAGTG 1924 | TTC |
| | | | CACTAGTTTAGA AACAT | |
| | | | | |
| | | | GTGATTAAATTT TTGTA | |
| | | | TC_ | |
| GAM187 | DKFZP564F013 | 3' | TATGTTGAATTATGTCAGTG 3640 | AG TTA |
| | | | CACT T GATTCAACATA | |
| | | | | |
| | | | GTGA G TTAAGTTGTAT | |
| | | | CT TA_ | |
| GAM187 | FN5 | 3' | TATGTTGAATCAAAGTG 1898 | AGT A |
| | | | CACT TT GATTCAACATA | |
| | | | | |
| | | | GTGA AA CTAAGTTGTAT | |
| | | | _ _ | |
| GAM187 | KIAA0416 | 3' | TATGCTGAAGACTGGT 1637 | TAGA A |
| | | | ACTAGTT TTCA CATA | |
| | | | | |
| | | | TGGTCAG AAGT GTAT | |
| | | | _ C | |
| GAM187 | KIAA0455 | 3' | TATGTTGATTCTACCTGTG 2948 | T TT T |
| | | | CAC AG TAGA TCAACATA | |
| | | | | |
| | | | GTG TC ATCT AGTTGTAT | |
| | | | _ C_ T | |
| GAM187 | KIAA0912 | 3' | GTATGTTTTACTTAACTAG 2689 | ATTC |
| | | | CTAGTTTAG AACATAC | |
| | | | | |
| | | | GATCAAATT TTGTATG | |
| | | | CATT | |
| GAM187 | KIAA0981 | 3' | ATGTTGAATTTTAACTAG 2597 | _ |
| | | | CTAGTTTAGA TTCAACAT | |
| | | | | |

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|--------|----------|----|-----------------------------|---------|--------|
| | | | GATCAAATTT AAGTTGTA | | |
| | | | T | | |
| GAM187 | KIAA1911 | 3' | TATGTTGAAAACTGCTGTG 2976 | T | TTAGA |
| | | | CAC AGT TTCAACATA | | |
| | | | | | |
| | | | GTG TCG AAGTTGTAT | | |
| | | | _ TCAAA | | |
| GAM187 | KRTHB2 | 3' | GTATGTTGAACCCAACTGTG 2310 | T | AGA |
| | | | CAC AGTTT TTCAACATAC | | |
| | | | | | |
| | | | GTG TCAAA AAGTTGTATG | | |
| | | | _ CCC | | |
| GAM187 | RPS6KC1 | 3' | GTATGTTGAATGTGGTCCCAG 1429 | AGT_ | G |
| | | | CT TTA ATTCAACATAC | | |
| | | | | | |
| | | | GA GGT TAAGTTGTATG | | |
| | | | CCCT G | | |
| GAM187 | TOMM70A | 3' | ATGTTGATTTTAAATTA 1558 | T_ | |
| | | | TAGTTTAGA TCAACAT | | |
| | | | | | |
| | | | ATTAAATTT AGTTGTA | | |
| | | | TT | | |
| GAM188 | CDC23 | 3' | TGCACAGTAGATGCTATGGA 1141 | | AAC |
| | | | TCTATAGCATCTACT TGTA | | |
| | | | | | |
| | | | AGGTATCGTAGATGA ACGT | | |
| | | | C_ | | |
| GAM188 | EGLN3 | 3' | TGGAGGTGGTAGATGCCACAGA 2330 | ATA | A G |
| | | | TCT GCATCTACTA CT TA | | |
| | | | | | |
| | | | AGA CGTAGATGGT GA GT | | |
| | | | CAC G G | | |
| GAM188 | EGLN3 | 3' | TGGAGGTGGTAGATGCCACAGA 1976 | ATA | A G |
| | | | TCT GCATCTACTA CT TA | | |
| | | | | | |
| | | | AGA CGTAGATGGT GA GT | | |
| | | | CAC G G | | |
| GAM188 | JAM3 | 3' | GTACACAGATGCTACAGA 2280 | A | ACTAAC |
| | | | TCT TAGCATCT TGTAC | | |
| | | | | | |
| | | | AGA ATCGTAGA ACATG | | |
| | | | C C_ | | |
| GAM188 | RNF7 | 3' | ACAGCTTAGAAGTGCTATA 1485 | T A | _ |
| | | | TATAGCA CT CTAA CTGT | | |
| | | | | | |
| | | | ATATCGT GA GATT GACA | | |
| | | | _ A C | | |
| GAM188 | WBSCR5 | 3' | GTACAGTTAACTTATAGA 1973 | CATCTAC | |
| | | | TCTATAG TAACTGTAC | | |
| | | | | | |

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|--------|--------------|----|------------------------|---------------|------------|
| | | | AGATATT | ATTGACATG | |
| | | | CA_____ | | |
| GAM188 | WBSCR5 | 3' | GTACAGTTAACTTATAGA | 2250 | CATCTAC |
| | | | TCTATAG | TAACTGTAC | |
| | | | | | |
| | | | AGATATT | ATTGACATG | |
| | | | CA_____ | | |
| GAM188 | WBSCR5 | 3' | GTACAGTTAACTTATAGA | 1479 | CATCTAC |
| | | | TCTATAG | TAACTGTAC | |
| | | | | | |
| | | | AGATATT | ATTGACATG | |
| | | | CA_____ | | |
| GAM188 | C8orf13 | 3' | TGCACAGCTGTTTAGGCTATAG | 3206 | ATCT TAA A |
| | A | | TCTATAGC | AC CTGT CA | |
| | | | | | |
| | | | AGATATCG | TG GACA GT | |
| | | | GATT TC_ | C | |
| GAM188 | CDT6 | 3' | TATAGTTAATAATAAATGCTGT | 1945 | C C__ |
| | A | | TATAGCAT TA | TAACTGTA | |
| | | | | | |
| | | | ATGTCGTA AT | ATTGATAT | |
| | | | A AATA | | |
| GAM188 | DKFZp566D234 | 3' | TGCAGCATGCTATAGA | 2613 | CTACTAA |
| | | | TCTATAGCAT | CTGTA | |
| | | | | | |
| | | | AGATATCGTA | GACGT | |
| | | | C_____ | | |
| GAM188 | FLJ10525 | 3' | GTACAGTTTTAGTATAGA | 1786 | GCAT CT |
| | | | TCTATA | CTA AACTGTAC | |
| | | | | | |
| | | | AGATAT | GAT TTGACATG | |
| | | | _____ | T_ | |
| GAM188 | FLJ12078 | 5' | TGCTAGAGTAATGCTATA | 2121 | C AACT |
| | | | TATAGCAT TACT | GTA | |
| | | | | | |
| | | | ATATCGTA ATGA | CGT | |
| | | | _ | GAT_ | |
| GAM188 | KIAA0007 | 3' | TGTACAGTTATATTTGTCTATA | 3154 | _ TC C |
| | | | TATAG CA TA | TAACTGTACA | |
| | | | | | |
| | | | ATATC GT AT | ATTGACATGT | |
| | | | T TT | _ | |
| GAM188 | KIAA1728 | 3' | TGTACAATTAGTACTTTATAG | 2819 | CATC C |
| | | | CTATAG | TACTAA TGTACA | |
| | | | | | |
| | | | GATATT | ATGATT ACATGT | |
| | | | TC__ | A | |
| GAM188 | MGC4643 | 3' | TGTACAGTCTAAAGCTACAGA | 2272 | A ATCTACTA |
| | | | TCT TAGC | ACTGTACA | |
| | | | | | |

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|--------|---------------|----|------------------------|----------|-------|-----|
| | | | AGA ATCG | TGACATGT | | |
| | | | C | AAATC__ | | |
| GAM188 | MPPE1 | 3' | TGTACAGTATGTAAATGCTAT | 2029 | C | TA |
| | | | ATAGCAT TAC ACTGTACA | | | |
| | | | | | | |
| | | | TATCGTA ATG TGACATGT | | | |
| | | | A | TA | | |
| GAM188 | RNPS1 | 3' | TGTACAGTCAGTACTATA | 2376 | CATC | A |
| | | | TATAG TACT ACTGTACA | | | |
| | | | | | | |
| | | | ATATC ATGA TGACATGT | | | |
| | | | _____ C | | | |
| GAM188 | RNPS1 | 3' | TGTACAGTCAGTACTATA | 1326 | CATC | A |
| | | | TATAG TACT ACTGTACA | | | |
| | | | | | | |
| | | | ATATC ATGA TGACATGT | | | |
| | | | _____ C | | | |
| GAM188 | TUSP | 3' | AGTAGAAGATGCTACAGA | 1907 | A | A A |
| | | | TCT TAGCATCT CTA CT | | | |
| | | | | | | |
| | | | AGA ATCGTAGA GAT GA | | | |
| | | | C A _ | | | |
| GAM188 | LOC153027 | 3' | TGTACAGTCAGTTCTATA | 2792 | CATCT | A |
| | | | TATAG ACT ACTGTACA | | | |
| | | | | | | |
| | | | ATATC TGA TGACATGT | | | |
| | | | T_____ C | | | |
| GAM188 | LOC153114 | 5' | GTGAGCAGACTGCTATAGA | 3367 | _ | A A |
| | | | TCTATAGCA TCT CT AC | | | |
| | | | | | | |
| | | | AGATATCGT AGA GA TG | | | |
| | | | C C G | | | |
| GAM189 | SORT1 | 3' | CATCAAAGCCAAAAGGACCTAC | 974 | A C | AAA |
| | A | | TGTA G TCTTTTTG TTGATG | | | |
| | | | | | | |
| | | | ACAT C AGGAAAAC AACTAC | | | |
| | | | _ C CGA | | | |
| GAM189 | ATP9A | 3' | CATCAATCTGGAAAGAACTTAC | 2618 | C | GAA |
| | A | | TGTAAG TCTTTTT ATTGATG | | | |
| | | | | | | |
| | | | ACATTC AGAAAGG TAACTAC | | | |
| | | | A TC_ | | | |
| GAM189 | DKFZP434K1772 | 3' | TTTCAAAAAGAGGTTACA | 2797 | G | |
| | | | TGTAA CTCTTTTTGAAA | | | |
| | | | | | | |
| | | | ACATT GAGAAAACTTT | | | |
| | | | G | | | |
| GAM189 | UNC5D | 3' | CAATTTCAAAGAGAACCCACA | 2392 | AAGC | |
| | | | TGT TCTTTTTGAAATTG | | | |
| | | | | | | |

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|--------|-----------|----|-----------------------------|-----------|
| | | | ACA AGAGAACTTTAAC | |
| | | | CCCA | |
| GAM190 | SCD | 3' | AGCCAGACAAAATTTGAGAATA 1176 | CA TG CCA |
| | | | TAT T A TTTGTCTGGCT | |
| | | | | |
| | | | ATA A T AAACAGACCGA | |
| | | | AG GT TA_ | |
| GAM190 | SOS2 | 3' | AGCCATATGTAGTCATTGA 2824 | T CATT C |
| | | | TCA TGAC TGT TGGCT | |
| | | | | |
| | | | AGT ACTG GTA ACCGA | |
| | | | T AT__ T | |
| GAM190 | BANP | 3' | CCAGACAAGTGCCCAACGA 2744 | A AC |
| | | | TC TTG CATTTGTCTGG | |
| | | | | |
| | | | AG AAC GTGAACAGACC | |
| | | | C CC | |
| GAM190 | KIAA0446 | 5' | AGCCAGACAAAAAGAATGATTC 2831 | T GACCA |
| | | | A ATCATT TTTGTCTGGCT | |
| | | | | |
| | | | C TAGTAA AAACAGACCGA | |
| | | | T GAA__ | |
| GAM190 | LOC115110 | 3' | GGCTGAAATGGTCAAT 2924 | GTC |
| | | | ATTGACCATT TGGCT | |
| | | | | |
| | | | TAACTGGTAAA GTCGG | |
| | | | _____ | |
| GAM190 | LOC148443 | 3' | AGCCAACACATATGGTCAATGA 3118 | T C_ |
| | | | TCATTGACCAT TGT TGGCT | |
| | | | | |
| | | | AGTAACTGGTA ACA ACCGA | |
| | | | T CA | |
| GAM190 | LOC151826 | 3' | TTATTCAAAGGCCAATGATA 3161 | A A TC |
| | | | TATCATTG CC TTTG TGG | |
| | | | | |
| | | | ATAGTAAC GG AAAC ATT | |
| | | | C _ TT | |
| GAM190 | LOC200609 | 5' | CCACCACCAATGGTCAAGATAT 3479 | A T C_ |
| | | | ATATC TTGACCATT GT TGG | |
| | | | | |
| | | | TATAG AACTGGTAA CA ACC | |
| | | | _ C CC | |
| GAM191 | BHLHB3 | 3' | TCAAGTGCATCTATTCCCA 2163 | AAATAC GT |
| | | | TGGGAATA TACT TGA | |
| | | | | |
| | | | ACCCTTAT GTGA ACT | |
| | | | CTAC__ _ | |
| GAM191 | ITK | 3' | CATGAGGTAATATTATTATTC 1223 | _ C GT_ |
| | CA | | TGGGAATAA AATA TACT TG | |
| | | | | |

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|--------|---------------|----|-----------------------------|-----------|--|
| | | | ACCCTTATT TTAT ATGG AC | | |
| | | | A A AGT | | |
| GAM191 | MPV17 | 3' | CTTGATAATAGTCTTATTCCCA 2888 | AAT C TG | |
| | | | TGGGAATAA ACTA TGT AG | | |
| | | | | | |
| | | | ACCCTTATT TGAT ATA TC | | |
| | | | C__ A GT | | |
| GAM191 | MSR1 | 3' | TCAGCATT TTTTATTCCCA 930 | TACTAC | |
| | | | TGGGAATAAAA TGTTGA | | |
| | | | | | |
| | | | ACCCTTATTTT ACGACT | | |
| | | | T_____ | | |
| GAM191 | RNMT | 3' | TCAGCACCATTATTCCCA 1061 | AATACTAC | |
| | | | TGGGAATAA TGTTGA | | |
| | | | | | |
| | | | ACCCTTATT ACGACT | | |
| | | | ACC_____ | | |
| GAM191 | SCP2 | 3' | CAGAAACAGTATTTTCTTCCCA 976 | T ACTG | |
| | | | TGGGAA AAAATACT TTG | | |
| | | | | | |
| | | | ACCCTT TTTTATGA GAC | | |
| | | | C CAAA | | |
| GAM191 | DKFZP564K0822 | 3' | CTCAACAATTTTGTATTCCCA 3630 | AAATACTAC | |
| | | | TGGGAATA TGTTGAG | | |
| | | | | | |
| | | | ACCCTTAT ACAACTC | | |
| | | | GTTTTA__ | | |
| GAM191 | KIAA0564 | 3' | CAAAATGTACCTTATTCCCA 2742 | AA TACTG | |
| | | | TGGGAATAA TAC TTG | | |
| | | | | | |
| | | | ACCCTTATT ATG AAC | | |
| | | | CC TAA__ | | |
| GAM191 | KIAA0769 | 3' | CGGCATTATTTTATTCCCA 1560 | CTAC | |
| | | | TGGGAATAAAATA TGTTG | | |
| | | | | | |
| | | | ACCCTTATTTTAT ACGGC | | |
| | | | T_____ | | |
| GAM191 | KIAA1163 | 3' | CTTGGTAGTATTTGATTCCCA 3122 | A CTG TG | |
| | | | TGGGAAT AAATACTA T AG | | |
| | | | | | |
| | | | ACCCTTA TTTATGAT G TC | | |
| | | | G T__GT | | |
| GAM191 | KIAA1332 | 3' | CAACAAAGGATTTTATTCC 2909 | A AC | |
| | | | GGAATAAAAT CT TGTTG | | |
| | | | | | |
| | | | CCTTATTTTA GG ACAAC | | |
| | | | _ AA | | |
| GAM191 | SFRS11 | 3' | AGTAATAATTTATTCCCA 1155 | A C | |
| | | | TGGGAATAAA TA TACT | | |
| | | | | | |

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|--------|-----------|----|-----------------------------|-----------|
| | | | ACCCTTATTT AT ATGA | |
| | | | A A | |
| GAM191 | ZNF387 | 3' | CTCAACAGTAATTCCTCCCA 1521 | ATAAAATAC |
| | | | TGGGA TACTGTTGAG | |
| | | | | |
| | | | ACCCT ATGACAACTC | |
| | | | CACCTTA__ | |
| GAM191 | LOC138639 | 3' | CTCAACACACCAAGCCTTATTC 3020 | AATACTAC_ |
| | | | CCA TGGGAATAA TGTTGAG | |
| | | | | |
| | | | ACCCTTATT ACAACTC | |
| | | | CCGAACCAC | |
| GAM191 | LOC147299 | 3' | CAACATTTTATTTCCA 3107 | TACTAC |
| | | | TGGGAATAAAA TGTTG | |
| | | | | |
| | | | ACCTTTATTTT ACAAC | |
| | | | _____ | |
| GAM191 | LOC90019 | 5' | CTCAACAGCTGCTTATTCCTCG 2445 | AATACTA |
| | | | TGGGAATAA CTGTTGAG | |
| | | | | |
| | | | GCCCTTATT GACAACTC | |
| | | | CGTC__ | |
| GAM192 | B3GALT5 | 5' | AGATCAGAGACTGTAAAAAGT 2320 | C_ C |
| | | | GCTT TACAGTCTTT GTTT | |
| | | | | |
| | | | TGAA ATGTCAGAGA TAGA | |
| | | | AA C | |
| GAM192 | BTEB1 | 3' | GAAACGAAAGAAAGCAAAGC 808 | CTACAG |
| | | | GCTT TCTTTCGTTTC | |
| | | | | |
| | | | CGAA AGAAAGCAAAG | |
| | | | ACGAA_ | |
| GAM192 | RP2 | 3' | GCTAAAACTGTAGAAGC 1340 | C C |
| | | | GCTTCTACAGT TTT GT | |
| | | | | |
| | | | CGAAGATGTCA AAA CG | |
| | | | _ T | |
| GAM192 | C12orf22 | 3' | AAACAAAACCTGTAGAAGC 2169 | C C |
| | | | GCTTCTACAGT TTT GTTT | |
| | | | | |
| | | | CGAAGATGTCA AAA CAAA | |
| | | | - - | |
| GAM192 | C20orf26 | 3' | GGAAACGCGCTCTGTAGAA 2879 | TCTTT |
| | | | TTCTACAG CGTTTCC | |
| | | | | |
| | | | AAGATGTC GCAAAGG | |
| | | | TCGC_ | |
| GAM192 | FLJ14627 | 5' | GAACCTGAAGACTGCAGAGC 2283 | T A C_ |
| | | | GCT CT CAGTCTTT GTTT | |
| | | | | |

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|--------|-----------|----|-----------------------------|-------|--------|
| | | | CGA GA GTCAGAAG CAAG | | |
| | | | _ C TT | | |
| GAM192 | GPR72 | 3' | GGAAACACACTCCTGCAGAAGC 2867 | A | TCTTTC |
| | TG | | TAGCTTCT CAG GTTTCC | | |
| | | | | | |
| | | | GTCGAAGA GTC CAAAGG | | |
| | | | C CTCACA | | |
| GAM192 | GPT2 | 3' | GAAAAGGTTAAATCGTAGAAGC 2418 | A | CTT_ G |
| | TA | | TAGCTTCTAC GT TC TTTC | | |
| | | | | | |
| | | | ATCGAAGATG TA GG AAAG | | |
| | | | C AATT A | | |
| GAM192 | KIAA0470 | 5' | GCCAAAGACTTAGAAGCTA 1556 | C | C |
| | | | TAGCTTCTA AGTCTTT GT | | |
| | | | | | |
| | | | ATCGAAGAT TCAGAAA CG | | |
| | | | _ C | | |
| GAM192 | KIAA1328 | 5' | GAAATCATACCTGCAGAAGCTA 2602 | A | TCTTTC |
| | | | TAGCTTCT CAG GTTTC | | |
| | | | | | |
| | | | ATCGAAGA GTC TAAAG | | |
| | | | C CATACT_ | | |
| GAM192 | KIAA1981 | 3' | AGATGAAACCATGGAAGC 3430 | CA | CT |
| | | | GCTTCTA GT TTCGTTT | | |
| | | | | | |
| | | | CGAAGGT CA AAGTAGA | | |
| | | | AC _ | | |
| GAM192 | MGC17330 | 3' | GGAAACGAGTTTGTACAGAAGT 2342 | _ | TCT |
| | | | GCTTCT ACAG TTCGTTTCC | | |
| | | | | | |
| | | | TGAAGA TGTT GAGCAAAGG | | |
| | | | CA T_ | | |
| GAM192 | MRPL35 | 3' | GAAACGAAAAAGTTAAGC 1701 | CT | AGTC |
| | | | GCTT AC TTTCGTTTC | | |
| | | | | | |
| | | | CGAA TG AAAGCAAAG | | |
| | | | T_ AA_ | | |
| GAM192 | LOC205011 | 5' | GAAAACAAGAGTAGAGGC 3492 | AG | TCG |
| | | | GCTTCTAC TCTT TTTC | | |
| | | | | | |
| | | | CGGAGATG AGAA AAAG | | |
| | | | _ CA_ | | |
| GAM193 | KIAA1228 | 3' | CGGAACACACCCTCTCA 2712 | AAA | |
| | | | TGAGA GTGTGTTCTG | | |
| | | | | | |
| | | | ACTCT CACACAAGGC | | |
| | | | CC_ | | |
| GAM193 | KIAA1655 | 5' | GCGACTCGGGGCACTGCTCCTC 2754 | AAA _ | A |
| | A | | TGAG AGT GTGTTCTGA TCGC | | |
| | | | | | |

ACTC TCG CACGGGGCT AGCG
 C__ T C
 GAM193 NDST3 3' TAGAACACACCTTTTCCA 1157 A _
 TG GAAAAG TGTGTTCTG
 || ||||| |||||
 AC CTTTTC ACACAAGAT
 _ C
 GAM193 PP1057 3' GCAATTTACACACTTGTCTCA 2189 A TCT C
 TGAGA AAGTGTGT GAAT GC
 ||||| ||||| |||||
 ACTCT TTCACACA TTTA CG
 G _ A
 GAM193 RNP24 3' CGACTCAGCATACATTTTCCCA 1333 A G T A
 TG GAAAA TGTGT CTGA TCG
 || ||||| ||||| |||||
 AC CTTTT ACATA GACT AGC
 C _ C C
 GAM193 LOC150142 5' CAGAACACCACCTCTCA 3142 AAA _
 TGAGA GTG TGTCTG
 ||||| ||||| |||||
 ACTCT CAC ACAAGAC
 C__ C
 GAM193 LOC199899 5' ATTCAAAACACACATTC 3473 AA C
 GAA GTGTGTT TGAAT
 ||||| ||||| |||||
 CTT CACACAA ACTTA
 A_ A
 GAM193 LOC222068 3' ATTTTAATACACTTCCCTCA 3573 AA CT
 TGAG AAGTGTGTT GAAT
 ||||| ||||| |||||
 ACTC TTCACATAA TTTA
 CC T_
 GAM194 HUS1 3' TTCCTATTATAATTACATCT 3509 A TC
 GGAT TAGTT ATAATAGGAA
 ||||| ||||| |||||
 TCTA ATTAA TATTATCCTT
 C _
 GAM194 TRPM8 3' TCCTATTGAAGGAACCACCCCC 2052 ATATA A_
 GG GTTTC TAATAGGA
 || ||||| |||||
 CC CAAGG GTTATCCT
 CCCAC AA
 GAM194 LOC148936 3' CCTACCTGATATTACATCCTA 3304 A T TAA
 TAGGAT TAGT TCA TAGG
 ||||| ||||| |||||
 ATCCTA ATTA AGT ATCC
 C T CC_
 GAM194 LOC148938 3' CCTACCTGATATTACATCCTA 3303 A T TAA
 TAGGAT TAGT TCA TAGG
 ||||| ||||| |||||

ATCCTA ATTA AGT ATCC
 C T CC_
 GAM194 LOC200803 3' TTCCTATTATATGGTATCC 3452 AGTTTC
 GGATAT ATAATAGGAA
 ||||| |||||
 CCTATG TATTATCCTT
 GTA__
 GAM194 LOC255332 5' TTCCTATTACTCTGCATATCTT 3696 A TTCA
 A TAGGATAT GT TAATAGGAA
 ||||| || |||||
 ATTCTATA CG ATTATCCTT
 _ TCTC
 GAM194 LOC90459 3' CTAGATGAAACCATATCTTA 2641 A AA
 TAGGATAT GTTTCAT TAG
 ||||| ||||| ||
 ATTCTATA CAAAGTA ATC
 C G_
 GAM195 DKFZp434E0519 5' TGGAAATCCGTGTGTAA 2241 ACG
 TTACACACGGA TTTA
 ||||| ||||| ||
 AATGTGTGCCT AGGT
 AA_
 GAM195 HSU84971 3' GTTATAAACATTCTTATGTGTA 1439 C_ C
 AT ATTACACA GGAA GTTTATAAC
 ||||| ||||| |||||
 TAATGTGT TCTT CAAATATTG
 AT A
 GAM195 LOC157663 3' AGCTTCCCATTGTGTAATA 3203 C_ C
 TATTACACA GGAA GTT
 ||||| ||||| ||
 ATAATGTGT CCTT CGA
 TAC _
 GAM196 EXT2 3' GAGAAGAGAAGCGTGTGA 737 G
 TAACACGCTTCT TTCTC
 ||||| ||||| |||||
 ATTGTGCGAAGA AAGAG
 G
 GAM196 MBNL 3' ATAGATGAGAGCGTGCATGC 1936 TTC_
 GC TGTTCTCATCTAT
 || |||||
 CG GCGAGAGTAGATA
 TACGT
 GAM196 PLN 3' AGATGAGAACTGGTGGTGA 946 A TCT
 TAAC CGCT GTTCTCATCT
 ||| ||| |||||
 ATTG GTGG CAAGAGTAGA
 _ T_
 GAM196 SLC12A2 3' AGCAATAAAAGCGTGTGA 796 C _
 TAACACGCTT TGTT CT
 ||||| ||||| ||

ATTGTGCGAA ATAA GA
 A C
 GAM196 SLC1A3 3' AGATGAGAAGACTAGCAGC 1092 T ____
 GCT CTG TTCTCATCT
 ||| ||| |||||
 CGA GAT AAGAGTAGA
 C CAG
 GAM196 BTBD3 3' ATAGATGATGAAAAGCTGTTA 1600 C CTG _
 TAACA GCTT TTC TCATCTAT
 ||||| ||||| ||| |||||
 ATTGT CGAA AAG AGTAGATA
 _ ____ T
 GAM196 KIAA1237 3' AGATGAGGATGAGCGT 3166 CT
 ACGCTT GTTCTCATCT
 ||||| |||||
 TGCGAG TAGGAGTAGA
 _
 GAM196 NAALAD2 3' ATAGATGAGAATTTTCCGT 1215 CTTCT
 ACG GTTCTCATCTAT
 ||| |||||
 TGC TAAGAGTAGATA
 CTTT_
 GAM196 PEG10 3' ATAGATGAATTAGTAAGC 1605 _ TTC
 GCTT CTG TCATCTAT
 ||||| ||| |||||
 CGAA GAT AGTAGATA
 T TA_
 GAM197 RAI2 5' AGAATTAGGCTTAAAAAATGCC 1959 CG TATGAT
 T AGGCATTT TAA ATTCT
 ||||| ||| |||||
 TCCGTAAA ATT TAAGA
 AA CGGAT_
 GAM197 UMPK 3' CATGGAGATGAAATGCCT 1436 AA_
 AGGCATTTCTG TATG
 ||||| ||||| |||||
 TCCGTAAAGTA GTAC
 GAG
 GAM197 ZNF134 3' GAAAATCATGAAATGCCT 1021 GTAAT A
 AGGCATTTTC ATGAT TTC
 ||||| ||||| |||||
 TCCGTAAAG TACTA AAG
 ____ A
 GAM197 ARL8 3' AGAATATCACATTATTCAATGC 3594 TC A
 GCATT GTAAT TGATATTCT
 ||||| ||||| |||||
 CGTAA TATTA ACTATAAGA
 CT C
 GAM197 KIAA0546 3' AATGTTAATTATGAAACACCT 2911 CA A
 AGG TTTCGTAAT TGATATT
 ||| ||||| |||||

TCC AAAGTATTA ATTGTAA
 AC _
 GAM197 KIAA0644 3' AGAACATCACTGAAAATGCCT 1557 _ TAATA A
 AGGCATTT CG TGAT TTCT
 ||||| || ||| |||
 TCCGTAAA GT ACTA AAGA
 A C _ C
 GAM197 KIAA1508 3' GGATATCACATAATGCC 2614 TCGTA A
 GGCATT AT TGATATTC
 |||| | |||||
 CCGTAA TA ACTATAGG
 _ C
 GAM197 MTHFS 3' ATTGTAATTATGAAATACCT 1302 C _ TG
 AGG ATTTCGTAAT A AT
 || ||||| | ||
 TCC TAAAGTATTA T TA
 A A GT
 GAM197 SUCLA2 3' GTCATATTAAGAAACACCT 1066 CA G
 AGG TTTC TAATATGAT
 || ||| |||||
 TCC AAAG ATTATACTG
 AC A
 GAM197 LOC149910 3' AGAACTTTATTTACCATGAAAT 3140 AAT _ TA
 GCCT AGGCATTTCTG ATGA TTCT
 ||||| ||| |||
 TCCGTAAAGTA TATT AAGA
 CCATT TC
 GAM197 LOC222171 3' GAATATTTACACAATGCCT 3575 TC ATAT
 AGGCATT GTA GATATTC
 ||||| || |||||
 TCCGTAA CAT TTATAAG
 CA _
 GAM198 ZNF24 3' GACAAATACATTATTTCTG 1342 _ AA
 TAGAAATAATG AT GTC
 ||||| || |||
 GTCTTTATTAC TA CAG
 A AA
 GAM198 ALS2CR12 3' GATGGTTGGCACACCATTCTG 2471 AA ATAAGT
 TA TATAGAAAT TG CCATC
 ||||| || |||
 ATGTCTTTA AC GGTAG
 CC ACGGTT
 GAM198 FLJ10508 3' GATGGCTCTTATCATCATCTTT 1783 A A T_
 ATA TATAGA AT ATGATAAG CCATC
 |||| | ||||| |||
 ATATTT TA TACTATTC GGTAG
 C C TC
 GAM198 FLJ13197 3' GATTCATCATTATTCCTA 2072 A A
 TAG AATAATGAT AGTC
 || ||||| |||

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|--------|-----------|--------------------------------|-----------|----|
| | | ATC TTATTACTA TTAG | | |
| | | C C | | |
| GAM198 | FLJ21934 | 3' GATGATGTCATTACTTCTATA 2085 | A | A_ |
| | | TATAGAA TAATGATA GTC | | |
| | | | | |
| | | ATATCTT ATTACTGT TAG | | |
| | | C AG | | |
| GAM198 | FLJ23132 | 3' ATGGACTTAATCTCTG 3691 | AATAAT | _ |
| | | TAGA GAT AAGTCCAT | | |
| | | | | |
| | | GTCT CTA TTCAGGTA | | |
| | | _____ A | | |
| GAM198 | KIAA0470 | 3' ATGGACTTCTTCATCTGTA 1555 | AATAA | T_ |
| | | TATAGA TGA AAGTCCAT | | |
| | | | | |
| | | ATGTCT ACT TTCAGGTA | | |
| | | _____ TC | | |
| GAM198 | LEPROTL1 | 3' GCTGCGTATTATTTCTATA 1620 | ATA | |
| | | TATAGAAATAATG AGT | | |
| | | | | |
| | | ATATCTTTATTAT TCG | | |
| | | GCG | | |
| GAM198 | LYSAL1 | 5' GACCCCAGCATTATTTCTATA 1164 | ATAA_ | |
| | | TATAGAAATAATG GTC | | |
| | | | | |
| | | ATATCTTTATTAC CAG | | |
| | | GACCC | | |
| GAM198 | RAB40A | 5' GATGGATGCATGCATTATTTT 3229 | ATAA_ | |
| | | GAAATAATG GTCCATC | | |
| | | | | |
| | | CTTTATTAC TAGGTAG | | |
| | | GTACG | | |
| GAM198 | STK38L | 3' GATAGGGTTTCATTTATTTCTA 2845 | _ TA GT _ | |
| | TA | TATAGAAATAA TGA A CC ATC | | |
| | | | | |
| | | ATATCTTTATT ACT T GG TAG | | |
| | | T _ TG A | | |
| GAM198 | ZNF363 | 3' GATAGACTTATCATAGCTCTAT 2974 | AA A C | |
| | A | TATAGA TA TGATAAGTC ATC | | |
| | | | | |
| | | ATATCT AT ACTATTCAG TAG | | |
| | | CG _ A | | |
| GAM198 | LOC146481 | 3' GACAGTCATGCATTTCTATA 3093 | A_ AA | |
| | | TATAGAAAT ATGAT GTC | | |
| | | | | |
| | | ATATCTTTA TACTG CAG | | |
| | | CG A_ | | |
| GAM198 | LOC152008 | 3' ATGGAGGCATTATTTCTA 3165 | ATAAG | |
| | | TAGAAATAATG TCCAT | | |
| | | | | |

ATCTTTATTAC AGGTA
 GG___
 GAM198 LOC153020 3' GATGGACCCCTTCAAGCAATTTC 3178 AA__ TAA
 TATA TATAGAAAT TGA GTCCATC
 ||||| || |||||
 ATATCTTTA ACT CAGGTAG
 ACGA TCC
 GAM198 LOC199786 3' GCTTAAGCCATTATTTCTG 3433 A__
 TAGAAATAATG TAAGT
 ||||| ||||
 GTCTTTATTAC ATTCG
 CGA
 GAM198 LOC220766 3' ATGGACTTCTTCATCTGTA 3498 AATAA T_
 TATAGA TGA AAGTCCAT
 |||| || |||||
 ATGTCT ACT TTCAGGTA
 ____ TC
 GAM199 ADAM12 3' CTAGAGCACTGCCACCAGTA 1029 A A AAT _
 TACT GGT GCA TG TCTAG
 ||| ||| || |||||
 ATGA CCA CGT AC AGATC
 _ C C__ G
 GAM199 HOXC13 3' CTAGATGTAGATGCTGCCTA 2538 AAT_
 TAGGTAGCA TGTCTAG
 ||||| |||||
 ATCCGTCGT GTAGATC
 AGAT
 GAM199 NRIP1 3' CTAGACAATTTCTTCTA 2549 T C
 TAGG AG AAATTGTCTAG
 ||| || |||||
 ATCT TC TTTAACAGATC
 _ _
 GAM199 RRM2B 3' CTAAACAATTTGCATTTA 2798 A C
 TAGGT GCAAATTGT TAG
 |||| ||||| |||
 ATTTA CGTTTAACA ATC
 _ A
 GAM199 BIRC4 3' TTAGCATTTGCTACCAAGTA 806 A T T
 TACT GGTAGCAAAT G CTAG
 ||| ||||| |||
 ATGA CCATCGTTTA C GATT
 A _ _
 GAM199 FLJ11301 3' GCGGTATTTACTACCTAG 1822 C _
 CTAGGTAG AAAT TGT
 ||||| ||| |||
 GATCCATC TTTA GCG
 A TG
 GAM199 LAP1B 5' AGGCAGGTTTGCTACACAG 2696 AG _
 CT GTAGCAAAT TGTCT
 || ||||| |||||

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|--------|-----------|----|-----------------------------|-----------|--|
| | | | GA CATCGTTTG ACGGA | | |
| | | | CA G | | |
| GAM199 | MGC11324 | 3' | TAGATCTGTACCTAGTA 2273 | G AATT | |
| | | | TACTAGGTA CA GTCTA | | |
| | | | | | |
| | | | ATGATCCAT GT TAGAT | | |
| | | | _ C _ | | |
| GAM199 | PRO2958 | 3' | ACACCTTTGCTACCAGTA 1841 | A T_ | |
| | | | TACT GGTAGCAAA TGT | | |
| | | | | | |
| | | | ATGA CCATCGTTT ACA | | |
| | | | _ CC | | |
| GAM199 | SH3BGRL2 | 3' | CTAGACAAAGCTACCCAG 2208 | A AAA | |
| | | | CT GGTAGC TTGTCTAG | | |
| | | | | | |
| | | | GA CCATCG AACAGATC | | |
| | | | C A_ | | |
| GAM199 | LOC144997 | 3' | CTAGACAGATATCCACTTAGTA 3271 | AGCAAA | |
| | | | TACTAGGT TTGTCTAG | | |
| | | | | | |
| | | | ATGATTCA GACAGATC | | |
| | | | CCTATA | | |
| GAM199 | LOC148809 | 3' | CTAGACAACATGACCCTACC 3125 | _ AA | |
| | | | GGTAG CA TTGTCTAG | | |
| | | | | | |
| | | | CCATC GT AACAGATC | | |
| | | | CCA AC | | |
| GAM199 | LOC219540 | 3' | CTAGACAATTTTTTTTAG 3612 | TAGC | |
| | | | CTAGG AAATTGTCTAG | | |
| | | | | | |
| | | | GATT TTAAACAGATC | | |
| | | | TT_ | | |
| GAM200 | PTGER3 | 3' | CTATAGAGTATTCCATAATTTG 790 | T AC _ | |
| | AA | | TTCAA TTAT GGAT TTCTATAG | | |
| | | | | | |
| | | | AAGTT AATA CTTA GAGATATC | | |
| | | | T C_ T | | |
| GAM200 | SIRT1 | 3' | CTATAGATGATATTTTAAATTG 1416 | TACGGATT | |
| | AA | | TTCAATTTA TCTATAG | | |
| | | | | | |
| | | | AAGTTAAAT AGATATC | | |
| | | | TTTATAGT | | |
| GAM200 | FLJ10898 | 3' | AGAACTGTAAATTGAA 2526 | T A | |
| | | | TTCAATTTA ACGG TTTCT | | |
| | | | | | |
| | | | AAGTTAAAT TGTC AAAGA | | |
| | | | _ _ | | |
| GAM201 | FLJ10511 | 3' | ATGCCTATAATACCATAATGCC 1784 | C _ ACACC | |
| | AG | | CT GT TTATG ATAGGCAT | | |
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|--------|-----------|----|-----------------------------|-----------|
| | | | GA CG AATAC TATCCGTA | |
| | | | C T CATAA | |
| GAM201 | KIAA1462 | 3' | ATGCCTATAATTAGGAAGGAGT 3521 | G A CACC |
| | | | ACTC TTT TGA ATAGGCAT | |
| | | | | |
| | | | TGAG AAG ATT TATCCGTA | |
| | | | G G AA__ | |
| GAM201 | MESDC2 | 3' | CCCTGGTGGCATAAACGAGT 2950 | A TA |
| | | | ACTCGTTTATG CACCA GG | |
| | | | | |
| | | | TGAGCAAATAC GTGGT CC | |
| | | | G C_ | |
| GAM201 | LOC149620 | 5' | ATGCCTACAAAGGAAATGAGT 3135 | ATGACACCA |
| | | | ACTCGTTT TAGGCAT | |
| | | | | |
| | | | TGAGTAAA ATCCGTA | |
| | | | GGAAAC__ | |
| GAM201 | LOC219988 | 5' | ATGCCTACAGTGTCTGTATTAG 3534 | GTT _ CA |
| | A | | TC TAT GACAC TAGGCAT | |
| | | | | |
| | | | AG ATG CTGTG ATCCGTA | |
| | | | ATT T AC | |
| GAM202 | BHMT2 | 3' | CTGAAATAATCGAACAGGAAA 1730 | A TA |
| | | | TTTCT GTTC ATTATTCAG | |
| | | | | |
| | | | AAAGG CAAG TAATAAAGTC | |
| | | | A C_ | |
| GAM202 | COL15A1 | 3' | AAATAATCTGAAACTAGAAA 862 | _ TA |
| | | | TTTCTAGTT C ATTATTT | |
| | | | | |
| | | | AAAGATCAA G TAATAAA | |
| | | | A TC | |
| GAM202 | PDGFRA | 3' | TCTGAAATAATGGGATTAGAAA 1280 | A |
| | | | TTTCTAGTTCTA TTATTCAGA | |
| | | | | |
| | | | AAAGATTAGGGT AATAAAGTCT | |
| | | | - | |
| GAM202 | DORFIN | 5' | TTCTGGCCTCCAGAACTAGA 1631 | AATTATT |
| | | | TCTAGTTCT TCAGAA | |
| | | | | |
| | | | AGATCAAGA GGTCTT | |
| | | | CCTCC__ | |
| GAM202 | FLJ20034 | 5' | TCTGTGATAAGCAGAACTAGAA 1732 | AA T |
| | A | | TTTCTAGTTCT TTATT CAGA | |
| | | | | |
| | | | AAAGATCAAGA AATAG GTCT | |
| | | | CG T | |
| GAM202 | KIAA0831 | 5' | TCTGCATTGAACTAGAAA 1589 | T TATTT |
| | | | TTTCTAGTTC AAT CAGA | |
| | | | | |

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|--------|-----------|----|-----------------------------|-------|------|
| | | | AAAGATCAAG TTA GTCT | | |
| | | | — C— | | |
| GAM202 | MBLL39 | 3' | TTCTGAAATAATCAGCAGAAA 1243 | A | CTA |
| | | | TTTCT GTT ATTATTT CAGAA | | |
| | | | | | |
| | | | AAAGA CGA TAATAAAGTCTT | | |
| | | | — C— | | |
| GAM202 | TSP-NY | 3' | CTGGGAGCAGAACTAGAAA 2261 | AATTA | TT |
| | | | TTTCTAGTTCT T CAG | | |
| | | | | | |
| | | | AAAGATCAAGA A GTC | | |
| | | | CG— GG | | |
| GAM202 | LOC112840 | 3' | CTGAAAGTAGAACTGAAA 2384 | T | ATTA |
| | | | TTTC AGTTCTA TTTCAG | | |
| | | | | | |
| | | | AAAG TCAAGAT AAAGTC | | |
| | | | — G— | | |
| GAM202 | LOC136895 | 3' | AAATATTAGAACTAGAAA 2458 | T | |
| | | | TTTCTAGTTCTAAT ATTT | | |
| | | | | | |
| | | | AAAGATCAAGATTA TAAA | | |
| | | | — | | |
| GAM202 | LOC145790 | 5' | TTCTGAAATAATCTCTGGAGG 3083 | TTCTA | |
| | | | TTTCTAG ATTATTT CAGAA | | |
| | | | | | |
| | | | GGAGGTC TAATAAAGTCTT | | |
| | | | TC— | | |
| GAM202 | LOC151040 | 3' | TCAGGGATCTAGAACTAGAAA 3153 | ATT | TT A |
| | | | TTTCTAGTTCTA AT C GA | | |
| | | | | | |
| | | | AAAGATCAAGAT TA G CT | | |
| | | | C— GG A | | |
| GAM202 | LOC157869 | 3' | TTCTGAAATAATTTCAAGC 3207 | CT— | |
| | | | GTT AATTATTT CAGAA | | |
| | | | | | |
| | | | CGA TTAATAAAGTCTT | | |
| | | | ACT | | |
| GAM202 | LOC222028 | 3' | TTCTAAGTAGTTAAAATTAGAA 3631 | C | C |
| | A | | TTTCTAGTT TAATTATTT AGAA | | |
| | | | | | |
| | | | AAAGATTAA ATTGATGAA TCTT | | |
| | | | A — | | |
| GAM202 | LOC222252 | 3' | TCAGGGATCTAGAACTAGAAA 3652 | ATT | TT A |
| | | | TTTCTAGTTCTA AT C GA | | |
| | | | | | |
| | | | AAAGATCAAGAT TA G CT | | |
| | | | C— GG A | | |
| GAM203 | FLJ20485 | 3' | TGTGATGGAGTATAC 1875 | CGA | T |
| | | | GTATACT CCATC ACG | | |
| | | | | | |

CATATGA GGTAG TGT

GAM203 LOC132617 3' CGTAGATGATGTGAATGA 3040 A TCGAC
TCGT TAC CATCTACG
||||| ||| |||||
AGTA GTG GTAGATGC
A TA__

GAM204 PER2 3' AGATATGTAAATAAGCTCTCA 2013 A T AC
A AG GC GTTTACATATCT
| || || |||||
A TC CG TAAATGTATAGA
C T AA

GAM204 SLC14A2 3' AGATATGTTTAGTTTAGACTTT 1360 GC__ GTTT
ATA TATAAAGT AC ACATATCT
||||| || |||||
ATATTTCA TG TGTATAGA
GATT ATT_

GAM204 C20orf82 3' ATGTAAACGCCACCTTA 3316 A CA
TAA GTG CGTTTACAT
||| ||| |||||
ATT CAC GCAAATGTA
C CC

GAM204 DKFZp566D234 3' ATATGTAAATTATGCTTTA 2610 CAC
TAAAGTG GTTTACATAT
||||| |||||
ATTTCTG TAAATGTATA
AT_

GAM204 EFS2 3' AGACATGGGTGTGCACCTTA 1257 A TTTA A
TAA GTGCACG CAT TCT
||| ||||| ||| |||
ATT CACGTGT GTA AGA
C GG__ C

GAM204 FLJ13194 3' ATGTTTATGCACACTTTATA 2140 CA TT
TATAAAGTG CGT ACAT
||||||| ||| |||
ATATTTTAC GTA TGTA
AC TT

GAM204 ZNF291 3' AGATATGGCATGTACTTTA 1930 C TTA
TAAAGTGCA GT CATATCT
||||||| || |||||
ATTTTCATGT CG GTATAGA
A __

GAM204 LOC157503 3' ATGAAACCATGCACTTTGTA 3380 C_ A
TATAAAGTGCA GTTT CAT
||||||| ||| |||
ATGTTTCACGT CAAA GTA
AC _

GAM204 LOC254431 3' AGATATGTAAACACTGGTAC 3716 AC__
GTGC GTTTACATATCT
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|--------|---------|----|---------------------------|---------|--|
| | | | CATG CAAATGTATAGA | | |
| | | | GTCA | | |
| GAM205 | BRCA1 | 3' | CTAATGAAGTGGGCTCCA 1390 | A A T | |
| | | | TG GA GTCT TTTCATTAG | | |
| | | | | | |
| | | | AC CT CGGG GAAGTAATC | | |
| | | | _ _ T | | |
| GAM205 | C18orf1 | 3' | AGTGAAGGACCTCTCA 2562 | A TT | |
| | | | TGAGA GTCT TTCATT | | |
| | | | | | |
| | | | ACTCT CAGG AAGTGA | | |
| | | | C _ | | |
| GAM205 | CENTD1 | 3' | GCTAATGATGACATCTCA 1614 | A TTTT | |
| | | | TGAGA GTC TCATTAGC | | |
| | | | | | |
| | | | ACTCT CAG AGTAATCG | | |
| | | | A T _ | | |
| GAM205 | CENTD1 | 3' | GCTAATGATGACATCTCA 2473 | A TTTT | |
| | | | TGAGA GTC TCATTAGC | | |
| | | | | | |
| | | | ACTCT CAG AGTAATCG | | |
| | | | A T _ | | |
| GAM205 | CPNE3 | 3' | CTAATGAAAACTGCTTA 1068 | A CT | |
| | | | TGAG AGT TTTCATTAG | | |
| | | | | | |
| | | | ATTC TCA AAAAGTAATC | | |
| | | | G _ | | |
| GAM205 | EPB72 | 3' | CTAATGAAAAACATTACTC 1086 | A C | |
| | | | GAG AGT TTTTTCATTAG | | |
| | | | | | |
| | | | CTC TTA AAAAAGTAATC | | |
| | | | A C | | |
| GAM205 | GBP1 | 3' | GCTAATGAAGAAAACTTCTC 894 | C | |
| | | | GAGAAGT TTTTTCATTAGC | | |
| | | | | | |
| | | | CTCTTCA AAGAAGTAATCG | | |
| | | | A | | |
| GAM205 | MMP2 | 3' | GCCAATGGAGACTGTCTCA 1124 | _ TTT A | |
| | | | TGAGA AGTCTT CATT GC | | |
| | | | | | |
| | | | ACTCT TCAGAG GTAA CG | | |
| | | | G _ C | | |
| GAM205 | PSCD4 | 3' | CTAACAGGAAACACTTCTCA 1447 | C CA | |
| | | | TGAGAAGT TTTTT TTAG | | |
| | | | | | |
| | | | ACTCTTCA AAAGG AATC | | |
| | | | C AC | | |
| GAM205 | SLC7A6 | 3' | GCTAATGAAATGGGAACCTC 1077 | AAG T | |
| | | | GAG TCT TTTCATTAGC | | |
| | | | | | |

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|--------|----------|----|-----------------------------|----------|--|
| | | | CTC GGG AAAGTAATCG | | |
| | | | CAA T | | |
| GAM205 | XKRY | 5' | CTAATGAAAATTATTCTC 1142 | GTCT | |
| | | | GAGAA TTTTCATTAG | | |
| | | | | | |
| | | | CTCTT AAAAGTAATC | | |
| | | | ATT_ | | |
| GAM205 | XKRY | 5' | CTAATGAAAATTATTCTC 2551 | GTCT | |
| | | | GAGAA TTTTCATTAG | | |
| | | | | | |
| | | | CTCTT AAAAGTAATC | | |
| | | | ATT_ | | |
| GAM205 | C1orf16 | 3' | GCCAATGGGAACCTTCTCA 1568 | CTT TT A | |
| | | | TGAGAAGT T CATT GC | | |
| | | | | | |
| | | | ACTCTTCA A GTAA CG | | |
| | | | ___ GG C | | |
| GAM205 | C3orf4 | 3' | GCTAATGTCTGTTAGACTTTTC 1890 | TTTT__ | |
| | A | | TGAGAAGTCT CATTAGC | | |
| | | | | | |
| | | | ACTTTTCAGA GTAATCG | | |
| | | | TTGTCT | | |
| GAM205 | FLJ10483 | 3' | GCCAATGAAAATGTGCTTC 1781 | CT_ A | |
| | | | GAAGT TTTTCATT GC | | |
| | | | | | |
| | | | CTTCG AAAAGTAA CG | | |
| | | | TGT C | | |
| GAM205 | FLJ12568 | 3' | GCTAATGAAAATGTTTTCT 2122 | TCT | |
| | | | AGAAG TTTTCATTAGC | | |
| | | | | | |
| | | | TCTTT AAAAGTAATCG | | |
| | | | TGT | | |
| GAM205 | FLJ20340 | 3' | GCTTTGAAAAACTTTTCA 1750 | CT TT | |
| | | | TGAGAAGT TTTTCA AGC | | |
| | | | | | |
| | | | ACTTTTCA AAAAGT TCG | | |
| | | | ___ T_ | | |
| GAM205 | FLJ20727 | 5' | GCTAATGGACTTGACTCTCA 1769 | A TTT | |
| | | | TGAGA GTC TTCATTAGC | | |
| | | | | | |
| | | | ACTCT CAG AGGTAATCG | | |
| | | | _ TTC | | |
| GAM205 | FLJ20736 | 3' | CTAATGGACATCTTCTCA 1770 | TCTTT | |
| | | | TGAGAAG TTCATTAG | | |
| | | | | | |
| | | | ACTCTTC AGGTAATC | | |
| | | | TAC__ | | |
| GAM205 | PDE1C | 3' | GCTAATGACCTGGCTTTCA 1172 | A TTTT | |
| | | | TGAGA GTC TCATTAGC | | |
| | | | | | |

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|--------|-----------|----|-----------------------------|----------|--|
| | | | ACTTT CGG AGTAATCG | | |
| | | | _ TCC_ | | |
| GAM205 | TOB2 | 5' | GCTAAGGGTGAACTTTTCA 3680 | C T A | |
| | | | TGAGAAGT TT TTC TTAGC | | |
| | | | | | |
| | | | ACTTTTCA AG GGG AATCG | | |
| | | | A T _ | | |
| GAM205 | TSC22 | 3' | CTAATGAAATGGATTTCCTCA 1264 | A T | |
| | | | TG GAAGTCT TTTTCATTAG | | |
| | | | | | |
| | | | AC CTTTAGG AAAGTAATC | | |
| | | | C T | | |
| GAM205 | TSP-NY | 3' | GCTAAGAATGAAAAAGACTTCT 2262 | | |
| | C | | GAGAAGTCTTTTTCAT TAGC | | |
| | | | | | |
| | | | CTCTTCAGAAAAAGTA ATCG | | |
| | | | AGA | | |
| GAM205 | TUCAN | 3' | GCTAACAAAAGCTTCTCA 1598 | T TCA | |
| | | | TGAGAAG CTTTT TTAGC | | |
| | | | | | |
| | | | ACTCTTC GAAAA AATCG | | |
| | | | _ C_ | | |
| GAM205 | LOC138241 | 5' | GCCAATGGGGGAATTCTCA 3019 | GTC TT A | |
| | | | TGAGAA TTT CATT GC | | |
| | | | | | |
| | | | ACTCTT AGG GTAA CG | | |
| | | | A_ GG C | | |
| GAM205 | LOC152345 | 3' | AATGGAGAGACTTCCG 3170 | A T | |
| | | | TG GAAGTCTTTT CATT | | |
| | | | | | |
| | | | GC CTTCAGAGAG GTAA | | |
| | | | _ _ | | |
| GAM205 | LOC154214 | 5' | CTAATGAAAAGGACCTTA 3189 | AA | |
| | | | TGAG GTCTTTTTCATTAG | | |
| | | | | | |
| | | | ATTC CAGGAAAAGTAATC | | |
| | | | _ | | |
| GAM205 | LOC154790 | 5' | AATGAAAAGAACTTCCCA 3192 | A CT | |
| | | | TG GAAGT TTTTCATT | | |
| | | | | | |
| | | | AC CTTCA AAAAGTAA | | |
| | | | C AG | | |
| GAM205 | LOC158427 | 3' | CTAATGAAAATAACTCCCA 2478 | A A CT | |
| | | | TG GA GT TTTTCATTAG | | |
| | | | | | |
| | | | AC CT CA AAAAGTAATC | | |
| | | | C _ AT | | |
| GAM205 | LOC161003 | 5' | AGTATAAAAGCTTCTCA 2520 | T TC | |
| | | | TGAGAAG CTTTT ATT | | |
| | | | | | |

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| | | ACTCTTC GAAAA TGA | | |
| | | — TA | | |
| GAM205 | LOC200830 3' | GCTAATGGGCTGACTACTCA 3480 | A | TTT |
| | | — TGAG AGTC TTCATTAGC | | |
| | | | | |
| | | ACTC TCAG GGGTAATCG | | |
| | | A TC_ | | |
| GAM205 | LOC221421 3' | GCTAATGAAAGAGATTCT 3558 | G | |
| | | AGAA TCTTTTTCATTAGC | | |
| | | | | |
| | | TCTT AGAGAAAGTAATCG | | |
| | | — | | |
| GAM205 | LOC257017 5' | CTAAGTTAAGACTTTTCA 3736 | | TTTCA |
| | | — TGAGAAGTCTT TTAG | | |
| | | | | |
| | | ACTTTTCAGAA AATC | | |
| | | TTG_ | | |
| GAM205 | LOC257353 5' | GCTAATAATGATGGCCTCTCA 3738 | A | T TTC |
| | | — TGAGA GTC TT ATTAGC | | |
| | | | | |
| | | ACTCT CGG AG TAATCG | | |
| | | C T TAA | | |
| GAM205 | LOC90459 3' | GCCAATGAATTTCTGCTTTTCA 2642 | CTTT_ | A |
| | | — TGAGAAGT TTCATT GC | | |
| | | | | |
| | | ACTTTTCG AAGTAA CG | | |
| | | TCTTT C | | |
| GAM206 | CXADR 3' | TATTGAGATGACACTAGGTGC 820 | _ | CA CCC |
| | | GCAC TAG TC TTTCAATA | | |
| | | | | |
| | | CGTG ATC AG AGAGTTAT | | |
| | | G AC T_ | | |
| GAM206 | EPB72 3' | TATTGAGGATTGAGCCAGTGC 1087 | A | A CCC |
| | | — GCACT GC TC TTTCAATA | | |
| | | | | |
| | | CGTGA CG AG GGAGTTAT | | |
| | | C _ TTA | | |
| GAM206 | FCAR 5' | ATTGAAAGGAGAGCAACGG 880 | CACTA | A C |
| | | CCG GC TC CCTTTCAAT | | |
| | | | | |
| | | GGC CG AG GGAAAGTTA | | |
| | | AA_ _ A | | |
| GAM206 | FCAR 5' | ATTGAAAGGAGAGCAACGG 2400 | CACTA | A C |
| | | CCG GC TC CCTTTCAAT | | |
| | | | | |
| | | GGC CG AG GGAAAGTTA | | |
| | | AA_ _ A | | |
| GAM206 | FCAR 5' | ATTGAAAGGAGAGCAACGG 2401 | CACTA | A C |
| | | CCG GC TC CCTTTCAAT | | |
| | | | | |

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| | | | GGC CG AG GGAAAGTTA | | |
| | | | AA__ _ A | | |
| GAM206 | FCAR | 5' | ATTGAAAGGAGAGCAACGG 2402 | CACTA A C | |
| | | | CCG GC TC CCTTTCAAT | | |
| | | | | | |
| | | | GGC CG AG GGAAAGTTA | | |
| | | | AA__ _ A | | |
| GAM206 | FCAR | 5' | ATTGAAAGGAGAGCAACGG 2403 | CACTA A C | |
| | | | CCG GC TC CCTTTCAAT | | |
| | | | | | |
| | | | GGC CG AG GGAAAGTTA | | |
| | | | AA__ _ A | | |
| GAM206 | FCAR | 5' | ATTGAAAGGAGAGCAACGG 2404 | CACTA A C | |
| | | | CCG GC TC CCTTTCAAT | | |
| | | | | | |
| | | | GGC CG AG GGAAAGTTA | | |
| | | | AA__ _ A | | |
| GAM206 | FCAR | 5' | ATTGAAAGGAGAGCAACGG 2406 | CACTA A C | |
| | | | CCG GC TC CCTTTCAAT | | |
| | | | | | |
| | | | GGC CG AG GGAAAGTTA | | |
| | | | AA__ _ A | | |
| GAM206 | KCNAB1 | 3' | TGAAAATGCTAGTGGG 2585 | G CCCC | |
| | | | CC CACTAGCAT TTTCA | | |
| | | | | | |
| | | | GG GTGATCGTA AAAGT | | |
| | | | — — | | |
| GAM206 | NCOA6 | 3' | TATTGAAAGGAGCTAATGC 1468 | C ATCC | |
| | | | GCA TAGC CCTTTCAATA | | |
| | | | | | |
| | | | CGT ATCG GGAAAGTTAT | | |
| | | | A A__ | | |
| GAM206 | SDHC | 3' | TATTGAAAGAAGAGAGGTGGGG 2856 | G AGCA CC | |
| | | | CC CACT TC CTTTCAATA | | |
| | | | | | |
| | | | GG GTGG AG GAAAGTTAT | | |
| | | | G AG__ AA | | |
| GAM206 | CBLN1 | 5' | GGAGGGGACGCTAGTCGCGG 1101 | _ A | |
| | | | CCGC ACTAGC TCCCCTTT | | |
| | | | | | |
| | | | GGCG TGATCG AGGGGAGG | | |
| | | | C C | | |
| GAM206 | CSTF2 | 3' | TATTGAAAAAAGATGACCTGC 819 | CTAG CCC | |
| | | | GCA CATC TTTCAATA | | |
| | | | | | |
| | | | CGT GTAG AAAGTTAT | | |
| | | | CCA_ AAA | | |
| GAM206 | GS3955 | 5' | AAAGGGGGTGCAGCGCGG 1953 | A A | |
| | | | CCGC CT GCATCCCCTTT | | |
| | | | | | |

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|--------|-----------|----|------------------------|------|------------|
| | | | GGCG GA CGTGGGGGAAA | | |
| | | | C _ | | |
| GAM206 | KIAA0184 | 3' | ATTGAAAGAGGTGTGCTGG | 2715 | TC _ |
| | | | CTAGCA CC CTTTCAAT | | |
| | | | | | |
| | | | GGTCGT GG GAAAGTTA | | |
| | | | GT A | | |
| GAM206 | MGC14697 | 5' | GTTGAAGGACACCAGCTGCGG | 2276 | CTA ATCCC_ |
| | | | CCGCA GC CTTTCAAT | | |
| | | | | | |
| | | | GGCGT CG GGAAGTTG | | |
| | | | ___ ACCACA | | |
| GAM206 | RRN3 | 3' | AGGTGGAAGTTGCTAGTGC | 1827 | ___ _ |
| | | | GCACTAGCA TCC CCT | | |
| | | | | | |
| | | | CGTGATCGT AGG GGA | | |
| | | | TGA T | | |
| GAM206 | WDR13 | 5' | AAGGAATGCTAGGCGG | 1759 | A CC |
| | | | CCGC CTAGCAT CCTT | | |
| | | | | | |
| | | | GGCG GATCGTA GGAA | | |
| | | | _ A_ | | |
| GAM206 | LOC219287 | 3' | GAAAGAGGGATGCTACACGG | 3609 | CAC _ |
| | | | CCG TAGCATCCC CTTTC | | |
| | | | | | |
| | | | GGC ATCGTAGGG GAAAG | | |
| | | | AC_ A | | |
| GAM206 | LOC221979 | 5' | ATTGAAACTGCTAGTG | 3571 | TCCCC |
| | | | CACTAGCA TTTCAAT | | |
| | | | | | |
| | | | GTGATCGT AAAGTTA | | |
| | | | C___ | | |
| GAM206 | LOC255328 | 3' | TATTGAAAGGGCTGCACCATGC | 3710 | CTA_ TC |
| | | | GCA GCA CCCTTTCAATA | | |
| | | | | | |
| | | | CGT CGT GGGAAAGTTAT | | |
| | | | ACCA C_ | | |
| GAM206 | LOC257115 | 3' | TATTGAAAGGAAAGTGCTATCG | 3709 | CAC CC_ |
| | | | CG TAGCAT CCTTTCAATA | | |
| | | | | | |
| | | | GC ATCGTG GGAAAGTTAT | | |
| | | | T_ AAA | | |
| GAM206 | LOC51145 | 3' | ATTGAAAGGGGAAATGTGTCA | 1666 | C TAGCA |
| | | | C GCAC TCCCCTTTCAAT | | |
| | | | | | |
| | | | A TGTG AGGGGAAAGTTA | | |
| | | | C TAA_ | | |
| GAM207 | BCL11A | 3' | AAACTAGAACAGGTATAT | 2018 | TA |
| | | | ATATACCTGTTTT TTT | | |
| | | | | | |

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|--------|----------|----|-------------------------|------|---------|
| | | | TATATGGACAAGA AAA | | |
| | | | TC | | |
| GAM207 | C8orf1 | 3' | GAAACCTTGACAGGTA | 1099 | TA TTTA |
| | | | TGA TACCTGTT TTTC | | |
| | | | | | |
| | | | ACT ATGGACAG AAAG | | |
| | | | TC TTCC | | |
| GAM207 | KPNA1 | 3' | AAATAAAAACAGTATC | 3159 | TAC |
| | | | GATA CTGTTTTTATTT | | |
| | | | | | |
| | | | CTAT GACAAAATAAA | | |
| | | | — | | |
| GAM207 | NRXN1 | 3' | AAATAAAAACAAGTATCTCA | 2457 | T C |
| | | | TGA ATAC TGTTTTTATTT | | |
| | | | | | |
| | | | ACT TATG ACAAAAATAAA | | |
| | | | C A | | |
| GAM207 | NRXN1 | 3' | AAATAAAAACAAGTATCTCA | 1158 | T C |
| | | | TGA ATAC TGTTTTTATTT | | |
| | | | | | |
| | | | ACT TATG ACAAAAATAAA | | |
| | | | C A | | |
| GAM207 | PCDHGA8 | 3' | AAATAATTTTAAAGGTGTATCA | 1459 | GTTT__ |
| | | | TGATATACCT TTATTT | | |
| | | | | | |
| | | | ACTATGTGGA AATAAA | | |
| | | | ATTTTT | | |
| GAM207 | SNX5 | 3' | GAAATATCTACAGGTATAT | 1500 | TTT |
| | | | ATATACCTGT TATTC | | |
| | | | | | |
| | | | TATATGGACA ATAAAG | | |
| | | | TCT | | |
| GAM207 | BNIP2 | 3' | GAAATATGCAGGTATAT | 2762 | TTT |
| | | | ATATACCTGT TATTC | | |
| | | | | | |
| | | | TATATGGACG ATAAAG | | |
| | | | T__ | | |
| GAM207 | DRIL2 | 3' | AAATGAAAACAGATCA | 1305 | ATAC |
| | | | TGAT CTGTTTTTATTT | | |
| | | | | | |
| | | | ACTA GACAAAAGTAAA | | |
| | | | — | | |
| GAM207 | DVS27 | 3' | AAATAAAAGCAGAAATGTATATC | 2335 | __ |
| | A | | TGATATAC CTGTTTTTATTT | | |
| | | | | | |
| | | | ACTATATG GACGAAAATAAA | | |
| | | | TAA | | |
| GAM207 | FLJ12960 | 3' | GAAGGGGGAGCAGGCACATCA | 2074 | ATA TA |
| | | | TGAT CCTGTTTT TTTC | | |
| | | | | | |

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|--------|-----------|----|---------------------------|------|----|
| | | | ACTA GGACGAGG GAAG | | |
| | | | CAC GG | | |
| GAM207 | FLJ20793 | 3' | GAATACTAACAGGTATTTCA 3542 | T | TT |
| | | | TGA ATACCTGTT TATTT | | |
| | | | | | |
| | | | ACT TATGGACAA ATAAG | | |
| | | | T TC | | |
| GAM207 | KIAA0040 | 3' | GAAATAAAATTAAAGGTATA 1515 | GT__ | |
| | | | TATACCT TTTTATTT | | |
| | | | | | |
| | | | ATATGGA AAAATAAAG | | |
| | | | AATT | | |
| GAM207 | KIAA1349 | 3' | GAAATAAAAGCAGCATCA 2893 | ATAC | |
| | | | TGAT CTGTTTTTATTT | | |
| | | | | | |
| | | | ACTA GACGAAAATAAAG | | |
| | | | C__ | | |
| GAM207 | KIAA1373 | 3' | AAATATTAACAGGTATAT 2903 | TT | |
| | | | ATATACCTGTT TATTT | | |
| | | | | | |
| | | | TATATGGACAA ATAAA | | |
| | | | TT | | |
| GAM207 | SCDGF-B | 3' | AAGTAGAAAGGTATATCA 2147 | GT | |
| | | | TGATATACCT TTTTATTT | | |
| | | | | | |
| | | | ACTATATGGA AAGATGAA | | |
| | | | — | | |
| GAM207 | SCDGF-B | 3' | AAGTAGAAAGGTATATCA 2314 | GT | |
| | | | TGATATACCT TTTTATTT | | |
| | | | | | |
| | | | ACTATATGGA AAGATGAA | | |
| | | | — | | |
| GAM207 | LOC121441 | 3' | AAATAAAACAGGAATATTA 2991 | A | |
| | | | TGATAT CCTGTTTTTATTT | | |
| | | | | | |
| | | | ATTATA GGACAAAAATAAA | | |
| | | | A | | |
| GAM207 | LOC157729 | 3' | AAATAAAGATAGCATGTCA 3205 | AC | |
| | | | TGATAT CTGTTTTTATTT | | |
| | | | | | |
| | | | ACTGTA GATAGAAATAAA | | |
| | | | C_ | | |
| GAM207 | LOC200339 | 3' | GAAGTTCACAGGTATATC 3475 | TTTT | |
| | | | GATATACCTGT ATTT | | |
| | | | | | |
| | | | CTATATGGACA TGAAG | | |
| | | | CT__ | | |
| GAM207 | LOC221300 | 3' | AAATGGCAAACAGGTATAT 3545 | _ | |
| | | | ATATACCTGTTT TTATTT | | |
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|--------|-----------|----|-----------------------------|-----|---------|
| | | | TATATGGACAAA GGTAAG | | |
| | | | C | | |
| GAM207 | LOC257235 | 5' | GAAACCATTCAGGTATTTCA 3728 | T | TTTTA |
| | | | TGA ATACCTGT TTTC | | |
| | | | | | |
| | | | ACT TATGGACG AAAG | | |
| | | | T TTACC | | |
| GAM207 | LOC93333 | 5' | AAATGGTTAAGGGTATATCA 2932 | | GTTT |
| | | | TGATATACCT TTATTT | | |
| | | | | | |
| | | | ACTATATGGG GGTAAG | | |
| | | | AATT | | |
| GAM208 | PCDH7 | 3' | AAACAGTATTAATGCAGAAATG 938 | A | _ |
| | | | CGT TC GCATTAATACTGTTT | | |
| | | | | | |
| | | | GTA AG CGTAATTATGACAAA | | |
| | | | A A | | |
| GAM208 | TRC8 | 3' | AAACAGTATCAATGTTGA 1365 | _ | A |
| | | | TCG CATT ATACTGTTT | | |
| | | | | | |
| | | | AGT GTAA TATGACAAA | | |
| | | | T C | | |
| GAM208 | LOC145225 | 3' | AAACAGTATTAACCCTGC 3275 | ___ | |
| | | | GCA TTAATACTGTTT | | |
| | | | | | |
| | | | CGT AATTATGACAAA | | |
| | | | CCC | | |
| GAM209 | BHMT2 | 3' | AGCATTATTGAAATAAATGTTT 1729 | C__ | TGG |
| | A | | TAGACATTTA CA GATGCT | | |
| | | | | | |
| | | | ATTTGTAAAT GT TTACGA | | |
| | | | AAA TA_ | | |
| GAM209 | CANX | 3' | AGCATCCTGATTAAATGTCTG 3409 | | CCA |
| | | | TAGACATTTA TGGGATGCT | | |
| | | | | | |
| | | | GTCTGTAAAT GTCCTACGA | | |
| | | | TA_ | | |
| GAM209 | COPG2 | 3' | AGCAGATCAAGCAAATGTCTA 3194 | | ACCA GA |
| | | | TAGACATTT TGG TGCT | | |
| | | | | | |
| | | | ATCTGTAAA ACT ACGA | | |
| | | | CGA_ AG | | |
| GAM209 | MS4A1 | 3' | CATTTACAAATGTTTAGT 711 | | ACCA GG |
| | | | ACTAGACATTT TG ATG | | |
| | | | | | |
| | | | TGATTTGTAAA AC TAC | | |
| | | | C__ TT | | |
| GAM209 | SEL1L | 3' | CATGTGTATTAATGTCTA 1180 | ___ | _ |
| | | | TAGACATT TAC CATG | | |
| | | | | | |

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|--------|-----------|----|-----------------------------|--------------|--|
| | | | ATCTGTAA ATG GTAC | | |
| | | | TT T | | |
| GAM209 | TPK1 | 3' | CATCCTTAAATGTCTA 1988 | CCAT | |
| | | | TAGACATTTA GGGATG | | |
| | | | | | |
| | | | ATCTGTAAAT TCCTAC | | |
| | | | _____ | | |
| GAM209 | CYorf14 | 3' | CTGTGGGCAATAAATGTCTG 1839 | _____ | |
| | | | TAGACATTTA CCATGG | | |
| | | | | | |
| | | | GTCTGTAAAT GGTGTC | | |
| | | | AACG | | |
| GAM209 | HSPC228 | 3' | AGCATTTCATAAATGTTTAGT 1688 | CCA GG | |
| | | | ACTAGACATTTA TG ATGCT | | |
| | | | | | |
| | | | TGATTTGTAAAT AC TACGA | | |
| | | | ____ TT | | |
| GAM209 | MGC1127 | 3' | AGCTGGGTAATAAATGTCTA 2336 | ____ ATGGGAT | |
| | | | TAGACATT TACC GCT | | |
| | | | | | |
| | | | ATCTGTAA ATGG CGA | | |
| | | | ATA GT_____ | | |
| GAM209 | SLC16A4 | 3' | AGCATTCTGAGAAATGTCTA 1144 | ACCA | |
| | | | TAGACATTT TGGGATGCT | | |
| | | | | | |
| | | | ATCTGTAAA GTCTTACGA | | |
| | | | GA__ | | |
| GAM209 | LOC147180 | 5' | CACCTGTTTAAATGTCTG 3292 | CC A | |
| | | | TAGACATTTA ATGGG TG | | |
| | | | | | |
| | | | GTCTGTAAAT TGTCC AC | | |
| | | | T_ _ | | |
| GAM209 | LOC148195 | 5' | GCATCCCATTTGGTGTCTAGT 3297 | A ATTT _ | |
| | | | ACT GAC ACCA TGGGATGC | | |
| | | | | | |
| | | | TGA CTG TGGT ACCCTACG | | |
| | | | _ ____ T | | |
| GAM209 | LOC158572 | 3' | AGCATCCTTTCAATAAATGCCT 3221 | A CCAT_ | |
| | G | | TAG CATTTA GGGATGCT | | |
| | | | | | |
| | | | GTC GTAAAT TCCTACGA | | |
| | | | C AACTT | | |
| GAM209 | LOC201595 | 3' | AGCACTGCTGTAAATGTCTAG 3453 | CATG A | |
| | | | CTAGACATTTAC GG TGCT | | |
| | | | | | |
| | | | GATCTGTAAATG TC ACGA | | |
| | | | TCG_ _ | | |
| GAM209 | LOC203427 | 5' | CATTTAGGAAGCAAGATGTCTA 3464 | ACCATG_ | |
| | G | | CTAGACATTT GGATG | | |
| | | | | | |

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|--------|---------------|----|------------------------------|-------|-----|--------|
| | | | GATCTGTAGA | TTTAC | | |
| | | | ACGAAGGA | | | |
| GAM210 | PDE1A | 3' | ATCAGCATGAAAACATCCTA | 1171 | AT | _ GA |
| | | | TAG TGTTTTCA GT GAT | | | |
| | | | | | | |
| | | | ATC ACAAAGT CG CTA | | | |
| | | | CT A A_ | | | |
| GAM210 | ELAC1 | 3' | AATCATCTCACCCCGAAATGCA | 3506 | _ | A__ |
| | | | TGT TTTC GTGAGATGATT | | | |
| | | | | | | |
| | | | ACG AAAG CACTCTACTAA | | | |
| | | | T CCC | | | |
| GAM210 | LOC154790 | 5' | AATCAGATCATATGAAAACAAT | 3191 | _ | GA |
| | | | CTA TAGATTGTTTTCA GTGA TGATT | | | |
| | | | | | | |
| | | | ATCTAACAAAAGT TACT ACTAA | | | |
| | | | A AG | | | |
| GAM210 | LOC158434 | 3' | CAGTCACTAAAAACAATC | 3389 | C | GA |
| | | | GATTGTTTT AGTGA TG | | | |
| | | | | | | |
| | | | CTAACAAA TCACT AC | | | |
| | | | A G_ | | | |
| GAM211 | MAP3K5 | 3' | TCTGAGTAGAAATGCGT | 1261 | A | TT |
| | | | ACGCAT TTCTACTC GGA | | | |
| | | | | | | |
| | | | TGCGTA AAGATGAG TCT | | | |
| | | | - - | | | |
| GAM211 | DKFZP564F0522 | 3' | TAATTCCACAGTCAGAACATGC | 2825 | A | _ CT |
| | | | GCAT TTCT ACT TGGAATTA | | | |
| | | | | | | |
| | | | CGTA AAGA TGA ACCTTAAT | | | |
| | | | C C C_ | | | |
| GAM211 | GPCR150 | 3' | TAATTCCAAGAAGTTTTTATAG | 1496 | GC | TTCT _ |
| | | | T AC ATA ACT CTTGGAATTA | | | |
| | | | | | | |
| | | | TG TAT TGA GAACCTTAAT | | | |
| | | | A_ TTT_ A | | | |
| GAM211 | SLC26A7 | 3' | TAATTCAGTATAGAATATGC | 2340 | CT | TG |
| | | | GCATATTCTA CT GAATTA | | | |
| | | | | | | |
| | | | CGTATAAGAT GA CTTAAT | | | |
| | | | AT _ | | | |
| GAM211 | SLC6A14 | 3' | TAATTTCAAATAGAATATG | 1369 | CTC | |
| | | | CATATTCTA TTGGAATTA | | | |
| | | | | | | |
| | | | GTATAAGAT AACTTTAAT | | | |
| | | | A_ | | | |
| GAM211 | LOC116228 | 3' | TAGTTCTGAATTAATAATATGC | 2980 | C | CTC TG |
| | | | GCATATT TA T GAATTA | | | |
| | | | | | | |

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|--------|-----------|----|----------------------------|----------|-----|
| | | | CGTATAA AT A CTTGAT | | |
| | | | A TA_ GT | | |
| GAM212 | CCNC | 3' | ATAATGTCTTCAGTGGAACAC 1192 | A_____ | III |
| | | | GTGTTCCA ACATTA T | | |
| | | | | | |
| | | | CACAAGGT TGTAAT A | | |
| | | | GACTTC III | | |
| GAM212 | MSL3L1 | 5' | TAATGGTTGGAACAGAA 1331 | G A | |
| | | | TTC TGTTCCAA CATTA | | |
| | | | | | |
| | | | AAG ACAAGGTT GTAAT | | |
| | | | _ G | | |
| GAM212 | THBS1 | 3' | TAATGTTTGCACACTGAA 1004 | _ TC | |
| | | | TTC GTGT CAAACATTA | | |
| | | | | | |
| | | | AAG CACA GTTTGTAAT | | |
| | | | T C_ | | |
| GAM212 | CSRP3 | 3' | TAATGCTTGGAATGGGAG 1031 | G A | |
| | | | TTC TGTTCCAA CATTA | | |
| | | | | | |
| | | | GAG GTAAGGTT GTAAT | | |
| | | | G C | | |
| GAM212 | FLJ11181 | 5' | TAATGTTCGGCAAACATGAA 1817 | _ A | |
| | | | TTCGTGTT CC AACATTA | | |
| | | | | | |
| | | | AAGTACAA GG TTGTAAT | | |
| | | | AC C | | |
| GAM212 | FLJ23132 | 3' | TAATGTTTCCAACATGAA 3692 | CC | |
| | | | TTCGTGTT AAACATTA | | |
| | | | | | |
| | | | AAGTACAA TTTGTAAT | | |
| | | | CC | | |
| GAM212 | GAB3 | 3' | TAATGTTTGTTACAGAA 2378 | G TC | |
| | | | TTC TGT CAAACATTA | | |
| | | | | | |
| | | | AAG ACA GTTTGTAAT | | |
| | | | _ TT | | |
| GAM212 | MGC13033 | 3' | TAATGTTTGGAATGGAG 2198 | G | |
| | | | TTC TGTTCCAAACATTA | | |
| | | | | | |
| | | | GAG GTAAGGTTTGTAAT | | |
| | | | - | | |
| GAM212 | PRO0386 | 5' | TAATGTTCTGTGGAACAT 1844 | _____ | |
| | | | GTGTTCCA AACATTA | | |
| | | | | | |
| | | | TACAAGGT TTGTAAT | | |
| | | | GTC | | |
| GAM212 | LOC149351 | 5' | TAATGTGAGGAAAAACACGGA 3132 | _____ AA | |
| | | | TTCGTGT TCC ACATTA | | |
| | | | | | |

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|--------|-----------------|------------------------|--------------|
| | | AGGCACA AGG TGTAAT | |
| | | AAA AG | |
| GAM212 | LOC163590 3' | TAATGTTTGGA | 2512 T T |
| | | TTCG GT CCAAACATTA | |
| | | | |
| | | AGGT CA GGTTTGTAAT | |
| | | T _ | |
| GAM212 | LOC256307 3' | TAATGCTACATGGAACATGAA | 3726 AA__ |
| | | TTCGTGTTCCA CATT | |
| | | | |
| | | AAGTACAAGGT GTAAT | |
| | | ACATC | |
| GAM212 | LOC87769 3' | TAATGTTGAGATACGAA | 2912 TC A |
| | | TTCGTGT CAA CATT | |
| | | | |
| | | AAGCATA GTT GTAAT | |
| | | GA _ | |
| GAM212 | LOC89890 3' | TAATGTTTGAAATACGAA | 2574 C |
| | | TTCGTGTT CAAACATTA | |
| | | | |
| | | AAGCATAA GTTTGTAAT | |
| | | A | |
| GAM213 | GDF8 5' | ACAAGAAAAAAGATTATA | 1196 CA |
| | | TATAATCTTTTT TCTTGT | |
| | | | |
| | | ATATTAGAAAAA AGAACA | |
| | | _ | |
| GAM213 | REGL 3' | ACCATATAGAAAAAGATTATA | 1306 ATCT A |
| | | TATAATCTTTTTC TGTG GT | |
| | | | |
| | | ATATTAGAAAAAG ATAC CA | |
| | | AT__ _ | |
| GAM213 | DKFZP434J214 3' | ACTCAGTGTGGAAAAGA | 2586 CTTG |
| | | TCTTTTTCAT TGAGT | |
| | | | |
| | | AGAAAAGGTG ACTCA | |
| | | TG__ | |
| GAM213 | KIAA0440 5' | CTTTTAAATGAAAAAGATTA | 1636 C T |
| | | TAATCTTTTTCAT TTG GAG | |
| | | | |
| | | ATTAGAAAAAGTA AAT TTC | |
| | | _ T | |
| GAM213 | LOC152756 3' | ACTCATGATCCAAAAAAGATTA | 3363 CATC TG |
| | | TAATCTTTTT T TGAGT | |
| | | | |
| | | ATTAGAAAAA A ACTCA | |
| | | ACCT GT | |
| GAM213 | LOC158428 3' | ACTCACATAGGTGAAAAA | 2889 _ |
| | | TTTTTCATCT TGTGAGT | |
| | | | |

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|--------|-----------|----|-----------------------------|---|---------|
| | | | AAAAAGTGGA ACACTCA | | |
| | | | T | | |
| GAM214 | BHLHB3 | 3' | TATGTAAGGGGTGAGACACAAC 2162 | | A A G _ |
| | | | GTTGTGTCT CA CC CT ACATA | | |
| | | | | | |
| | | | CAACACAGA GT GG GA TGTAT | | |
| | | | _ _ G A | | |
| GAM214 | F9 | 3' | GCGTGTGTGTAGACACAC 709 T | | _ _ |
| | | | GT GTGTCTACA AC CGC | | |
| | | | | | |
| | | | CA CACAGATGT TG GCG | | |
| | | | _ G T | | |
| GAM214 | FLJ31737 | 3' | TAGCACTGTAGACACAAC 2504 | | ACC |
| | | | GTTGTGTCTACA GCTA | | |
| | | | | | |
| | | | CAACACAGATGT CGAT | | |
| | | | CA_ | | |
| GAM214 | KIAA1505 | 5' | GCATTTAGTAGACACCACG 3638 | T | _ CC |
| | | | CGT GTGTCTAC AA GC | | |
| | | | | | |
| | | | GCA CACAGATG TT CG | | |
| | | | C A TA | | |
| GAM214 | PHRET1 | 3' | GGCGCTGTAGACACAAC 1947 | | AC |
| | | | GTTGTGTCTACA CGCT | | |
| | | | | | |
| | | | CAACACAGATGT GCGG | | |
| | | | C_ | | |
| GAM214 | RYD5 | 3' | AGCAGCCGTGGACACAACG 3103 | | AACC |
| | | | CGTTGTGTCTAC GCT | | |
| | | | | | |
| | | | GCAACACAGGTG CGA | | |
| | | | CCGA | | |
| GAM214 | LOC221337 | 5' | TAGTTCAAGTAAACACAATG 3556 | | C AACC |
| | | | CGTTGTGT TAC GCTA | | |
| | | | | | |
| | | | GTAACACA ATG TGAT | | |
| | | | A AACT | | |
| GAM215 | ADCY9 | 3' | GTGGTCATTTTCAGCCCTA 801 | T | A |
| | | | TAGG GCTGAAAT ACCAC | | |
| | | | | | |
| | | | ATCC CGACTTTA TGGTG | | |
| | | | _ C | | |
| GAM215 | CRAT | 3' | GTGGGTCATCCCAGCACCTG 1079 | | AA A A |
| | | | TAGGTGCTG AT ACC CAT | | |
| | | | | | |
| | | | GTCCACGAC TA TGG GTG | | |
| | | | CC C _ | | |
| GAM215 | CRAT | 3' | GTGGGTCATCCCAGCACCTG 771 | | AA A A |
| | | | TAGGTGCTG AT ACC CAT | | |
| | | | | | |

GTCCACGAC TA TGG GTG
 CC C _
 GAM215 CXCR4 3' CAGGAGTGGGTTGATTTTCAGCA 1028 AA__ AT
 CCTA TAGGTGCTGAAAT CCAC CTG
 ||||| ||| |||
 ATCCACGACTTTA GGTG GAC
 GTTG AG
 GAM215 AGMAT 3' CAGACGTGGTGTGGTGCACACC 2087 C AAATA_ A
 GGTG TG ACCAC TCTG
 ||| || |||| ||||
 CCAC AC TGGTG AGAC
 _ GTGGTG C
 GAM215 DKFZp434E0519 3' CAGATGCGGTGGCTCACACCTA 2240 C AATA A
 TAGGTG TGA ACC CATCTG
 |||| || || ||||
 ATCCAC ACT TGG GTAGAC
 _ CGG_ C
 GAM215 DKFZp762E1312 5' CAGACATGGCCTTAGTACCTA 1823 AATAA CA
 TAGGTGCTGA CCA TCTG
 ||||| || |||
 ATCCATGATT GGT AGAC
 CC__ AC
 GAM215 FLJ20619 3' CAGTGAGGTAGCATCTA 1760 GAAATA A T
 TAGGTGCT ACC CA CTG
 ||||| || |||
 ATCTACGA TGG GT GAC
 _____ A _
 GAM215 FLJ20716 3' CAGATTGCCACCCCAGCACCTA 1768 AAATAAC C
 TAGGTGCTG CA ATCTG
 ||||| || ||||
 ATCCACGAC GT TAGAC
 CCCACC_ _
 GAM215 FRAT1 3' CAGATGTGGCTACTGACATATC 1217 C AAA_ A
 TA TAGGTG TG TA CCACATCTG
 |||| || || |||||
 ATCTAT AC AT GGTGTAGAC
 _ AGTC C
 GAM215 KIAA1656 3' CAGATGTGGCCATCCCTCCCTG 2729 TGCT AATAA
 TAGG GA CCACATCTG
 ||| || |||||
 GTCC CT GGTGTAGAC
 CTCC ACC__
 GAM215 Rab11-FIP3 3' CAGATGTGGTCACCTCAGTCC 1524 T AATA
 GG GCTGA ACCACATCTG
 || ||| |||||
 CC TGA CT TGGTGTAGAC
 _ CCAC
 GAM215 TOMM34 3' AGACATGGTTGTTGCACC 1332 TGA CA
 GGTGC AATAACCA TCT
 |||| ||||| |||

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|--------|--------------|-----------------------------|--------------|------|
| | | CCACG TTGTTGGT AGA | | |
| | | ____ AC | | |
| GAM215 | LOC146337 3' | CAGATGCATCTGTTTCAGCCCT 3285 | T | ACCA |
| | A | TAGG GCTGAAATA CATCTG | | |
| | | | | |
| | | ATCC CGACTTTGT GTAGAC | | |
| | | ____ CTAC | | |
| GAM215 | LOC147229 3' | AGATGCAGGCTCAGCACT 3105 | AATAA A_ | |
| | | GGTGCTGA CC CATCT | | |
| | | | | |
| | | TCACGACT GG GTAGA | | |
| | | C____ AC | | |
| GAM215 | LOC158332 3' | GGTACTAATTCAGCACCTA 3217 | A ____ | |
| | | TAGGTGCTGAA TA ACC | | |
| | | | | |
| | | ATCCACGACTT AT TGG | | |
| | | A CA | | |
| GAM215 | LOC163131 5' | AGATGTGATTACATTACT 3245 | C AAA C | |
| | | GGTG TG TAA CACATCT | | |
| | | | | |
| | | TCAT AC ATT GTGTAGA | | |
| | | T ____ A | | |
| GAM215 | LOC221423 3' | AGATGTGGCTACAACAT 3551 | C AAA A | |
| | | GTG TG TA CCACATCT | | |
| | | | | |
| | | TAC AC AT GGTGTAGA | | |
| | | A ____ C | | |
| GAM215 | LOC222182 5' | CAGACATGTGCCCAGCACCT 3639 | AAATAAC ____ | |
| | | AGGTGCTG CACA TCTG | | |
| | | | | |
| | | TCCACGAC GTGT AGAC | | |
| | | CC____ AC | | |
| GAM216 | B3GALT3 3' | GAAGATTACAGTTATGTA 1056 | CG_ | |
| | | TACGTAAC AATCTTC | | |
| | | | | |
| | | ATGTATTG TTAGAAG | | |
| | | ACA | | |
| GAM216 | LOC159199 5' | GAAGATCAAGAGGTTACGTG 3237 | GA____ | |
| | | TACGTAACC ATCTTC | | |
| | | | | |
| | | GTGCATTGG TAGAAG | | |
| | | AGAAC | | |
| GAM217 | ACCN2 3' | CCACCAGACACTCCTTC 1891 | TCT | |
| | | GAAGGAGTGTTT TGG | | |
| | | | | |
| | | CTTCCTCACAGA ACC | | |
| | | CC_ | | |
| GAM217 | BLAME TG 3' | CCAAAAAACACAAAGTGCTTC 1892 | GA____ C | |
| | | TAGAAG GTGTTTT TTGG | | |
| | | | | |

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|--------|--------|----|------------------------|---------------|------|--------|--|
| | | | GTCTTC | CACAAAA | AACC | | |
| | | | GTGAAA | A | | | |
| GAM217 | DLX4 | 3' | TTGCCACTCCCCACTCCTTCT | 2432 | | TTTTCT | |
| | | | AGAAGGAGTG | TGGCAA | | | |
| | | | | | | | |
| | | | TCTTCCTCAC | ACCGTT | | | |
| | | | CCCCTC | | | | |
| GAM217 | DLX4 | 3' | TTGCCACTCCCCACTCCTTCT | 870 | | TTTTCT | |
| | | | AGAAGGAGTG | TGGCAA | | | |
| | | | | | | | |
| | | | TCTTCCTCAC | ACCGTT | | | |
| | | | CCCCTC | | | | |
| GAM217 | IGSF6 | 3' | TTTGCCAAGAAAAAAATTCTA | 1256 | | GGAGTG | |
| | | | TAGAA | TTTTCTTGGCAA | | | |
| | | | | | | | |
| | | | ATCTT | AAAAGAACCGTTT | | | |
| | | | AAAA__ | | | | |
| GAM217 | ITPR2 | 3' | CAGGAACAAAACACTGCCT | 912 | - | __ | |
| | | | AGG AGTGTTT | TCTTG | | | |
| | | | | | | | |
| | | | TCC TCACAAA | AGGAC | | | |
| | | | G | ACA | | | |
| GAM217 | IVD | 5' | GCTAAAAACACTCATCCTA | 913 | AAG | CT | |
| | | | TAG GAGTGTTTT | TGGC | | | |
| | | | | | | | |
| | | | ATC CTCACAAA | ATCG | | | |
| | | | CTA | __ | | | |
| GAM217 | MAP4K2 | 3' | TGCCAAGAGCCTGCCCCT | 1127 | A | TT | |
| | | | AGG GTG TTCTTGGCA | | | | |
| | | | | | | | |
| | | | TCC CGT GAGAACCGT | | | | |
| | | | C | CC | | | |
| GAM217 | POLG | 3' | TGCCAAGAAGATTCCTTCTA | 948 | | GT | |
| | | | TAGAAGGA | GTTTTCTTGGCA | | | |
| | | | | | | | |
| | | | ATCTTCCT | TAGAAGAACCGT | | | |
| | | | __ | | | | |
| GAM217 | RET | 3' | TTGCCAAAACCTCCTTCT | 1920 | | GTTTTC | |
| | | | AGAAGGAGT | TTGGCAA | | | |
| | | | | | | | |
| | | | TCTTCCTCA | AACCGTT | | | |
| | | | A__ | | | | |
| GAM217 | SALL2 | 3' | TTGCCAAGAGGTCTCC | 2672 | | TGT | |
| | | | GGAG | TTTCTTGGCAA | | | |
| | | | | | | | |
| | | | CCTC | GGAGAACCGTT | | | |
| | | | T__ | | | | |
| GAM217 | SLC9A1 | 3' | CCAAGGTCTCACACTCCTCCTG | 2886 | A | TT__ | |
| | | | TAG AGGAGTGT | TCTTGG | | | |
| | | | | | | | |

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|--------|------------|----|-----------------------------|----------|
| | | | GTC TCCTCACA GGAACC | |
| | | | C CTCT | |
| GAM217 | ZNF132 | 5' | CCAAGAAAGCTAACTCCT 1020 | — |
| | | | AGGAGT GTTTTCTTGG | |
| | | | | |
| | | | TCCTCA CGAAAGAACC | |
| | | | AT | |
| GAM217 | AD-020 | 3' | TTTGCCAAGAAAATCTGGGCCT 1893 | AGT— |
| | | | AGG GTTTTCTTGGCAAA | |
| | | | | |
| | | | TCC TAAAAGAACCGTTT | |
| | | | GGGTC | |
| GAM217 | AD-020 | 3' | TTTGCCAAGAAAATCTGGGCCT 2524 | AGT— |
| | | | AGG GTTTTCTTGGCAAA | |
| | | | | |
| | | | TCC TAAAAGAACCGTTT | |
| | | | GGGTC | |
| GAM217 | APOL3 | 3' | CCAAGAAAAACAGTCTCA 1494 | A G _ |
| | | | A GGA TGTTTT CTTGG | |
| | | | | |
| | | | A TCT ACAAAA GAACC | |
| | | | C G A | |
| GAM217 | DJ473B4 | 3' | TTTGCCAAAAAAGTCCCCTA 1881 | AA GTG C |
| | | | TAG GGA TTTT TTGGCAAA | |
| | | | | |
| | | | ATC CCT GAAA AACCGTTT | |
| | | | C_ _ _ A | |
| GAM217 | KIAA0475 | 3' | TTTGCCAAAAGCAGTCCTTC 1571 | G CT |
| | | | GAAGGA TGTTTT TGGCAAA | |
| | | | | |
| | | | CTTCCT ACGAAA ACCGTTT | |
| | | | G _ | |
| GAM217 | KIAA1729 | 3' | CCAGGAACACTCCTTC 3458 | TT |
| | | | GAAGGAGTGT TCTTGG | |
| | | | | |
| | | | CTTCCTCACA AGGACC | |
| | | | — | |
| GAM217 | PHYHIP | 3' | CCACCGGGACACTCCCCCTG 1541 | AA CT |
| | | | TAG GGAGTGTTTT TGG | |
| | | | | |
| | | | GTC CCTCACAGGG ACC | |
| | | | CC CC | |
| GAM217 | SCAMP-4 | 3' | TGCCAAGAGGCACCCCCTTC 2372 | A_ T |
| | | | GAAGG GTGTTT CTTGGCA | |
| | | | | |
| | | | CTTCC CACGGA GAACCGT | |
| | | | CC _ | |
| GAM217 | ST6GalNAcI | 3' | TGCTGAAAAACACTCTTC 1824 | G C TG |
| | | | GAAG AGTGTTTT T GCA | |
| | | | | |

CTTC TCACAAAA A CGT
 _ _GT
 GAM217 TTTY2 5' TGCCAAAAAACAGGTACTCTT 3396 G ____ C
 CTA TAGAAG AGT GTTTT TTGGCA
 ||||| ||| ||||| |||||
 ATCTTC TCA CAAAA AACCGT
 _ TGGA A
 GAM217 LOC126917 3' TTGCCAAGAAAGACCCC 3001 A G
 GG GT TTTTCTTGGCAA
 || || ||||| |||||
 CC CA GAAAGAACCGTT
 C _
 GAM217 LOC128077 3' TTGCTTCTGAAACCCCTCCT 3007 T_ CTT
 AGGAG GTTTT GGCAA
 ||||| ||||| |||||
 TCCTC CAAAG TCGTT
 CC TCT
 GAM217 LOC152485 3' TCACCCAAACACTCCTTC 3171 TCT
 GAAGGAGTGTTT TGG
 ||||| ||||| |||
 CTTCTCACAAA ACT
 CCC
 GAM217 LOC159148 5' TGCCAAAAAACAGGTACTCTT 3397 G ____ C
 CTA TAGAAG AGT GTTTT TTGGCA
 ||||| ||| ||||| |||||
 ATCTTC TCA CAAAA AACCGT
 _ TGGA A
 GAM217 LOC159989 3' GCCAAGAAAAAAGCTCT 3238 G_
 GGAGT TTTTCTTGGC
 ||||| ||||| |||||
 TCTCG AAAAGAACCG
 AAA
 GAM217 LOC164584 5' TTGCCAAGAAAACAATCT 3250 G
 GGA TGTTTTCTTGGCAA
 ||| ||||| ||||| |||||
 TCT ACAAAGAACCGTT
 A
 GAM218 RAG1 3' CCAGTATTAAATTATCC 745 ACTACT
 GGATAATTTA ATATTGG
 ||||| ||||| |||||
 CCTATTAAAT TATGACC

 GAM218 LOC221964 3' GCCAGTAATAGTCAAATTAACC 3628 A A CTA
 GG TAATTT ACTA TATTGGC
 || ||||| ||||| |||||
 CC ATTAAA TGAT ATGACCG
 A C A_
 GAM219 ADAM12 3' TGA CTATGGATAAACTAAA 1030 AT
 TTTAGTTTATTCATA GTTA
 ||||| ||||| ||||| |||||

AAATCAAATAGGTAT CAGT

GAM219 KIAA1789 5' TAACATTATGTGATTCTAAATG 2780 TTTATT
TATTTAG CATAATGTTA
||||| |||||||
GTAAATC GTATTACAAT
TTAGT_

GAM220 NR4A2 3' AACAAACAAAACTGTTGCTAT 1276 TC__ CTA
TTC GAAATAGC GTTT TTTGTT
||||| ||| |||||
CTTTATCG CAAA AAACAA
TTGT AAC

GAM220 LOC51145 3' GCAAAAACGAGCTCTTCA 1667 AT CTAT
TGAA AGCTCGTTT TTGT
||| ||||||| |||
ACTT TCGAGCAAA AACG
C_ _

GAM221 HFE 3' GCAGGTGCTTCAGGATA 738 AC _
TATCCTGA AGCAT TGC
||||| |||||
ATAGGACT TCGTG ACG
_ G

GAM221 HFE 3' GCAGGTGCTTCAGGATA 2464 AC _
TATCCTGA AGCAT TGC
||||| |||||
ATAGGACT TCGTG ACG
_ G

GAM221 PKIA 3' CAATGCTGTATGATACTATTT 1334 A CTGA
AGATA TATC ACAGCATTG
||||| ||| |||||||
TTTAT ATAG TGTCGTAAC
C TA_

GAM221 PLAG1 3' GCAATGCTATCCATTGATGT 943 C_ AAC
ATATC TG AGCATTGC
||||| || |||||||
TGTAG AC TCGTAACG
TT CTA

GAM221 FLJ20371 3' GCCTATTCAGGATATTA ACT 1752 A CA_
AG TAATATCCTGAA GC
|| ||||||||| ||
TC ATTATAGGACTT CG
A ATC

GAM221 LOC202052 3' GCATCTGTT CAGGACAACATC 3485 AATA CAT
GAT TCCTGAACAG TGC
||| ||||||||| |||
CTA AGGACTTGTC ACG
CAAC T_

GAM222 EIF2C1 3' TGCCCTCAAGCTTATACTA 1413 CGTC A A
TAGTATAG GTTT AG GCA
||||| ||||| |||

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|--------|-----------|----|-----------------------------|---------|
| | | | ATCATATT CGAA TC CGT | |
| | | | _____ C C | |
| GAM222 | FMR2 | 3' | CTCTTAAAAAGATGCTATGC 888 | G_ |
| | | | GTATAGCGTC TTAAAGAG | |
| | | | | |
| | | | CGTATCGTAG AAATTCTC | |
| | | | AA | |
| GAM222 | FLJ13612 | 3' | CTCTTAAATACTGTACTA 2146 | CGTC |
| | | | TAGTATAG GTTTAAGAG | |
| | | | | |
| | | | ATCATGTC TAAATTCTC | |
| | | | A_____ | |
| GAM223 | HPS4 | 5' | TGTTTGAAGTGGAACTTCAA 1977 | AA T |
| | | | TTGAAGTTTCCA TTT GATA | |
| | | | | |
| | | | AACTTCAAAGGT AAG TTGT | |
| | | | C_ T | |
| GAM223 | TEKT1 | 5' | GGAATTTGGAAACCTCAA 2359 | A |
| | | | TTGA GTTTCCAAATTTT | |
| | | | | |
| | | | AACT CAAAGGTTTAAGG | |
| | | | C | |
| GAM223 | LOC145783 | 3' | CGGAATTTGGAAACCCCAG 3082 | AA |
| | | | TTG GTTTCCAAATTTTG | |
| | | | | |
| | | | GAC CAAAGGTTTAAGGC | |
| | | | CC | |
| GAM223 | LOC154321 | 3' | TATTAGCTTTGGAACTT 3190 | T T |
| | | | AAGTTTCCAAA TT GATA | |
| | | | | |
| | | | TTCAAAGGTTT GA TTAT | |
| | | | C T | |
| GAM224 | FEZ1 | 3' | AGGATATGTCCACATAAGAA 1993 | _ ATTTT |
| | | | TTCTT TGT GGCATATCCT | |
| | | | | |
| | | | AAGAA ACA CTGTATAGGA | |
| | | | T C_____ | |
| GAM224 | GOLGA4 | 5' | AGGATATTGAACACAAAGAA 2554 | A TGGC |
| | | | TTCTTTGT TTT ATATCCT | |
| | | | | |
| | | | AAGAAACA AAG TATAGGA | |
| | | | C T_____ | |
| GAM224 | HAS3 | 3' | AGGACAAATCTAAAATGCAAAG 1199 | CATA_ |
| | AA | | TTCTTTGTATTTTGG TCCT | |
| | | | | |
| | | | AAGAAACGTAAAATC AGGA | |
| | | | TAAAC | |
| GAM224 | JUN | 3' | AGGATATTTAAGAAAATACAA 914 | GGC_ |
| | | | TTGTATTTT ATATCCT | |
| | | | | |

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|--------|----------|----|------------------------|---------|-----|----------|
| | | | AACATAAAA | TATAGGA | | |
| | | | GAATT | | | |
| GAM224 | MADH9 | 3' | ATGTGTAAATACATAGAA | 1260 | T | TG |
| | | | TTCT TGTATTT GCATAT | | | |
| | | | | | | |
| | | | AAGA ACATAAA TGTGTA | | | |
| | | | T | — | | |
| GAM224 | NR2C2 | 3' | AGGACCGTTCACATACAAAGAA | 1007 | | TTT ATA |
| | | | TTCTTTGTAT GGC TCCT | | | |
| | | | | | | |
| | | | AAGAAACATA TTG AGGA | | | |
| | | | CAC CC_ | | | |
| GAM224 | AP1S3 | 3' | AGGACTATAGAAATGCAAAGAA | 3010 | | GGCATA |
| | | | TTCTTTGTATTTT TCCT | | | |
| | | | | | | |
| | | | AAGAAACGTAAAG AGGA | | | |
| | | | ATATC_ | | | |
| GAM224 | ARHE | 3' | ATATGCCAAAAAATGAGAG | 1190 | | TGTA |
| | | | TTCTT TTTTGGCATAT | | | |
| | | | | | | |
| | | | GAGAG AAAACCGTATA | | | |
| | | | TAA_ | | | |
| GAM224 | FLJ11000 | 3' | AGGACACATGGGGTACAAAGA | 1812 | | TT GCATA |
| | | | TCTTTGTATT G TCCT | | | |
| | | | | | | |
| | | | AGAAACATGG T AGGA | | | |
| | | | GG ACAC_ | | | |
| GAM224 | FLJ11996 | 5' | ATAGATCTAAATACAAAGGA | 2120 | | T CA |
| | | | TTCTTTGTATTT GG TAT | | | |
| | | | | | | |
| | | | AGGAAACATAAA CT ATA | | | |
| | | | T AG | | | |
| GAM224 | GADD45A | 3' | AGGAACAAAAATTACAAAGAA | 869 | | T GGCATA |
| | | | TTCTTTGTA TTT TCCT | | | |
| | | | | | | |
| | | | AAGAAACAT AAA AGGA | | | |
| | | | T AACA_ | | | |
| GAM224 | HNRPA3 | 3' | AGGATATGATGGTTACAATGAA | 1244 | T | TTTTGG |
| | | | TTC TTGTA CATATCCT | | | |
| | | | | | | |
| | | | AAG AACAT GTATAGGA | | | |
| | | | T TGGTA_ | | | |
| GAM224 | KIAA0179 | 3' | AGAATATGTCACATAAAGAA | 2704 | ATT | C |
| | | | TTCTTTGT TGGCATAT CT | | | |
| | | | | | | |
| | | | AAGAAATA ACTGTATA GA | | | |
| | | | C_ A | | | |
| GAM224 | KIAA1831 | 3' | GGAAAAAATACAAAGAA | 2667 | | GGCATA |
| | | | TTCTTTGTATTTT TCC | | | |
| | | | | | | |

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|--------|-----------|----|------------------------|------|----------|
| | | | AAGAAACATAAAA | AGG | |
| | | | AA____ | | |
| GAM224 | KLHL4 | 3' | AGGATATGTGTGCTATATAAA | 1880 | TTTG_ |
| | | | TTTGTAT GCATATCCT | | |
| | | | | | |
| | | | AAATATA TGTATAGGA | | |
| | | | TCGTG | | |
| GAM224 | PANX3 | 3' | AGGATAGTATAAATAAAAAGAA | 2350 | G TG A |
| | | | TTCTTT TATTT GC TATCCT | | |
| | | | | | |
| | | | AAGAAA ATAAA TG ATAGGA | | |
| | | | A TA _ | | |
| GAM224 | TRAF3 | 5' | ATATGCTAAACAAAAGAA | 2541 | GTAT |
| | | | TTCTTT TTTGGCATAT | | |
| | | | | | |
| | | | AAGAAA AAATCGTATA | | |
| | | | AC__ | | |
| GAM224 | TRAF3 | 3' | ATATGCTAAACAAAAGAA | 1008 | GTAT |
| | | | TTCTTT TTTGGCATAT | | |
| | | | | | |
| | | | AAGAAA AAATCGTATA | | |
| | | | AC__ | | |
| GAM224 | ZFD25 | 3' | GATTGTACAAATACAAGGAA | 1672 | TG T |
| | | | TTCTTTGTATTT GCA ATC | | |
| | | | | | |
| | | | AAGGAACATAAA TGT TAG | | |
| | | | CA _ | | |
| GAM224 | ZID | 3' | ATATGCCAAAAGGAA | 1315 | TTGTA |
| | | | TTCT TTTTGGCATAT | | |
| | | | | | |
| | | | AAGG AAAACCGTATA | | |
| | | | _____ | | |
| GAM224 | LOC151742 | 5' | AGGACTACGAGAAAGACAAAGA | 2477 | A GGCATA |
| | A | | TTCTTTGT TTTT TCCT | | |
| | | | | | |
| | | | AAGAAACA AAAG AGGA | | |
| | | | G AGCATC | | |
| GAM224 | LOC152179 | 3' | TGCTTCAAAATCAAAGAA | 3352 | T _ |
| | | | TTCTTTG ATTTTG GCA | | |
| | | | | | |
| | | | AAGAAAC TAAAC CGT | | |
| | | | _ TT | | |
| GAM224 | LOC51266 | 3' | GATATGTATGAATGCAAA | 1691 | TG |
| | | | TTTGTATTT GCATATC | | |
| | | | | | |
| | | | AAACGTAAG TGTATAG | | |
| | | | TA | | |
| GAM224 | LOC90317 | 5' | AGGATACATACTACAGAGAA | 2629 | TTT GCA |
| | | | TTCTTTGTA TG TATCCT | | |
| | | | | | |

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|--------|-----------|----|----------------------------|------|------|
| | | | AAGAGACAT AC ATAGGA | | |
| | | | CAT ____ | | |
| GAM224 | LOC90470 | 3' | AGAATATGCTCAATACAAAG 2645 | TT | C |
| | | | CTTTGTATT GGCATAT CT | | |
| | | | | | |
| | | | GAAACATAA TCGTATA GA | | |
| | | | C_ A | | |
| GAM224 | LOC90786 | 5' | ATATGCCAAAATTGAGA 2678 | TGT | |
| | | | TCTT ATTTTGGCATAT | | |
| | | | | | |
| | | | AGAG TAAAACCGTATA | | |
| | | | T__ | | |
| GAM225 | ATRX | 3' | ATCACGTCAGTAAAATACTA 751 | T A | C |
| | | | TAGTATTTT CT ACGT GGT | | |
| | | | | | |
| | | | ATCATAAAA GA TGCA CTA | | |
| | | | T C _ | | |
| GAM225 | ATRX | 3' | ATCACGTCAGTAAAATACTA 2431 | T A | C |
| | | | TAGTATTTT CT ACGT GGT | | |
| | | | | | |
| | | | ATCATAAAA GA TGCA CTA | | |
| | | | T C _ | | |
| GAM225 | D10S170 | 3' | ATACCATTAGAAAATACTA 1211 | T | CGTC |
| | | | TAGTATTTT CTAA GGTAT | | |
| | | | | | |
| | | | ATCATAAAA GATT CCATA | | |
| | | | _ A__ | | |
| GAM225 | RAB27A | 3' | ACTGTAATTAGAAAAATAC 1128 | CGT | |
| | | | GTATTTTCTAA CGGT | | |
| | | | | | |
| | | | CATAAAAAGATT GTCA | | |
| | | | AAT | | |
| GAM225 | CYLD | 3' | AATAGTGGTCAGAAAAATACT 1616 | A GT | G |
| | | | AGTATTTTCT AC CG TATT | | |
| | | | | | |
| | | | TCATAAAAAGA TG GT ATAA | | |
| | | | C _ G | | |
| GAM225 | LOC145945 | 5' | ATTTATGGTGAGAAAAATAC 3279 | AA_ | CG |
| | | | GTATTTTCT CGT GT | | |
| | | | | | |
| | | | CATAAAAAGA GTA TA | | |
| | | | GTG TT | | |
| GAM225 | LOC200273 | 3' | ACCGACGTCAAAAAGTCTG 2895 | T | CTA |
| | | | TAG ATTTT ACGTCGGT | | |
| | | | | | |
| | | | GTC TGAAAA TGCAGCCA | | |
| | | | _ AC_ | | |
| GAM225 | LOC220758 | 3' | GCGATTAGAAAAACACTA 3497 | A | _ |
| | | | TAGT TTTTCTAA CGT | | |
| | | | | | |

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|--------|----------|----|-----------------------------|--------|--------|
| | | | ATCA AAAAAGATT GCG | | |
| | | | C A | | |
| GAM226 | KNSL1 | 3' | TTAGTGGTTATTTCTAAAAT 1123 | — | |
| | | | ATTTTAGAAATAAC ATTAG | | |
| | | | | | |
| | | | TAAAATCTTTATTG TGATT | | |
| | | | G | | |
| GAM226 | PLAC1 | 3' | TGAAGATGCTATTTCTAGAATT 1960 | A | AG |
| | | | AATTTTAGAAATA CATT CG | | |
| | | | | | |
| | | | TTAAGATCTTTAT GTAG GT | | |
| | | | C AA | | |
| GAM226 | SCP2 | 3' | CTAATGTTATTTCTTAAAATT 977 | — | |
| | | | AATTTTA GAAATAACATTAG | | |
| | | | | | |
| | | | TTAAAAT CTTTATTGTAATC | | |
| | | | T | | |
| GAM226 | STIM1 | 3' | GTGTTATTTTCATAAAATT 2558 | — | |
| | | | AATTTTA GAAATAACAT | | |
| | | | | | |
| | | | TTAAAAT CTTTATTGTG | | |
| | | | A | | |
| GAM226 | CORTBP2 | 3' | AATGTTACTTCTAAAATT 2334 | A | |
| | | | AATTTTAGAA TAACATT | | |
| | | | | | |
| | | | TTAAAATCTT ATTGTAA | | |
| | | | C | | |
| GAM226 | VAMP3 | 3' | CTACTGTTATCTCTAAAATT 1156 | A | T |
| | | | AATTTTAGA ATAACA TAG | | |
| | | | | | |
| | | | TTAAAATCT TATTGT ATC | | |
| | | | C C | | |
| GAM226 | LOC90148 | 3' | TCCTTGTGTTATTTCTAAAA 2603 | T | C |
| | | | TTTAGAAATAACAT AG GA | | |
| | | | | | |
| | | | AAAATCTTTATTGTG TC CT | | |
| | | | T | | |
| GAM227 | AK2 | 3' | TGAAAAAGGAAGTTGGTTATGC 1449 | TACA | — C |
| | CA | | TGGC AACT TTTCTTTT CA | | |
| | | | | | |
| | | | ACCG TTGG GAAGGAAAA GT | | |
| | | | TA__ TT A | | |
| GAM227 | CRTAP | 3' | GGAAAAGGAAGAAAGCCA 1291 | ACAAAC | |
| | | | TGGCT TTTCTTTTCC | | |
| | | | | | |
| | | | ACCGA AGAAGGAAAAGG | | |
| | | | A_____ | | |
| GAM227 | CXorf6 | 5' | TGGAAAAGTCGGCTTGTAATCA 1218 | GC | A TTTC |
| | | | TG TACAA CT CTTTCCA | | |
| | | | | | |

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|--------|--------------|----|-----------------------------|-----------|--|
| | | | AC ATGTT GG GAAAAGGT | | |
| | | | TA C CT__ | | |
| GAM227 | EPHB2 | 3' | TGGAAAAGAAAACTGGTGCCA 1113 | T AAAC C | |
| | | | TGGC AC TTTTC TTTTCCA | | |
| | | | | | |
| | | | ACCG TG AAAAG AAAAGGT | | |
| | | | _ GTCA _ | | |
| GAM227 | FZD3 | 3' | TGGAAAAATTTTAATTTGTAGC 1717 | CTTTTCC | |
| | CA | | TGGCTACAAA TTTTCCA | | |
| | | | | | |
| | | | ACCGATGTTT AAAAGGT | | |
| | | | AATTTTA | | |
| GAM227 | HMGA2 | 3' | GAAAAAAAAGCTTGTGGCCA 1033 | A CC | |
| | | | TGGCTACAA CTTTT TTTTC | | |
| | | | | | |
| | | | ACCGGTGTT GAAAA AAAAG | | |
| | | | C A_ | | |
| GAM227 | SLC2A4 | 3' | TGGAAAAGAATCCCTGCAGCC 794 | A AACTT C | |
| | | | GGCT CA TTC TTTTCCA | | |
| | | | | | |
| | | | CCGA GT AAG AAAAGGT | | |
| | | | C CCCT_ _ | | |
| GAM227 | ATP10B | 3' | AGGGAAAAGTTATAACCA 2654 | C CA | |
| | | | TGG TA AACTTTTCCTT | | |
| | | | | | |
| | | | ACC AT TTGAAAAGGGA | | |
| | | | A A_ | | |
| GAM227 | BCCIP | 3' | GAAAAGGAATAGTCA 2369 | CAAACCTT | |
| | | | TGGCTA TTCCTTTTC | | |
| | | | | | |
| | | | ACTGAT AAGGAAAAG | | |
| | | | _____ | | |
| GAM227 | C20orf30 | 3' | GGAAAAGTGTTCCTGCCA 1478 | TA_ _ | |
| | | | TGGC CAA ACTTTTCC | | |
| | | | | | |
| | | | ACCG GTT TGAAAAGG | | |
| | | | TCC G | | |
| GAM227 | DKFZP564O043 | 3' | GGAAGGGAAAAATTTATAGCTA 3565 | C C | |
| | | | TGGCTA AAA TTTTCCTTTTC | | |
| | | | | | |
| | | | ATCGAT TTT AAAAGGGAAGG | | |
| | | | A A | | |
| GAM227 | FLJ11710 | 3' | TGGAAAGGGGAATCTATGCCA 2097 | TACAACT | |
| | | | TGGC TTTCTTTTCCA | | |
| | | | | | |
| | | | ACCG AAGGGGAAAGGT | | |
| | | | TATCT__ | | |
| GAM227 | JDD1 | 3' | TGGAAAGGCAAGTTTGTACCCA 2653 | C TTC | |
| | | | TGG TACAACTT CTTTCCA | | |
| | | | | | |

ACC ATGTTTGAA GGAAAGGT
C C__

GAM227 KIAA0265 3' GAAAAGGAAAAGGAATAATCA 2871 GC CAAA
TG TA CTTTTCCTTTTC
|| || ||||||||
AC AT GAAAAGGAAAAG
TA AAG_

GAM227 KIAA0663 3' GGAAAAGGAAGAAAGCCA 1561 ACAAAC
TGGCT TTTTCCTTTTCC
|||| ||||||||
ACCGA AGAAGGAAAAGG
A_____

GAM227 KIAA1010 3' TGGAAAGGAGAACTTGCAGTC 2934 A AC T
A TGGCT CAA TTTTCCTTT CCA
|||| || |||||| ||
ACTGA GTT AAGAGGAAA GGT
C CA _

GAM227 KIAA1576 3' GGTCAAAAGTTTGAGCCA 2734 A _
TGGCT CAAACTTTT CC
|||| |||||| ||
ACCGA GTTTGAAAA GG
_ CT

GAM227 KIAA1634 3' TGAAAAAGGAAAGAAAGTAACC 2658 C AAAC C
A TGG TAC TTTTCCTTTT CA
||| || |||||| ||
ACC ATG GAAAGGAAAA GT
A AAA_ A

GAM227 KIAA1798 3' GAAAGTAAGTTTGTAGC 2575 TTC
GCTACAACTT CTTTT
|||||| ||||
CGATGTTTGAA GAAAG
T_

GAM227 KNSL7 3' AAAAATAAAAGCCTGTAGCTA 1904 AA CC
TGGCTACA CTTTT TTTT
|||| |||| |||
ATCGATGT GAAAA AAAA
CC TA

GAM227 LALP1 3' GAAATGAAATTTGTAGC 1916 CT CT
GCTACAAA TTTC TTTC
|||| |||| |||
CGATGTTT AAAG AAAG
_ T_

GAM227 MGC2488 3' GAAAAGGAAGCATGTAGC 2044 AACT
GCTACA TTTCCTTTTC
|||| ||||||
CGATGT GAAGGAAAAG
AC_

GAM227 nexilin 3' AAAAGGAAACCAGGAGTGCCA 2484 T AAA _
TGGC AC CT TTTTCCTTT
|||| || || ||||||

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|--------|-----------|----|-----------------------------|------------|--|
| | | | ACCG TG GA AAAGGAAAA | | |
| | | | _ AG_ CC | | |
| GAM227 | NKX2B | 3' | TGGAAAAGAAAACCCTGTAGGC 934 | G AAC C | |
| | A | | TG CTACA TTTTC TTTCCA | | |
| | | | | | |
| | | | AC GATGT AAAAG AAAAGGT | | |
| | | | G CCC _ | | |
| GAM227 | STX18 | 3' | TGAAAAAGGAAACAGTGCACAC 1715 | CTACAA _ C | |
| | CA | | TGG ACT TTTCTTTT CA | | |
| | | | | | |
| | | | ACC TGA AAAGGAAAA GT | | |
| | | | ACACG_ C A | | |
| GAM227 | ZNF271 | 5' | AGTAAAAGTTTTAGCCA 3670 | C C | |
| | | | TGGCTA AAACCTTT CT | | |
| | | | | | |
| | | | ACCGAT TTTGAAAA GA | | |
| | | | _ T | | |
| GAM227 | LOC115207 | 3' | GAAAGTTGGAAGTTTGTACCA 2440 | C CC | |
| | | | TGG TACAACTTTT TTTTC | | |
| | | | | | |
| | | | ACC ATGTTTGAAGG GAAAG | | |
| | | | _ TT | | |
| GAM227 | LOC133482 | 5' | AAAAGGAAAAAAGCCA 3014 | ACAAAC | |
| | | | TGGCT TTTCTTTT | | |
| | | | | | |
| | | | ACCGA AAAAGGAAAA | | |
| | | | A_____ | | |
| GAM227 | LOC147080 | 5' | TGGAAATCGCCAAATTTGTAGC 3290 | CTTTTCCT | |
| | CA | | TGGCTACAAA TTTCCA | | |
| | | | | | |
| | | | ACCGATGTTT AAAGGT | | |
| | | | AAACCGCT | | |
| GAM227 | LOC147990 | 3' | GAAAAGGAAATAAAAAAGCCA 3295 | ACAAACT | |
| | | | TGGCT TTTCTTTTC | | |
| | | | | | |
| | | | ACCGA AAAGGAAAAG | | |
| | | | AAAAAT_ | | |
| GAM227 | LOC149529 | 3' | AAAAGGCAAAAGTTTGCAGC 3134 | A _ | |
| | | | GCT CAACTTTT CCTTTT | | |
| | | | | | |
| | | | CGA GTTTGAAAA GGAAAA | | |
| | | | C C | | |
| GAM227 | LOC158130 | 3' | AAAGGAAAATTCTAGCCA 2847 | C AC | |
| | | | TGGCTA AA TTTCTTTT | | |
| | | | | | |
| | | | ACCGAT TT AAAAGGAAA | | |
| | | | C _ | | |
| GAM227 | LOC196478 | 5' | GAAAATGGATTTGTAGC 3413 | CTTT _ | |
| | | | GCTACAAA TCC TTTTC | | |
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|--------|--------------|-----------------------------|-----------|---|
| | | CGATGTTT AGG AAAAG | | |
| | | _____ T | | |
| GAM227 | LOC219894 3' | AGAAGAAAAGTTTGAAACCA 3595 | CTA | C |
| | | TGG CAAACTTTTC TTTT | | |
| | | | | |
| | | ACC GTTTGAAAAG AAGA | | |
| | | AAA _____ | | |
| GAM227 | LOC219988 5' | GAAAGCACAAAATTTGTAGC 3535 | C TC_ | |
| | | GCTACAAA TTT CTTTT | | |
| | | | | |
| | | CGATGTTT AAA GAAAG | | |
| | | A CAC | | |
| GAM227 | LOC221272 3' | GAAAAGGAAAAGTTTACCTGC 3613 | TAC_ | |
| | | GC AAACTTTTCCTTTTC | | |
| | | | | |
| | | CG TTTGAAAAGGAAAAG | | |
| | | TCCA | | |
| GAM227 | LOC221272 3' | GAAAAGGAAAGTAGCTA 3614 | AAACT | |
| | | TGGCTAC TTTCCTTTTC | | |
| | | | | |
| | | ATCGATG AAAGGAAAAG | | |
| | | _____ | | |
| GAM227 | LOC245771 5' | TGAAAAAGGAGAGATCATCAGC 3584 | ACAAAC | C |
| | CA | TGGCT TTTTCCTTTT CA | | |
| | | | | |
| | | ACCGA GAGAGGAAAA GT | | |
| | | CTACTA A | | |
| GAM227 | LOC253019 3' | GGAAAAGGAAGAAAGCCA 3673 | ACAAAC | |
| | | TGGCT TTTTCCTTTTCC | | |
| | | | | |
| | | ACCGA AGAAGGAAAAGG | | |
| | | A_____ | | |
| GAM227 | LOC253975 3' | GGAAAAGGAAGAAAGCCA 3687 | ACAAAC | |
| | | TGGCT TTTTCCTTTTCC | | |
| | | | | |
| | | ACCGA AGAAGGAAAAGG | | |
| | | A_____ | | |
| GAM227 | LOC254873 3' | TGAAAAAGAATCCCTGCAGCC 3659 | A AACTT C | |
| | | GGCT CA TTC TTTTCCA | | |
| | | | | |
| | | CCGA GT AAG AAAAGGT | | |
| | | C CCCT_ _ | | |
| GAM227 | LOC51634 3' | AAATGAAACCCTGTAGCCA 1655 | AACT C | |
| | | TGGCTACA TTTC TTTT | | |
| | | | | |
| | | ACCGATGT AAAG AAAA | | |
| | | CCC_ T | | |
| GAM228 | ABCE1 3' | AAATATACAGAATGGAA 2532 | GCTG | |
| | | TTCCG TTGTATATTT | | |
| | | | | |

AAGGT GACATATAAA
 AA__
 GAM228 WWP1 3' ATTTAAATACCCCAGCCAAGAA 1345 C_ TTGTA
 A TTTT GGCTG TATTTAAAT
 ||| ||| |||||
 AAAG CCGAC ATAAATTTA
 AA CCC__
 GAM229 GDF8 3' ATGAAGAATAAACTGATGCTA 1197 C GAG C
 TAGCATCG TTT ATTCT CAT
 ||||| || ||| |||
 ATCGTAGT AAA TAAGA GTA
 C __ A
 GAM229 DIO2 3' TGGAGAGGAAGAAACGCTA 773 ATCG GAGA
 TAGC CTTT TTCTCCA
 ||| ||| |||||
 ATCG GAAG GAGAGGT
 CAAA ____
 GAM229 DIO2 3' TGGAGAGGAAGAAACGCTA 1454 ATCG GAGA
 TAGC CTTT TTCTCCA
 ||| ||| |||||
 ATCG GAAG GAGAGGT
 CAAA ____
 GAM229 FLJ21007 5' ATGAAGAATCTCAGGCTGC 2167 TC T C
 GCA GCTT GAGATTCT CAT
 || ||| ||||| |||
 CGT CGGA CTCTAAGA GTA
 __ _ A
 GAM229 KIAA0478 3' ATGGAGAAAAAGCAGGGATGCT 1573 __ GAGA
 A TAGCATC GCTTT TTCTCCAT
 ||||| ||| |||||
 ATCGTAG CGAAA AAGAGGTA
 GGA ____
 GAM229 KIAA0513 3' GATCTCAAAACAGTGCTA 1535 CGC
 TAGCAT TTTGAGATT
 |||| |||||
 ATCGTG AACTCTAG
 ACA
 GAM229 KIAA1323 5' ATGGAGAATGGGCTGAAGCGAT 2647 G ____
 GCT AGCATCGCTTT AG ATTCTCCAT
 ||||| || |||||
 TCGTAGCGAAG TC TAAGAGGTA
 _ GGG
 GAM229 P450RAI-2 3' GAGAATCTTGGGGATGCTG 1888 G TT
 TAGCATC CT GAGATTCTC
 ||||| || |||||
 GTCGTAG GG TTCTAAGAG
 G __
 GAM229 XYLT1 3' GAAACTCACAAAGCAATGCT 3089 C __ A
 AGCAT GCTT TGAG TTC
 |||| ||| ||| |||

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|--------|-----------|----|-----------------------------|------------|
| | | | TCGTA CGAA ACTC AAG | |
| | | | A AC A | |
| GAM229 | LOC143282 | 3' | ATGGAGAATCTCTGGGATAGC 3055 | _ G TT |
| | | | GC ATC CT GAGATTCTCCAT | |
| | | | | |
| | | | CG TAG GG CTCTAAGAGGTA | |
| | | | A _ T_ | |
| GAM229 | LOC200132 | 3' | ATGGAGAAAATTAGCAATGCTG 3438 | C TT GA |
| | | | TAGCAT GCT GA TTCTCCAT | |
| | | | | |
| | | | GTCGTA CGA TT AAGAGGTA | |
| | | | A _ _ AA | |
| GAM230 | FGFR1 | 5' | CCGCAGCGCGCGGAGGAA 759 | GAGA ACA A |
| | | | TTCCTCTG TG CT CGG | |
| | | | | |
| | | | AAGGAGGC GC GA GCC | |
| | | | _ GC_ C | |
| GAM230 | FGFR1 | 5' | CCGCAGCGCGCGGAGGAA 1647 | GAGA ACA A |
| | | | TTCCTCTG TG CT CGG | |
| | | | | |
| | | | AAGGAGGC GC GA GCC | |
| | | | _ GC_ C | |
| GAM230 | FGFR1 | 5' | CCGCAGCGCGCGGAGGAA 2031 | GAGA ACA A |
| | | | TTCCTCTG TG CT CGG | |
| | | | | |
| | | | AAGGAGGC GC GA GCC | |
| | | | _ GC_ C | |
| GAM230 | FGFR1 | 5' | CCGCAGCGCGCGGAGGAA 2033 | GAGA ACA A |
| | | | TTCCTCTG TG CT CGG | |
| | | | | |
| | | | AAGGAGGC GC GA GCC | |
| | | | _ GC_ C | |
| GAM230 | FGFR1 | 5' | CCGCAGCGCGCGGAGGAA 2035 | GAGA ACA A |
| | | | TTCCTCTG TG CT CGG | |
| | | | | |
| | | | AAGGAGGC GC GA GCC | |
| | | | _ GC_ C | |
| GAM230 | FGFR1 | 5' | CCGCAGCGCGCGGAGGAA 2036 | GAGA ACA A |
| | | | TTCCTCTG TG CT CGG | |
| | | | | |
| | | | AAGGAGGC GC GA GCC | |
| | | | _ GC_ C | |
| GAM230 | ITGB3 | 3' | CCTCTCATTCCAGAGGAA 718 | A CACTAC |
| | | | TTCCTCTGGAG TGA GG | |
| | | | | |
| | | | AAGGAGACCTT ACT CC | |
| | | | _ CT_ | |
| GAM230 | PCSK2 | 3' | GCCATGCAATTCATCCCAGAGG 940 | A CACTAC_ |
| | AA | | TTCCTCTGG GATGA GGC | |
| | | | | |

AAGGAGACC CTACT CCG
 _ TAACGTA
 GAM230 STK24 3' CCATAGTGCACATATTCCAGG 1038 _ A_ C
 TCTGGAG ATG CACTA GG
 ||||| || ||||| ||
 GGACCTT TAC GTGAT CC
 A AC A
 GAM230 TIMP3 5' CCTGCTCTCTCCAGAG 733 T _ CTAC
 CTCTGGAGA GA CA GG
 ||||| || || ||
 GAGACCTCT CT GT CC
 _ C _
 GAM230 AF038169 3' GCCAGGGGGCATCTCCAAAGGA 1440 C ACA AC
 A TTCCT TGGAGATG CT GGC
 ||||| ||||| || |||||
 AAGGA ACCTCTAC GG CCG
 A GG_ GA
 GAM230 CRTAM 3' GCCGCA GTGTCACCTCAGTGGA 1883 T G A A
 TCC CTG AG TGACACT CGGC
 || || || ||||| |||||
 AGG GAC TC ACTGTGA GCCG
 T _ C C
 GAM230 DKFZP564J0863 3' GCCACAGGTTTCATATCCAGAGG 2815 G CA AC
 AA TTCCTCTGGA ATGA CT GGC
 ||||| ||||| || |||||
 AAGGAGACCT TACT GA CCG
 A TG CA
 GAM230 FLJ14297 5' GCCATAGAATTCTCTCCAGAAG 2108 C T CA_ C
 AG TTC TCTGGAGA GA CTA GGC
 || ||||| || ||||| |||||
 GAG AGACCTCT CT GAT CCG
 A _ TAA A
 GAM230 FLJ20508 3' GCTGTTACCATCTCAGAGGAA 1757 G ACACT
 TTCCTCTG AGATG ACGGC
 ||||| ||||| |||||
 AAGGAGAC TCTAC TGTCTG
 _ CAT_
 GAM230 FLJ23462 3' GCTTCTGT CATCTCCAGAG 2096 CTAC
 CTCTGGAGATGACA GGC
 ||||| ||||| |||||
 GAGACCTCTACTGT TCG
 CT_
 GAM230 LOC126167 3' CCAAGAATTTATCTCCAAAGGA 2998 C CACTAC
 A TTCCT TGGAGATGA GG
 ||||| ||||| || |||||
 AAGGA ACCTCTATT CC
 A TAAGAA
 GAM230 LOC157247 5' CCACAGTGT CATCCCACAG 3200 C A AC
 CT TGG GATGACACT GG
 || ||||| ||||| || |||||

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|--------|-----------|----|-------------------------------|-------|--------|
| | | | GA ACC CTACTGTGA CC | | |
| | | | C _ CA | | |
| GAM230 | LOC161357 | 5' | CCGTAGTGGCTCCAAAG 3240 | C | ATGA |
| | | | CT TGGAG CACTACGG | | |
| | | | | | |
| | | | GA ACCTC GTGATGCC | | |
| | | | A G__ | | |
| GAM230 | LOC201965 | 3' | CCGTAAATTACTTCAGAG 3455 | A | CAC |
| | | | CTCTGGAG TGA TACGG | | |
| | | | | | |
| | | | GAGACTTC ATT ATGCC | | |
| | | | _ AA_ | | |
| GAM230 | LOC253758 | 5' | GCCGTCTCACCTCCAAAGG 3723 | C | A CACT |
| | | | CCT TGGAG TGA ACGGC | | |
| | | | | | |
| | | | GGA ACCTC ACT TGCCG | | |
| | | | A C C__ | | |
| GAM230 | LOC91661 | 3' | CCACTGCATCTCAGAGGAA 2438 | G | A CTAC |
| | | | TTCTCTG AGATG CA GG | | |
| | | | | | |
| | | | AAGGAGAC TCTAC GT CC | | |
| | | | _ _ CA__ | | |
| GAM231 | SPG4 | 3' | AATCTACAGACATTAAACAAT 1595 | C | TA |
| | | | ATTGTTTAAT GTTT TAGATT | | |
| | | | | | |
| | | | TAACAAATTA CAGA ATCTAA | | |
| | | | _ C_ | | |
| GAM231 | KIAA0672 | 3' | AATCTATAAAACAAAACAA 1569 | AATC | |
| | | | TTGTTT GTTTTATAGATT | | |
| | | | | | |
| | | | AACAAA CAAAATATCTAA | | |
| | | | A__ | | |
| GAM231 | MGC32104 | 3' | AATCTATAAAGAACTCAAACAA 2495 | AATCG | |
| | | | TTGTTT TTTTATAGATT | | |
| | | | | | |
| | | | AACAAA GAAATATCTAA | | |
| | | | CTCAA | | |
| GAM231 | PRO0082 | 3' | AATCTATGGCTTGATTA AAAAAT 1851 | G | TT |
| | A | | TATT TTTAATCG TTATAGATT | | |
| | | | | | |
| | | | ATAA AAATTAGT GGTATCTAA | | |
| | | | _ TC | | |
| GAM232 | TRAP1 | 3' | GATGACAGCCCCACCTCC 1678 | A | A_ |
| | | | GGAGGTGG GT TCGTC | | |
| | | | | | |
| | | | CCTCCACC CG AGTAG | | |
| | | | C AC | | |
| GAM232 | ASAH | 3' | TGGTGA ACTCCACCTCC 1098 | A | GT |
| | | | GGAGGTGGAGT TC CA | | |
| | | | | | |

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|--------|------------|----|-----------------------------|------|--------|
| | | | CCTCCACCTCA AG GT | | |
| | | | — TG | | |
| GAM232 | CNNM1 | 3' | ATTATTGACTTCACCACACCCC 1913 | A | GA ATC |
| | | | GG GGTG GT GTCAATAAT | | |
| | | | | | |
| | | | CC CCAC CA CAGTTATTA | | |
| | | | — AC CTT | | |
| GAM232 | Rab11-FIP2 | 3' | ATTATGCATTACTCCACATCC 1582 | G | TC CA |
| | | | GGA GTGGAGTA GT ATAAT | | |
| | | | | | |
| | | | CCT CACCTCAT CG TATTA | | |
| | | | A TA — | | |
| GAM232 | RNF38 | 3' | ATTGAATACTCCATCCC 2009 | A | CG |
| | | | GG GGTGGAGTAT TCAAT | | |
| | | | | | |
| | | | CC CTACCTCATA AGTTA | | |
| | | | — — | | |
| GAM232 | LOC152283 | 3' | TGGTCGACATCCCACCTCC 3357 | AG A | — |
| | | | GGAGGTGG T TCG TCA | | |
| | | | | | |
| | | | CCTCCACC A AGC GGT | | |
| | | | CT C T | | |
| GAM232 | LOC160484 | 5' | TATTGGCCTGACAGTCCACCTC 3239 | — | ATC |
| | C | | GGAGGTGGA GT GTCAATA | | |
| | | | | | |
| | | | CCTCCACCT CA CGGTTAT | | |
| | | | GA GTC | | |
| GAM232 | LOC90119 | 3' | ATTATTGACAACACCAT 2600 | A | ATC |
| | | | GTGG GT GTCAATAAT | | |
| | | | | | |
| | | | TACC CA CAGTTATTA | | |
| | | | A A— | | |
| GAM233 | MTMR2 | 3' | GATCAAAATCATTTGATA 1664 | T | |
| | | | TATCAGATGATTTTG ATT | | |
| | | | | | |
| | | | ATAGTTTACTAAAAC TAG | | |
| | | | — | | |
| GAM233 | PCDHGA8 | 5' | GATCTAATCTGATCATTTAATA 2227 | C | TTGT |
| | | | TAT AGATGATT ATTAGATC | | |
| | | | | | |
| | | | ATA TTTACTAG TAATCTAG | | |
| | | | A TC— | | |
| GAM233 | PCDHGA8 | 5' | GATCTAATCTGATCATTTAATA 1460 | C | TTGT |
| | | | TAT AGATGATT ATTAGATC | | |
| | | | | | |
| | | | ATA TTTACTAG TAATCTAG | | |
| | | | A TC— | | |
| GAM233 | PTGES | 3' | CTAATGATCATCTGA 1162 | TTGT | |
| | | | TCAGATGATT ATTAG | | |
| | | | | | |

AGTCTACTAG TAATC

GAM233 SOX11 3' AATCATAATCATCTGATA 991 T T
TATCAGATGATT TG ATT
||||||| || |||
ATAGTCTACTAA AC TAA
T _

GAM234 C6 5' TGGGAGGACAAAGGCAGT 3656 A A_
ACT CCTTTGTC CCCA
||| ||||| ||||
TGA GGAAACAG GGGT
C GA

GAM234 CGB 5' ATAAAGCCAGGTACACGAGGCA 770 A _ C CAA
G CT CCTT TGT ACC CTTTAT
|| ||| ||| ||| |||||
GA GGAG ACA TGG GAAATA
C C _ ACC

GAM234 CUL3 3' AGTTGGGTAACAAAAATGG 1040 CC C
CTA TTTGT ACCCAACT
||| ||||| |||||
GGT AAACA TGGGTTGA
AA A

GAM234 GRINL1A 3' ATAAAGTTACACAAAGGTAGT 2863 CACCC
ACTACCTTTGT AACTTTAT
||||||| |||||
TGATGGAAACA TTGAAATA
CA__

GAM234 PRKG1 3' AGTTGAGAGACAAAGGTA 1283 ACC
TACCTTTGTC CAACT
||||||| |||||
ATGGAAACAG GTTGA
AGA

GAM234 WHSC1 3' AAAGTTGGGTTGATAGG 2409 TT _
CCT GTCA CCCAACTTT
||| ||| |||||
GGA TAGT GGGTTGAAA
_ T

GAM234 CGB5 5' ATAAAGCCAGGTACACGAGGCA 2311 A _ C CAA
G CT CCTT TGT ACC CTTTAT
|| ||| ||| ||| |||||
GA GGAG ACA TGG GAAATA
C C _ ACC

GAM234 DDX33 3' ATAAAATTGGGTTTCATAAAG 1895 C_ C
CTTTGT ACCCAA TTTAT
||||| ||||| |||||
GAAATA TGGGTT AAATA
CT A

GAM234 FLJ20296 5' TAAAGCTGGTTAAGGTGGT 1749 TGTCAC A
ACTACCTT CCA CTTTA
||||||| ||| |||||

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|--------|-----------|----|-----------------------|-------------------|-----|---------|
| | | | TGGTGGAA | GGT GAAAT | | |
| | | | TT_____ | C | | |
| GAM234 | IRO039700 | 5' | GTGGGGCAGACAAAGGCAG | 1858 | A | A_ A |
| | | | CT CCTTTGTC | CCC AC | | |
| | | | | | | |
| | | | GA GGAAACAG | GGG TG | | |
| | | | C | AC G | | |
| GAM234 | KIAA0594 | 3' | ATAAAATTAGGTGACAAGGGT | 2706 | | C C |
| | | | ACCTTTGTCACC | AA TTTAT | | |
| | | | | | | |
| | | | TGGGAACAGTGG | TT AAATA | | |
| | | | A | A | | |
| GAM234 | MAL2 | 3' | AGTTGAATGACAAAGCAGT | 2343 | AC | CC |
| | | | ACT CTTTGTCA | CAACT | | |
| | | | | | | |
| | | | TGA GAAACAGT | GTTGA | | |
| | | | C_ | AA | | |
| GAM234 | LOC145622 | 3' | AAAGTTGTGTAAAGTGACGAA | 3080 | | C_____ |
| | | | TTTGTAC | CAACTTT | | |
| | | | | | | |
| | | | AAGCAGTG | GTTGAAA | | |
| | | | AAATGT | | | |
| GAM234 | LOC152982 | 3' | ATAAAGTTACACAAAGGTAGT | 3176 | | CACCC |
| | | | ACTACCTTTGT | AACTTTAT | | |
| | | | | | | |
| | | | TGATGGAAACA | TTGAAATA | | |
| | | | CA_____ | | | |
| GAM234 | LOC256174 | 5' | ATAAAGTTGGATGGAAAGG | 3742 | G | C |
| | | | CCTTT TCA | CCAACCTTTAT | | |
| | | | | | | |
| | | | GGAAA GGT | GGTTGAAATA | | |
| | | | _ | A | | |
| GAM235 | CALCR | 3' | GAGGGGAAAAAATTA | ACTGCTC | 854 | A A _ G |
| | CA | | TG AGTA | TTAATTTTT CT CCTC | | |
| | | | | | | |
| | | | AC TCGT | AATTAAAAA GG GGAG | | |
| | | | C | C A _ | | |
| GAM235 | IL1F9 | 3' | GAAGAAGCAATTACTTCA | 1886 | AA | |
| | | | TGAAGTAATT | TTTTTC | | |
| | | | | | | |
| | | | ACTTCATTAA | AAGAAG | | |
| | | | CG | | | |
| GAM235 | LTA | 3' | AGGCAAAAAAATTA | AATTATTT | 757 | _ C |
| | | | AAGTAATT | AATTTTT TGCCT | | |
| | | | | | | |
| | | | TTTATTAA | TTAAAAA ACGGA | | |
| | | | A | A | | |
| GAM235 | PPP1R12B | 3' | AGGCAGGGTCTAACCCTTCA | 2229 | TAA | ATTT |
| | | | TGAAG TTA | TTCTGCCT | | |
| | | | | | | |

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|--------|---------------|----|----------------------|------|---------|
| | | | ACTTC AAT GGGACGGA | | |
| | | | CC_ CT__ | | |
| GAM235 | TFF3 | 3' | GCAGAAAAAATACATTTC | 2661 | AAT A |
| | | | TGAAGT TA TTTTCTGC | | |
| | | | | | |
| | | | ACTTTA AT AAAAAGACG | | |
| | | | C__ A | | |
| GAM235 | ZHX1 | 3' | AGGAGAATCAATTCTTCA | 1366 | T A |
| | | | TGAAG AATT ATTTTCT | | |
| | | | | | |
| | | | ACTTC TTAA TAAGAGGA | | |
| | | | _ C | | |
| GAM235 | DKFZP434C1715 | 3' | AGGCAGAAGGATCACTT | 3371 | AATTA |
| | | | AAGT ATTTTCTGCCT | | |
| | | | | | |
| | | | TTCA TAGGAAGACGGA | | |
| | | | C__ | | |
| GAM235 | FLJ21075 | 3' | GAGGCAGAAAATTCCACTT | 2130 | AATTAAT |
| | | | AAGT TTTTCTGCCTC | | |
| | | | | | |
| | | | TTCA AAAAGACGGAG | | |
| | | | CCTT__ | | |
| GAM235 | FLJ23556 | 3' | AGGCAGAAGGATCACTT | 2101 | AATTA |
| | | | AAGT ATTTTCTGCCT | | |
| | | | | | |
| | | | TTCA TAGGAAGACGGA | | |
| | | | C__ | | |
| GAM235 | HSD17B7 | 3' | AGGCAGAAGGATCACTT | 1682 | AATTA |
| | | | AAGT ATTTTCTGCCT | | |
| | | | | | |
| | | | TTCA TAGGAAGACGGA | | |
| | | | C__ | | |
| GAM235 | IDN3 | 3' | AGGCAGAAAACTTGAAATAC | 2415 | A_ _ |
| | | | GTA TTAA TTTTCTGCCT | | |
| | | | | | |
| | | | CAT AGTT AAAAAGACGGA | | |
| | | | AA C | | |
| GAM235 | KIAA1456 | 3' | AGGCAGAAGGATCACTT | 2772 | AATTA |
| | | | AAGT ATTTTCTGCCT | | |
| | | | | | |
| | | | TTCA TAGGAAGACGGA | | |
| | | | C__ | | |
| GAM235 | NXPH3 | 3' | AGACAGAAATGTTACTTC | 2727 | TAATT C |
| | | | GAAGTAAT TTTCTG CT | | |
| | | | | | |
| | | | CTTCATTG AAAGAC GA | | |
| | | | T__ A | | |
| GAM235 | PNPASE | 3' | GAGGCAGAAGAATCACTTCA | 2901 | AATTA |
| | | | TGAAGT ATTTTCTGCCTC | | |
| | | | | | |

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|--------|-----------|----|------------------------|---------------|--------|--------|
| | | | ACTTCA | TAAGAAGACGGAG | | |
| | | | C_____ | | | |
| GAM235 | SPRY4 | 3' | AGGCAGAAGAATCACTT | 2176 | AATTA | |
| | | | AAGT | ATTTTTCTGCCT | | |
| | | | | | | |
| | | | TTCA | TAAGAAGACGGA | | |
| | | | C_____ | | | |
| GAM235 | ZNF33A | 3' | AGGCAGAAGAATCACTT | 3519 | AATTA | |
| | | | AAGT | ATTTTTCTGCCT | | |
| | | | | | | |
| | | | TTCA | TAAGAAGACGGA | | |
| | | | C_____ | | | |
| GAM235 | LOC126282 | 3' | AGGCAGGATAATCACTT | 2999 | A | ATTT |
| | | | AAGT | ATTA TTCTGCCT | | |
| | | | | | | |
| | | | TTCA | TAAT AGGACGGA | | |
| | | | C _____ | | | |
| GAM235 | LOC144583 | 3' | AGGCAGGATAATCACTT | 3068 | A | ATTT |
| | | | AAGT | ATTA TTCTGCCT | | |
| | | | | | | |
| | | | TTCA | TAAT AGGACGGA | | |
| | | | C _____ | | | |
| GAM235 | LOC145231 | 3' | AGGCAGGCGAATTACTTCA | 3273 | | AATTTT |
| | | | TGAAGTAATT | TCTGCCT | | |
| | | | | | | |
| | | | ACTTCATTAA | GGACGGA | | |
| | | | GC_____ | | | |
| GAM235 | LOC147837 | 3' | AGGCAGGATAATCACTT | 3113 | A | ATTT |
| | | | AAGT | ATTA TTCTGCCT | | |
| | | | | | | |
| | | | TTCA | TAAT AGGACGGA | | |
| | | | C _____ | | | |
| GAM235 | LOC149910 | 3' | GAGACAGAATCTTTAGTTACTT | 3141 | TTT | C |
| | CA | | TGAAGTAATTAA | TTCTG CTC | | |
| | | | | | | |
| | | | ACTTCATTGATT | AAGAC GAG | | |
| | | | TCT | A | | |
| GAM235 | LOC158160 | 3' | AGGCAGAAGGATCACTT | 2967 | AATTA | |
| | | | AAGT | ATTTTTCTGCCT | | |
| | | | | | | |
| | | | TTCA | TAGGAAGACGGA | | |
| | | | C_____ | | | |
| GAM235 | LOC158292 | 5' | AGGCAGAAGAATCACTT | 3385 | AATTA | |
| | | | AAGT | ATTTTTCTGCCT | | |
| | | | | | | |
| | | | TTCA | TAAGAAGACGGA | | |
| | | | C_____ | | | |
| GAM235 | LOC162333 | 5' | GAAGCAGAAGATACTACTTTA | 3401 | ATTAAT | C |
| | | | TGAAGTA | TTTTCTGC TC | | |
| | | | | | | |

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|--------|-----------|----|-------------------------|-------------|--------|-------|
| | | | ATTTCAT | AGAAGACG AG | | |
| | | | CAT___ | A | | |
| GAM235 | LOC200057 | 5' | GAAGCAGAAAGAGGTTACTT | 3437 | AA | C |
| | | | AAGTAATT TTTTCTGC TC | | | |
| | | | | | | |
| | | | TTCATTGG AGAAAGACG AG | | | |
| | | | ___ | A | | |
| GAM235 | LOC202018 | 3' | GCTTTAAACTAATTACTTCA | 3460 | A | TCT |
| | | | TGAAGTAATTA TTTT GC | | | |
| | | | | | | |
| | | | ACTTCATTAAT AAAA CG | | | |
| | | | C TTT | | | |
| GAM235 | LOC219392 | 5' | GCAGAGGGAACCAGCTTCA | 3511 | AATTAA | |
| | | | TGAAGT TTTTCTGC | | | |
| | | | | | | |
| | | | ACTTCG AGGGAGACG | | | |
| | | | ACCA___ | | | |
| GAM236 | TACC1 | 3' | TAATTGGTAGCCATCTCATG | 1285 | C | _ |
| | | | CGTGA GTGGT ATCAATTA | | | |
| | | | | | | |
| | | | GTACT TACCG TGGTTAAT | | | |
| | | | C A | | | |
| GAM237 | EIF4G2 | 3' | AAGCAGAGGCAGTCTATTG | 827 | T | GTAAG |
| | | | CAAT AGAC TTCTGCTT | | | |
| | | | | | | |
| | | | GTTA TCTG GAGACGAA | | | |
| | | | _ ACG___ | | | |
| GAM237 | PEX12 | 3' | AAGCAAAATACTAATCTAATTG | 727 | CGTAA | C |
| | TG | | TACAATTAGA GTT TGCTT | | | |
| | | | | | | |
| | | | GTGTTAATCT TAA ACGAA | | | |
| | | | AATCA A | | | |
| GAM237 | LOC130162 | 3' | AAGCAGAACAGATACCTAATT | 3009 | AC | AA |
| | | | AATTAG GT GTTCTGCTT | | | |
| | | | | | | |
| | | | TTAATC TA CAAGACGAA | | | |
| | | | CA GA | | | |
| GAM237 | LOC152573 | 3' | AAGCAAAGAAAAATACCTAATT | 3172 | AC | AG_ _ |
| | GTA | | TACAATTAG GTA TTCT GCTT | | | |
| | | | | | | |
| | | | ATGTTAATC CAT AAGA CGAA | | | |
| | | | _ AAA AA | | | |
| GAM238 | FACL2 | 3' | AGAGTACATGTATTATAT | 1942 | TTT | A |
| | | | ATGTAATACA TG ACTCT | | | |
| | | | | | | |
| | | | TATATTATGT AC TGAGA | | | |
| | | | _ A | | | |
| GAM238 | PTER | 3' | AGTCAAAATATATTACAT | 2154 | C | A |
| | | | ATGTAATA ATTTTGA CT | | | |
| | | | | | | |

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|--------|-----------|----|-----------------------------|--------|--------|
| | | | TACATTAT TAAAACT GA | | |
| | | | A _ | | |
| GAM238 | ATP6V1G1 | 3' | AGAATTCAAGAACTTGTTACAT 1163 | CA_ | C |
| | | | GTA TACATGTAATA TTTTGAA TCT | | |
| | | | | | |
| | | | ATGTACATTGT AGAACTT AGA | | |
| | | | TCA A | | |
| GAM238 | GFR | 3' | AGATGCAAATGTATTACTGTA 1423 | T | T AAC |
| | | | TACA GTAATACATTT G TCT | | |
| | | | | | |
| | | | ATGT CATTATGTAAA C AGA | | |
| | | | _ _GT_ | | |
| GAM238 | KIAA0349 | 3' | TTTGGAATGTATCATATGTA 3562 | A | TG |
| | | | TACATGT ATACATTT AA | | |
| | | | | | |
| | | | ATGTATA TATGTAAG TT | | |
| | | | C GT | | |
| GAM238 | RGS20 | 3' | AAGATGTGACCACTACATGTA 1049 | A_____ | |
| | | | TACATGTA TACATTTT | | |
| | | | | | |
| | | | ATGTACAT GTGTAGAA | | |
| | | | CACCA | | |
| GAM238 | LOC253573 | 3' | GAGTTCAAAAGTACCACA 3725 | AA A | |
| | | | TGT TAC TTTTGAACTC | | |
| | | | | | |
| | | | ACA ATG AAAACTTGAG | | |
| | | | CC _ | | |
| GAM238 | LOC83690 | 3' | AGATGAACTAATGTATTACATT 2203 | C | TTGAAC |
| | | | A A ATGTAATACATT TCT | | |
| | | | | | |
| | | | A TACATTATGTAA AGA | | |
| | | | T TCAAGT | | |
| GAM239 | RBM8A | 3' | AATGTTCCATTTTGTGTTTC 1186 | A_ | |
| | | | GAAAACAAAAAT GATATT | | |
| | | | | | |
| | | | CTTTTGTTTTTA TTGTAA | | |
| | | | CC | | |
| GAM239 | SLC7A6 | 3' | GTCTGTTTTTGTTCCTGA 1078 | AA | |
| | | | TCG AACAAAAATAGAT | | |
| | | | | | |
| | | | AGC TTGTTTTTGTCTG | | |
| | | | CC | | |
| GAM239 | SEMA3E | 3' | AGTGTTTATTTTCAAGTTTC 1432 | AA | |
| | | | GAAAAC AAATAGATATT | | |
| | | | | | |
| | | | CTTTTG TTTATTTGTGA | | |
| | | | AC | | |
| GAM239 | LOC151201 | 3' | AATGTCATTTTGTGTTTT 3339 | A | |
| | | | GAAAACAAAAAT GATATT | | |
| | | | | | |

TTTTTGTTTTTA CTGTAA

GAM239 LOC90979 3' AATAATATTTTTTTTGT T 2692
—
AAAACAAAAA AGATATTATT
||||||| |||||||
TTTTGTTTTT TTTATAATAA

GAM240 ZIC1 3' CGAATCAAACAACCCCCACAC 1017 ATAGA AC
—
A TGT GG GTTTTGATTG
||| || |||||||
ACA CC CAAACTAAGC
CACCC AA

GAM240 KIAA1550 3' CAGGACGTCCTCTACACA 2752 A
TGT TAGAGGACGTTTTG
||| |||||||||
ACA ATCTCCTGCAGGAC
C

GAM240 LOC143720 3' TCAAAGCTCCCCTATACA 2568 A C
TGTATAG GGA GTTTTGA
||||| ||| |||||
ACATATC CCT CGAACT
C _

GAM240 LOC150848 5' TCAAATCCCTTTTGTCTCTATA 3335 G TTTT_ C
CA TGTATAGAG ACG GATT GA
||||||| ||| ||| ||
ACATATCTC TGT CTA CT
_ TTTCC A

GAM241 MAIL 3' AGTCTTTGTAGATAAA 2194 AC
TTTATCTACAG AGACT
||||||| |||||
AAATAGATGTT TCTGA

GAM241 LOC151414 3' ATTATTCTTAGATCTGTAGATA 3157 C__ C
—
TATCTACAGA AGA TAAT
||||||| ||| |||||
ATAGATGTCT TCT ATTA
AGAT T

GAM241 LOC155038 3' AGCTATTTGTAGATAAA 3197 C A
TTTATCTACAGA AG CT
||||||| ||| |||
AAATAGATGTTT TC GA
A _

GAM242 CRH 3' TTAGCTAGCATGCACAAA 772 A GA
TTTGT CA CTAAGTAA
||||| || |||||||
AAACA GT GATTCATT
C AC

GAM242 C1orf24 3' AAGAATTTTCTGTACA 2351 CTAAGT
TGTACAGA AATTCTT
||||||| |||||||

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|--------|-----------|----|------------------------|------------|---------|-------|
| | | | ACATGTCT | TTAAGAA | | |
| | | | T_____ | | | |
| GAM242 | C21orf67 | 5' | AAAGATACTCACCTGTACAAA | 2367 | ACTA | AT |
| | | | TTTGTACAG | AGTA TCTTT | | |
| | | | | | | |
| | | | AAACATGTC | TCAT AGAAA | | |
| | | | CAC_ _ | | | |
| GAM242 | KIAA0940 | 3' | AAGAAATGTCTGTACAAA | 1585 | TAAGTAA | |
| | | | TTTGTACAGAC | TTCTT | | |
| | | | | | | |
| | | | AAACATGTCTG | AAGAA | | |
| | | | TA_____ | | | |
| GAM242 | LOC158722 | 3' | AAAGAATTATATTGCTGACAAA | 3225 | A | ACTAA |
| | | | TTTGT CAG | GTAATTCTTT | | |
| | | | | | | |
| | | | AAACA GTC | TATTAAGAAA | | |
| | | | _ GTTA_ | | | |
| GAM242 | LOC220705 | 3' | AATGTCTTAGTTGTACAAA | 3514 | A | TA |
| | | | TTTGTACAG | CTAAG ATT | | |
| | | | | | | |
| | | | AAACATGTT | GATTC TAA | | |
| | | | _ TG | | | |
| GAM243 | ACVR1 | 3' | AAGCAAAGATTTTCAGTAGA | 800 | _ | A |
| | | | TCT TTGAAATCTTT | CTT | | |
| | | | | | | |
| | | | AGA GACTTTAGAAA | GAA | | |
| | | | T | C | | |
| GAM243 | CELSR1 | 3' | AAGTAAATGCAAAGATGT | 1486 | AAATC | |
| | | | ACATCTTTG | TTTACTT | | |
| | | | | | | |
| | | | TGTAGAAAC | AAATGAA | | |
| | | | GTA_ | | | |
| GAM243 | GJA1 | 3' | AAGTAGTGGATTCAAAGA | 715 | A | T |
| | | | TCTTTGAA | TC TTACTT | | |
| | | | | | | |
| | | | AGAAACTT | GG GATGAA | | |
| | | | A | T | | |
| GAM243 | PLN | 3' | AAGTAATTTTTTCAAAGA | 945 | TCT | |
| | | | TCTTTGAAA | TTACTT | | |
| | | | | | | |
| | | | AGAAACTTT | AATGAA | | |
| | | | TTT | | | |
| GAM243 | CNOT7 | 3' | AAGTAAAGATATAATTAGAGAT | 2363 | A | _____ |
| | | | ATCTTTGA | ATCTTTACTT | | |
| | | | | | | |
| | | | TAGAGATT | TAGAAATGAA | | |
| | | | AATA | | | |
| GAM243 | Grcc9 | 3' | AAGTAAAAATAGTAAGAGATGT | 2268 | GAA_ | C |
| | | T | AACATCTTT | AT TTTACTT | | |
| | | | | | | |

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|--------|-----------|----|-----------------------------|----------|
| | | | TTGTAGAGA TA AAATGAA | |
| | | | ATGA A | |
| GAM243 | KIAA1287 | 3' | AAGTAGAAATCTCAAAGAT 3106 | A C |
| | | | ATCTTTGA AT TTTACTT | |
| | | | | |
| | | | TAGAAACT TA AGATGAA | |
| | | | C A | |
| GAM243 | KIAA1673 | 3' | AAGTGTTTGATTGAGAGATGT 2894 | A TT_ |
| | | | ACATCTTTGAA TC TACTT | |
| | | | | |
| | | | TGTAGAGACTT AG GTGAA | |
| | | | _ TTT | |
| GAM243 | LHFP | 3' | AAGCAAGGTACCCCCAAAGATG 1248 | AAAT__ A |
| | TT | | AACATCTTTG CTTT CTT | |
| | | | | |
| | | | TTGTAGAAAC GGAA GAA | |
| | | | CCCCAT C | |
| GAM243 | PDE10A | 3' | AAGTAGCAGTTCAAAAGATGT 1320 | GA CT |
| | | | ACATCTTT AAT TTACTT | |
| | | | | |
| | | | TGTAGAAA TTG GATGAA | |
| | | | AC AC | |
| GAM243 | TBDN100 | 3' | AAGTAAAGATTTATCTGAT 2135 | TTTG |
| | | | ATC AAATCTTTACTT | |
| | | | | |
| | | | TAG TTTAGAAATGAA | |
| | | | TCTA | |
| GAM243 | LOC149448 | 3' | GTAATTTTCAAAGATG 3310 | TCT |
| | | | CATCTTTGAAA TTAC | |
| | | | | |
| | | | GTAGAAACTTT AATG | |
| | | | T__ | |
| GAM243 | LOC155434 | 3' | AGTGGCGATTCAAAGATG 3375 | A T |
| | | | CATCTTTGAA TC TTACT | |
| | | | | |
| | | | GTAGAAACTT AG GGTGA | |
| | | | _ C | |
| GAM243 | LOC221583 | 3' | AAGTATACTACTCTCAAAGGTG 3557 | AATCTT__ |
| | T | | ACATCTTTGA TACTT | |
| | | | | |
| | | | TGTGGAAACT ATGAA | |
| | | | CTCATCAT | |
| GAM243 | LOC54466 | 3' | AAGTGGCAACTGTCAAAGATG 1871 | AATCT_ |
| | | | CATCTTTGA TTACTT | |
| | | | | |
| | | | GTAGAAACT GGTGAA | |
| | | | GTCAAC | |
| GAM244 | MECP2 | 3' | CCAGAGACAAATATTTCTAGA 1167 | C C AA_ |
| | | | TC AGAGATAT TTGT TGG | |
| | | | | |

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|--------|-----------|----|-----------------------------|------|-------|
| | | | AG TCTTTATA AACA ACC | | |
| | | | A _ GAG | | |
| GAM244 | ATP10B | 3' | CCAGGCAATATCTCAGGATA 2655 | A | CT AA |
| | | | TATCC GAGATAT TGT TGG | | |
| | | | | | |
| | | | ATAGG CTCTATA ACG ACC | | |
| | | | A _ G_ | | |
| GAM244 | BDG-29 | 3' | CCATTACAGTGGCCTGGATA 2943 | AGA | CT |
| | | | TATCCAG TAT TGTAATGG | | |
| | | | | | |
| | | | ATAGGTC GTG ACATTACC | | |
| | | | CG_ _ | | |
| GAM244 | GW112 | 3' | CCACTTACTTAGATATCTGCAG 1298 | CAG | T_ _ |
| | ATA | | TATC AGATATCT GTAA TGG | | |
| | | | | | |
| | | | ATAG TCTATAGA CATT ACC | | |
| | | | ACG TT C | | |
| GAM244 | HSPB7 | 3' | CCATTACAACAGCTCCAGGA 1498 | A_ | ATATC |
| | | | TCC GAG TTGTAATGG | | |
| | | | | | |
| | | | AGG CTC AACATTACC | | |
| | | | AC GAC_ | | |
| GAM244 | KIAA1464 | 3' | CCAGTATTTATCTCTGGA 2813 | TCTT | A |
| | | | TCCAGAGATA GTA TGG | | |
| | | | | | |
| | | | AGGTCTCTAT TAT ACC | | |
| | | | T_ G | | |
| GAM244 | KIAA1634 | 3' | CCACCAACTATTTCTGGATA 2656 | TC | TAA |
| | | | TATCCAGAGATA TTG TGG | | |
| | | | | | |
| | | | ATAGGTCTTTAT AAC ACC | | |
| | | | C_ C_ | | |
| GAM244 | NETO1 | 3' | CCATCATCTCATCTCTGGATG 2463 | ATCT | TA |
| | | | TATCCAGAGAT TG ATGG | | |
| | | | | | |
| | | | GTAGGTCTCTA AC TACC | | |
| | | | CTCT _ | | |
| GAM244 | PRO2533 | 3' | CCATTACAAAATGTAATGG 1854 | GAG | C |
| | | | CCA ATAT TTGTAATGG | | |
| | | | | | |
| | | | GGT TGTA AACATTACC | | |
| | | | AA_ A | | |
| GAM244 | LOC151201 | 3' | TGTAATAACCTCTGGATA 3343 | A | C |
| | | | TATCCAGAG TAT TTGTA | | |
| | | | | | |
| | | | ATAGGTCTC ATA AATGT | | |
| | | | C A | | |
| GAM245 | FLJ14124 | 3' | CAAAACGAGTAAAGAGCAG 2099 | T | TAAAG |
| | | | CT CTT TACTCGTTTTG | | |
| | | | | | |

| | | | | |
|--------|--------------|-----------------------------|------|---------|
| | | GA GAG ATGAGCAAAAC | | |
| | | C AA__ | | |
| GAM245 | FLJ20039 3' | TGGGATAACTACTTTAAAGAA 1735 | | _____ |
| | | TTCTTTAAAGTA CTCG | | |
| | | | | |
| | | AAGAAATTCAT GGGT | | |
| | | CAATA | | |
| GAM245 | FLJ21369 5' | CAAAACCTGAACTTTAAAGGA 2090 | | ACTC_ |
| | | TTCTTTAAAGT GTTTG | | |
| | | | | |
| | | AGGAAATTTCA CAAAC | | |
| | | AAGTC | | |
| GAM245 | KIAA1577 5' | ATGGGTACCCCAGAGAAG 2690 | | AAA |
| | | CTTCTTT GTACTCGT | | |
| | | | | |
| | | GAAGAGA CATGGGTA | | |
| | | CCC | | |
| GAM245 | LOC144524 3' | CAAAACAAGGCATAAAGAAGT 3269 | | AAGTA C |
| | | ACTTCTTTA CT GTTTTG | | |
| | | | | |
| | | TGAAGAAAT GA CAAAC | | |
| | | ACG__ A | | |
| GAM245 | LOC150170 5' | CAAAATGGAACCTTTAAACAGT 3143 | TC | A T |
| | A | TACT TTTAAAGT C CGTTTG | | |
| | | | | |
| | | ATGA AAATTTCA G GTAAAC | | |
| | | CA A_ | | |
| GAM245 | LOC150175 5' | CAAAATGGAACCTTTAAACAGT 3144 | TC | A T |
| | A | TACT TTTAAAGT C CGTTTG | | |
| | | | | |
| | | ATGA AAATTTCA G GTAAAC | | |
| | | CA A_ | | |
| GAM245 | LOC150215 5' | CAAAATGGAACCTTTAAACAGT 3145 | TC | A T |
| | A | TACT TTTAAAGT C CGTTTG | | |
| | | | | |
| | | ATGA AAATTTCA G GTAAAC | | |
| | | CA A_ | | |
| GAM245 | LOC150218 5' | CAAAATGGAACCTTTAAACAGT 3146 | TC | A T |
| | A | TACT TTTAAAGT C CGTTTG | | |
| | | | | |
| | | ATGA AAATTTCA G GTAAAC | | |
| | | CA A_ | | |
| GAM246 | CCRL1 3' | TGTAACCTCCTGTGAATTTA 1697 | G | A C |
| | | TAAATTCG CAGGAA GT ACA | | |
| | | | | |
| | | ATTTAAGT GTCCTT CA TGT | | |
| | | _ _ A | | |
| GAM246 | PAFAH1B1 3' | TGTGACTTCCAAGTAGAATTTA 741 | G A_ | A |
| | | TAAATTC GC GGAA GTCACA | | |
| | | | | |

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|--------|----------|----|------------------------------|-------------|
| | | | ATTTAAG TG CCTT CAGTGT | |
| | | | A AA _ | |
| GAM246 | PSMB9 | 3' | TGACTTTCTTCTCAAACCTGGA 956 | AA C C |
| | | | TCTA TT GG AGGAAAGTCA | |
| | | | | |
| | | | AGGT AA CT TTCTTTCAGT | |
| | | | CC A C | |
| GAM246 | SLC4A4 | 3' | TGTGACTTTTTATGGAATTAAGA 1055 | A GG G |
| | | | TCT AATTC CA GAAAGTCACA | |
| | | | | |
| | | | AGA TTAAG GT TTTTCAGTGT | |
| | | | A _ A | |
| GAM246 | TNFAIP1 | 3' | TGACTTTCCACAGAGACTGGA 1944 | AA GGCA |
| | | | TCTA TTC GGAAAGTCA | |
| | | | | |
| | | | AGGT GAG CCTTTCAGT | |
| | | | CA ACAC | |
| GAM246 | CAT56 | 3' | GTGACTTCCCAGCACTAGA 2149 | AATTCTG A A |
| | | | TCTA GC GG AAGTCAC | |
| | | | | |
| | | | AGAT CG CC TTCAGTG | |
| | | | CA_ A C | |
| GAM246 | FLJ10520 | 3' | TGTGACTTTCTGGACCTTAGA 1785 | ATTC CA_ |
| | | | TCTAA GG GGAAAGTCACA | |
| | | | | |
| | | | AGATT CC TCTTTCAGTGT | |
| | | | _ AGG | |
| GAM246 | FLJ14001 | 5' | TGCGACCCCCCTGCCCGAAT 2081 | _ AAA A |
| | | | ATTC GGCAGG GTC CA | |
| | | | | |
| | | | TAAG CCGTCC CAG GT | |
| | | | CC CCC C | |
| GAM246 | FLJ14917 | 3' | TGTGACTTTCCTGGTGCATCCA 2290 | AA T G |
| | GG | | TCT AT CG CAGGAAAGTCACA | |
| | | | | |
| | | | GGA TA GT GTCCTTTCAGTGT | |
| | | | CC C G | |
| GAM246 | KIAA0618 | 3' | TGTGACTTTGCCCAAATTTG 1564 | C CA _ |
| | | | TAAATT GG GG AAAGTCACA | |
| | | | | |
| | | | GTTTAA CC CC TTTTCAGTGT | |
| | | | A _ G | |
| GAM246 | KIAA1750 | 3' | GACTTTCCCATTTTAG 2812 | TTC CA |
| | | | CTAAA GG GGAAAGTC | |
| | | | | |
| | | | GATTT CC CCTTTCAG | |
| | | | TA_ _ | |
| GAM246 | MAGEF1 | 3' | GTGACTTTAAGGATTTAGA 2555 | GGCAGG |
| | | | TCTAAATTC AAAGTCAC | |
| | | | | |

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|--------|-----------|----|------------------------|----------|---------|
| | | | AGATTTAGG | TTTCAGTG | |
| | | | AA | | |
| GAM246 | LOC253017 | 5' | TGACTTTACCAATTTA | 3685 | C CAG |
| | | | TAAATT GG GAAAGTCA | | |
| | | | | | |
| | | | ATTTAA CC CTTTCAGT | | |
| | | | _ A _ | | |
| GAM246 | LOC51705 | 3' | TGACTTTCCTTAATGTTTA | 1674 | TCGGC |
| | | | TAAAT AGGAAAGTCA | | |
| | | | | | |
| | | | ATTTG TCCTTTCAGT | | |
| | | | TAAT _ | | |
| GAM247 | BCL11B | 3' | AATGGTGGGTCTATAAATTTGT | 2019 | AT TT |
| | | | ATAAATTTATA G CGCCATT | | |
| | | | | | |
| | | | TGTTTAAATAT T GTGGTAA | | |
| | | | C _ GG | | |
| GAM247 | FGFR4 | 3' | AATGGCGTTTTATAAATT | 2022 | TGTT |
| | | | AATTTATAA CGCCATT | | |
| | | | | | |
| | | | TTAAATATT GCGGTAA | | |
| | | | TT _ | | |
| GAM247 | FGFR4 | 3' | AATGGCGTTTTATAAATT | 887 | TGTT |
| | | | AATTTATAA CGCCATT | | |
| | | | | | |
| | | | TTAAATATT GCGGTAA | | |
| | | | TT _ | | |
| GAM247 | FLJ22833 | 3' | AATGGCCGGGGACTTATAAAT | 2015 | T _ _ |
| | | | ATTTATAA GTTC GCCATT | | |
| | | | | | |
| | | | TAAATATT CAGG CGGTAA | | |
| | | | _ GGC | | |
| GAM247 | SSH2 | 3' | AATGGCCGGCTCTGCAAATTTA | 2625 | A AT TC |
| | T | | ATAAATTT TA GT GCCATT | | |
| | | | | | |
| | | | TATTTAAA GT CG CGGTAA | | |
| | | | C CT GC | | |
| GAM248 | RARB | 3' | TTCACAAGCCATTAGGGA | 792 | AA C |
| | | | TCCCTAAT CTT GTGAA | | |
| | | | | | |
| | | | AGGGATTA GAA CACTT | | |
| | | | CC _ | | |
| GAM248 | RARB | 3' | TTCACAAGCCATTAGGGA | 1663 | AA C |
| | | | TCCCTAAT CTT GTGAA | | |
| | | | | | |
| | | | AGGGATTA GAA CACTT | | |
| | | | CC _ | | |
| GAM248 | BTN2A2 | 3' | CACTTAGAAGTTATTGAGGA | 1344 | C _ _ |
| | | | TCC TAATAACTTC GTG | | |
| | | | | | |

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|--------|---------------|----|---------------------------|----------|--|
| | | | AGG GTTATTGAAG CAC | | |
| | | | A ATT | | |
| GAM248 | ZNF337 | 3' | TTACCTGGGCTATTGGGGA 2806 | A_ TC | |
| | | | TCCCTAATA CT GTGA | | |
| | | | | | |
| | | | AGGGGTTAT GG CATT | | |
| | | | CG TC | | |
| GAM248 | LOC139231 | 3' | TCACTTGAGAAGTTGTTAGG 3021 | _____ | |
| | | | CCTAATAACTTC GTGA | | |
| | | | | | |
| | | | GGATTGTTGAAG CACT | | |
| | | | AGTT | | |
| GAM248 | LOC221399 | 5' | CACTCAAGTCATTAGGGA 3622 | A C_ | |
| | | | TCCCTAAT ACTT GTG | | |
| | | | | | |
| | | | AGGGATTA TGAA CAC | | |
| | | | C CT | | |
| GAM249 | DKFZp762E1511 | 3' | AGGTTGGAAATGCACTGAA 2530 | C AT | |
| | | | TTCAG GTG TTTCCAACCT | | |
| | | | | | |
| | | | AAGTC CGT AAAGGTTGGA | | |
| | | | A _ | | |
| GAM249 | LOC123591 | 5' | AGGTTGGAAAAGGCTCCGC 3032 | T _ | |
| | | | GCG GA TTTTCCAACCT | | |
| | | | | | |
| | | | CGC CT AAAAGGTTGGA | | |
| | | | _ CGG | | |
| GAM250 | EFNB2 | 3' | GTTGAAAAGCCAAAGGT 1085 | C TTA | |
| | | | GCCT TGGCTTT TCAGC | | |
| | | | | | |
| | | | TGGA ACCGAAA AGTTG | | |
| | | | A _ | | |
| GAM250 | FACL4 | 5' | AGGCTTTCAAAAGCCAAAG 2025 | C TATC | |
| | | | CT TGGCTTTT AGCCT | | |
| | | | | | |
| | | | GA ACCGAAAA TCGGA | | |
| | | | A CTT_ | | |
| GAM250 | GATA2 | 3' | AGGCTGGGCTGAGCCAAAGC 892 | CTC TTTA | |
| | | | GC TGGCTT TCAGCCT | | |
| | | | | | |
| | | | CG ACCGAG GGTCGGA | | |
| | | | AA_ TCG_ | | |
| GAM250 | IRS2 | 3' | CTGATAAAAAGAGGC 2540 | GGCT | |
| | | | GCCTCT TTTTATCAG | | |
| | | | | | |
| | | | CGGAGA AAAATAGTC | | |
| | | | _____ | | |
| GAM250 | PAH | 5' | AGGCCCTAAAAAGCCAGAG 725 | TCA | |
| | | | CTCTGGCTTTTTA GCCT | | |
| | | | | | |

GAGACCGAAAAAT CGGA
 CC_
 GAM250 PODXL 3' GCTGCACAGGAGGCCAGA 1207 AT_
 TCTGGCTTTTT CAGC
 ||||| |||
 AGACCGGAGGA GTCG
 CAC
 GAM250 RPL15 3' GCTGGTGAGCCAGTGGC 973 T TTT
 GCC CTGGCTT ATCAGC
 || ||||| |||||
 CGG GACCGAG TGGTCG
 T ____
 GAM250 SERPINE1 3' AGGCTGGTGACAGGCCAAAGGC 758 C T
 GCCT TGGCTT TTATCAGCCT
 ||| ||||| |||||
 CGGA ACCGGA AGTGGTCGGA
 A C
 GAM250 ABIN-2 3' GCTTAAGCCAGAGCTA 2057 C TTTATC
 TAGC TCTGGCTT AGC
 ||| ||||| |||
 ATCG AGACCGAA TCG
 - T____
 GAM250 C20orf48 5' GGCCGAGGGACAAAGGCTA 2118 C G TTTA A
 TAGCCT TG CTT TC GCC
 ||||| || ||| |||
 ATCGGA AC GGG AG CGG
 A A ____ C
 GAM250 C9orf7 3' AGACTGGCTTAAGCCAGGAGC 1724 CT TTTA C
 GC CTGGCTT TCAG CT
 || ||||| ||| ||
 CG GACCGAA GGTC GA
 AG TTC_ A
 GAM250 DUSP10 3' CTGACAAATTAAGGAGGTTA 1364 GGCTT A
 TAGCCTCT TTT TCAG
 ||||| ||| |||
 ATTGGAGG AAA AGTC
 AATT_ C
 GAM250 DUSP10 3' CTGACAAATTAAGGAGGTTA 2501 GGCTT A
 TAGCCTCT TTT TCAG
 ||||| ||| |||
 ATTGGAGG AAA AGTC
 AATT_ C
 GAM250 ERMAP 3' GCTGATGGTCCTGTCCAAAGGC 1838 C _TTT_
 TA TAGCCT TGG C TTATCAGC
 ||||| ||| | |||||
 ATCGGA ACC G GGTAGTCG
 A T TCCT
 GAM250 FLJ12892 3' GCTGATAAAGAAGTGCTA 2802 CT GGC C
 TAGC CT TTTTATCAG C
 ||| || ||||| |||

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|--------|----------|----|-----------------------------|-----|---------|
| | | | ATCG GA AGAAATAGTC G | | |
| | | | T_ ____ A | | |
| GAM250 | FLJ22059 | 5' | GA CTGGAGAGCCAGAGGC 2003 | | — |
| | | | GCCTCTGGCTTTTTA TC | | |
| | | | | | |
| | | | CGGAGACCGAGAGGT AG | | |
| | | | C | | |
| GAM250 | HEMK | 3' | GGCCAAAGCCAGAGACT 1669 C | | TTATCA |
| | | | AG CTCTGGCTTT GCC | | |
| | | | | | |
| | | | TC GAGACCGAAA CGG | | |
| | | | A C_____ | | |
| GAM250 | KIAA0227 | 3' | GGGCCCCAAAAGACCAGAGGC 2578 | | — TATCA |
| | | | GCCTCTGG CTTT GCCT | | |
| | | | | | |
| | | | CGGAGACC GAAAA CGGG | | |
| | | | A CCC__ | | |
| GAM250 | KIAA0527 | 3' | GAATAAAAGCCAGAGACTG 3684 C | | TA |
| | | | TAG CTCTGGCTTT TC | | |
| | | | | | |
| | | | GTC GAGACCGAAAA AG | | |
| | | | A TA | | |
| GAM250 | KIAA1244 | 3' | AGGCTTCAGTAAAGCAGAGGCT 2930 | | G TTATC |
| | A | | TAGCCTCTG CTTT AGCCT | | |
| | | | | | |
| | | | ATCGGAGAC GAAA TCGGA | | |
| | | | — TGA CT | | |
| GAM250 | KIAA1649 | 3' | TGAAAAAAACCAGAGACT 2771 C | C | A |
| | | | AG CTCTGG TTTT TCA | | |
| | | | | | |
| | | | TC GAGACC AAAAA AGT | | |
| | | | A — A | | |
| GAM250 | KIAA1981 | 3' | AGGCCACGGGAGCCGAGGC 3431 | T | TATCA |
| | | | GCCTC GGCTTT GCCT | | |
| | | | | | |
| | | | CGGAG CCGAGGG CGGA | | |
| | | | — CAC__ | | |
| GAM250 | MGC2306 | 3' | AGGCTGGGCTGAGCCAAAGC 2266 | CTC | TTTA |
| | | | GC TGGCTT TCAGCCT | | |
| | | | | | |
| | | | CG ACCGAG GGTCGGA | | |
| | | | AA_ TCG_ | | |
| GAM250 | RPL39L | 5' | GTGGGAAAAAAGCAGAGGC 2352 | G | A A |
| | | | GCCTCTG CTTTTT TC GC | | |
| | | | | | |
| | | | CGGAGAC GAAAAA GG TG | | |
| | | | — A G | | |
| GAM250 | SNPH | 3' | CTGAAAAAGCCAGAGGC 1531 | | TA |
| | | | GCCTCTGGCTTT TCAG | | |
| | | | | | |

CGGAGACCGAAAA AGTC

GAM250 TMG3 3' GCCCCCGGGAAGAGCCAAAGGC 2053 C ATCA__
GCCT TGGCTTTTT GC
||||| ||
CGGA ACCGAGAAG CG
A GGCCCC

GAM250 LOC145240 3' GCTCGAAAAGGCAAAGGCTA 3076 C G ATC
TAGCCT TG CTTTTT AGC
||||| || |||
ATCGGA AC GAAAAG TCG
A G C__

GAM250 LOC146287 5' AGGCTGAACAGCAAACCCAGAG 3284 C TTA__
GC GCCTCTGG TTT TCAGCCT
||||| || |||
CGGAGACC AAA AGTCGGA
C CGACA

GAM250 LOC148696 5' AGACTGTACAGGAAACCTAAGG 3301 CT C AT_ C
C GCCT GG TTTTT CAG CT
||| || ||| |||
CGGA CC AAGGA GTC GA
AT A CAT A

GAM250 LOC150577 3' AGGCCGACAACCACCAGAAGCT 3330 C CTTTTTA A
G TAGC TCTGG TC GCCT
||||| || |||
GTCG AGACC AG CGGA
A ACCAAC_ C

GAM250 LOC151521 3' TGTTTAAAAACCCAAAGGC 3347 C C T_
GCCT TGG TTTTCA CA
||||| ||| ||
CGGA ACC AAAAAT GT
A C TT

GAM250 LOC157273 5' AGGCTGGATGAAGCCAGGGGCT 3379 TTA
A TAGCCTCTGGCTTT TCAGCCT
||||| |||
ATCGGGGACCGAAG GGTCGGA
TA_

GAM250 LOC163682 5' GAGCCAAAAGCCAGAGCCTA 3398 C TA_
TAG CTCTGGCTTTT TC
||| ||| ||| ||
ATC GAGACCGAAAA AG
C CCG

GAM250 LOC221749 3' GCTGAGGTCACAGCCGGAGGC 3549 TTTTA_
GCCTCTGGCT TCAGC
||||| |||
CGGAGGCCGA AGTCG
CACTGG

GAM250 LOC222234 3' AGGCTGATGCCCCAAAAGGC 3646 C_ CTTTT
GCCT TGG TATCAGCCT
||| ||| ||| |||

CGGA ACC GTAGTCGGA
AA CC___

GAM251 ADAMTSL1 3' AACCATTAGAGGTGCAATCTAC 2479 _ CA_ TTA
A TG AGAT ACT TCTAATGGTT
|| ||| ||| |||||
AC TCTA TGG AGATTACCAA
A ACG ___

GAM251 KIAA1862 3' AACCACCAGCCGTTCTGATCT 2834 ACTTTAT AA
CA TGAGATCA CT TGGTT
||||| || |||
ACTCTAGT GA ACCAA
CCTTGCC CC

GAM251 LOC153951 5' AACCATGAAAGACAGAGTTGAT 3184 A A_
CTCA TGAGATCAACTTT TCT ATGGTT
||||||| ||| |||
ACTCTAGTTGAGA AGA TACCAA
C AAG

GAM251 LOC221596 3' AACCATTAGACAAAACCTTTCT 3548 TCAAC A
AGA TTT TCTAATGGTT
||| ||| |||||
TCT AAA AGATTACCAA
TCTCA C

GAM252 ESAM 3' CTTTACTGTGGGAAAACCATCT 2461 GA A AC
CA TG ATGTTTTT TAGTAAAG
|| || ||||| |||||
AC TA CAAAAGG GTCATTTT
TC C GT

GAM252 KIAA0379 3' ACTAAGAAAACCTATTCA 2809 AC
TGGAATAGTTTTTT TAGT
||||||| |||
ACTTTATCAAAAGA ATCA

GAM252 LOC161784 3' CTTTAATTTTAAAAAACGTATT 3241 _ CTAG
CCA TGGAATA GTTTTTTA TAAAG
||||| ||||| |||
ACCTTAT CAAAAAAT ATTTC
G TTTA

GAM252 LOC255229 3' CTTTAATTTTAAAAAACGTATT 3676 _ CTAG
CCA TGGAATA GTTTTTTA TAAAG
||||| ||||| |||
ACCTTAT CAAAAAAT ATTTC
G TTTA

GAM253 HIP2 3' TGTTTTTAACATGGATC 1201 G
GAT CCATGTTAAAAATG
||| |||||
CTA GGTACAATTTTGT

GAM253 ITK 3' TATTTTAAACATGAATC 1224 GC
GAT CATGTTAAAAATG
||| |||||

CTA GTACAATTTTAT
A_
GAM253 ONECUT1 3' GCGGACATCTTTTAAGAT 2622 G _
AT TTA AAA ATGTCCGC
|| ||||| |||||
TA AATTTT TACAGGCG
G C
GAM253 BTN3A2 5' GACATTTTTGGCAGAGCAT 1354 CA
ATGC TGT TAAAAATGTC
|||| |||||
TACG ACGGTTTTTACAG
AG
GAM253 BTN3A3 5' GACATTTTTGGCAGAGCAT 1343 CA
ATGC TGT TAAAAATGTC
|||| |||||
TACG ACGGTTTTTACAG
AG
GAM253 IDN3 3' GGCAAACATTTTTGTGG 2416 GTT CC
CCAT AAAAATGT GCC
|||| ||||| ||
GGTG TTTTACA CGG
_ AA
GAM253 KIAA1635 3' CGGACATTTATTTGCATC 2803 CAT TAA
GATGC GT AAATGTCCG
|||| || |||||
CTACG TA TTTACAGGC
TT_ _
GAM253 LOC130106 3' GGCAAACACCTGACATGGCA 3008 AAAA CC
TGCCATGTTA TGT GCC
||||||| ||| ||
ACGGTACAGT ACA CGG
CC_ AA
GAM253 LOC151031 3' GGCATCTTAACATGGCATT 3403 AA
GATGCCATGT TAA ATGTC
||||||| ||||
TTACGGTACAATT TACGG
C_
GAM253 LOC162545 3' GGCATCTACATGGCATC 3402 TAAAA
GATGCCATGT ATGTC
||||||| ||||
CTACGGTACA TACGG
TC_
GAM253 LOC165666 5' GGCAGGGTTTTTAAATAGCATC 3257 CATG GT _
GATGC TTA AAAAT CC GCC
|||| ||||| ||| ||
CTACG AATTTTGT GG CGG
ATA_ _ A
GAM254 MEN1 5' AATGACTTGGGGATGATGC 3599 A
GCATCATCTTTAG TCATT
||||||| ||||

CGTAGTAGGGGTT AGTAA
C
GAM254 SRD5A2 5' AATTAATGATGAGGTTACATGC 2525 C__ TAG
T AGCAT ATCTT ATCATTAATT
||||| ||||| |||||
TCGTA TGGAG TAGTAATTAA
CAT ____
GAM254 DKFZP564O043 3' TGATGTCTGAAGATAATGCT 3566 C T
AGCAT ATCTTTAGA CATTA
||||| ||||| |||||
TCGTA TAGAAGTCT GTAGT
A _
GAM254 FLJ22794 5' AATTAATGACAGCTTTGAAGAT 3533 ____
ATCTTTAGA TCATTAATT
||||| |||||
TAGAAGTTT AGTAATTAA
CGAC
GAM254 HTMP10 3' AATTGTTATCTAAAGATGATTC 2322 C CAT
T AG ATCATCTTTAGAT TAATT
|| ||||| |||||
TC TAGTAGAAATCTA GTTAA
T TT_
GAM254 SEC24B 3' AATTAATGGTAACGATGATGCT 1288 TTTAG
AGCATCATC ATCATTAATT
||||| |||||
TCGTAGTAG TGGTAATTAA
CAA_
GAM254 LOC196812 5' AATGATCTAGTCAGAAGCT 3466 A ATCT
AGC TC TTAGATCATT
||| || |||||
TCG AG GATCTAGTAA
A ACT_
GAM255 ATRN 3' TAAGGGAGGTCTGTGCATTTTA 2480 A AAT A
TAAAAT CA GAC TTCCCTTA
||||| || ||| |||||
ATTTTA GT CTG GAGGGAAT
C GT_ _
GAM255 CD59 3' AATGACATTTGTATTTTA 760 A
TAAAATACAAATG CATT
||||| ||||| |||||
ATTTTATGTTTAC GTAA
A
GAM255 CENTD1 3' GGATCATTTGTATTTTG 1615 CAT
TAAAATACAAATGA TCC
||||| ||||| |||||
GTTTTATGTTTACT AGG

GAM255 CENTD1 3' GGATCATTTGTATTTTG 2474 CAT
TAAAATACAAATGA TCC
||||| ||||| |||||

GTTTTATGTTTACT AGG

GAM255 CLNS1A 3' GAGGGTATTTGTAGTTTA 816 A ACATT
TAAA TACAAATG CCCTT
|||| ||||| ||||
ATTT ATGTTTAT GGGAG
G

GAM255 NDUFA5 3' AGTGTCATTTTATTTTA 1169 C
TAAAATA AAATGACATT
||||| |||||
ATTTTAT TTTACTGTGA

GAM255 PBX3 3' GGAATCATAATCATTTGTATTT 1279 C____
AAATACAAATGA ATTCC
||||||| ||||
TTTATGTTTACT TAAGG
AATAC

GAM255 SCD 3' TAAGGGAAGATCACTGTAGTTT 1178 A AA CA
A TAAA TACA TGA TTCCCTTA
|||| ||| ||| |||||
ATTT ATGT ACT AAGGGAAT
G C_ AG

GAM255 SLC2A2 3' TAAGGGAACCGTCTGTTTTTA 731 T AAT A_
TAAAA ACA GAC TTCCCTTA
|||| ||| ||| |||||
ATTTT TGT CTG AAGGGAAT
_ _ _ CC

GAM255 TCF7 3' TAAGGGAATCCCTTGTA 998 AT CA
TACAA GA TTCCCTTA
|||| || |||||
ATGTT CT AAGGGAAT
CC _

GAM255 DKFZP586B0923 3' AAGACATGTGATTTGTATTTTA 3589 G TCC
TAAAATACAAAT ACAT CTT
||||||| ||| |||
ATTTTATGTTTA TGTA GAA
G CA_

GAM255 DKFZp761K1824 3' TAAGAGAATGTTGTGTATTT 1726 AA C
AAATACA TGACATTC CTTA
||||| ||||| |||
TTTATGT GTTGTAAAG GAAT
_ A

GAM255 FLJ14624 3' TAAGGAAATATTTATTTGTATT 2913 C_ C
TT AAAATACAAATGA ATT CCTTA
||||||| ||| |||
TTTTATGTTTATT TAA GGAAT
TA A

GAM255 GRO3 3' TAAGGGAATGTATGTA 2636 AATG
TACA ACATTCCCTTA
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|--------|-----------|--------------------------------|--------|------|
| | | ATGT TGTAAGGGAAT | | |
| | | A__ | | |
| GAM255 | KIAA0907 | 3' AAGAAAGTTTTATTTGTATTTT 1596 | C | CC |
| | A | TAAATACAAATGA ATT CTT | | |
| | | | | |
| | | ATTTTATGTTTATT TGA GAA | | |
| | | T AA | | |
| GAM255 | MGC14289 | 3' AAGGATACTGTCATTTGCATTT 2382 | A | TTC_ |
| | T | AAAATCAAATGACA CCTT | | |
| | | | | |
| | | TTTTA GTTTACTGT GGAA | | |
| | | C CATA | | |
| GAM255 | NLP_1 | 3' AAGGGAATTTTTTTTGTA 1395 | T | C |
| | | TACAAA GA ATTCCCTT | | |
| | | | | |
| | | ATGTTT TT TAAGGGAA | | |
| | | T _ | | |
| GAM255 | PARVA | 3' GAGTGCTCCTTTTGTATTTTA 1802 | T_ _ | |
| | | TAAAATACAAA GA CATTC | | |
| | | | | |
| | | ATTTTATGTTT CT GTGAG | | |
| | | TC C | | |
| GAM255 | PRO2176 | 3' AAGGGCTGCATTGTATTTTA 1833 | A | A TT |
| | | TAAAATACAA TG CA CCCTT | | |
| | | | | |
| | | ATTTTATGTT AC GT GGGAA | | |
| | | _ _ C_ | | |
| GAM255 | TIMM22 | 3' AAGGTTGGTTTATTTGTATTTT 3104 | _ | ATTC |
| | A | TAAAATACAAATGA C CCTT | | |
| | | | | |
| | | ATTTTATGTTTATT G GGAA | | |
| | | T GTT_ | | |
| GAM255 | LOC143914 | 5' GAGGGAGTCATTTTATT 3061 | C | AT |
| | | AATA AAATGAC TCCCTT | | |
| | | | | |
| | | TTAT TTTACTG AGGGAG | | |
| | | - - | | |
| GAM255 | LOC154862 | 3' AAGGGTGAAATTTGTGTTTTA 3193 | GA | TT |
| | | TAAAATACAAAT CA CCCTT | | |
| | | | | |
| | | ATTTTGTGTTTA GT GGGAA | | |
| | | AA _ | | |
| GAM255 | LOC158314 | 3' AAGGGAATGTTTAAGCCATTT 3386 | ACAAAT | |
| | | AAAT GACATTCCCTT | | |
| | | | | |
| | | TTTA TTGTAAGGGAA | | |
| | | CCGAAT | | |
| GAM255 | LOC221405 | 3' AAGGGACTATTTGTATT 3623 | ACAT | |
| | | AATACAAATG TCCCTT | | |
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|--------|-----------|----|-----------------------------|---------|----------|
| | | | TTATGTTTAT AGGGAA | | |
| | | | C___ | | |
| GAM256 | YES1 | 3' | ATGATGAATTTATCAGCGT 1209 | A | CCG |
| | | | AC CTGATAAA CATTAT | | |
| | | | | | |
| | | | TG GACTATTT GTAGTA | | |
| | | | C AA_ | | |
| GAM256 | ACTR3 | 3' | GATGGGATTTATCAGTGT 1238 | | _ G |
| | | | ACACTGATAAA CC CATT | | |
| | | | | | |
| | | | TGTGACTATTT GG GTAG | | |
| | | | A _ | | |
| GAM256 | GENX-3414 | 3' | CAGATAATGCTTCCAGTG 1073 | | ATAAACC |
| | | | CACTG GCATTATCTG | | |
| | | | | | |
| | | | GTGAC CGTAATAGAC | | |
| | | | CTT___ | | |
| GAM256 | HT007 | 3' | ACAGATAATAAATATCCAGTGT 1832 | | _ AACCGC |
| | | | ACACTG ATA ATTATCTGT | | |
| | | | | | |
| | | | TGTGAC TAT TAATAGACA | | |
| | | | C AAA___ | | |
| GAM256 | SPRY4 | 3' | ACAGACAATGCAGGGGCAG 2175 | ATAAA _ | A |
| | | | CTG CC GCATT TCTGT | | |
| | | | | | |
| | | | GAC GG CGTAA AGACA | | |
| | | | GG___ A C | | |
| GAM257 | POF1B | 3' | GAACCATGCTGCTACCCAA 2114 | | _ TG A |
| | | | TTGGGTAGT GT ATG TTC | | |
| | | | | | |
| | | | AACCCATCG CG TAC AAG | | |
| | | | T _ C | | |
| GAM257 | RODH-4 | 5' | CATGGGTAGCTACCCAATAAG 1050 | | GT_ G |
| | | | TTTATTGGGTAGT T ATG | | |
| | | | | | |
| | | | GAATAACCCATCG G TAC | | |
| | | | ATG G | | |
| GAM257 | SFRS12 | 3' | GAATCATTGGGACTACCCA 2472 | | G TG |
| | | | TGGGTAGT T ATGATTC | | |
| | | | | | |
| | | | ACCCATCA G TACTAAG | | |
| | | | G GT | | |
| GAM257 | TCBAP0758 | 3' | GAATCCCCAACACCCAATAAA 2181 | | AGT AT |
| | | | TTTATTGGGT GTTG GATTC | | |
| | | | | | |
| | | | AAATAACCCA CAAC CTAAG | | |
| | | | _ CC | | |
| GAM258 | HYOU1 | 3' | CTCTGTTTTCCCCATTCA 2537 | T TA | |
| | | | C AGTG GAAAACAGAG | | |
| | | | | | |

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|--------|----------|----|---------------------------|----------|--|
| | | | A TTAC CTTTTGTCTC | | |
| | | | C CC | | |
| GAM258 | ITGB1 | 3' | ATCTTGTTTCACACTAGT 910 | A A G | |
| | | | ACTAGTGT GAAA CA AGAT | | |
| | | | | | |
| | | | TGATCACA CTTT GT TCTA | | |
| | | | — — — | | |
| GAM258 | MAGEA4 | 3' | TATCTCTGTTTCCTTTTACA 922 | — | |
| | | | TGTAGAA AACAGAGATA | | |
| | | | | | |
| | | | ACATTTT TTGTCTCTAT | | |
| | | | CCT | | |
| GAM258 | PTTG1IP | 3' | ATCTCTGTTTCTAGATTAGT 1100 | _ G A | |
| | | | ACTAG T TAGAAA CAGAGAT | | |
| | | | | | |
| | | | TGATT A ATCTTT GTCTCTA | | |
| | | | T G _ | | |
| GAM258 | RAB27A | 3' | ATCTCTGTCTTTACCAGC 1129 | _ AA | |
| | | | GT GTAGA ACAGAGAT | | |
| | | | | | |
| | | | CG CATT TGTCTCTA | | |
| | | | AC C_ | | |
| GAM258 | SALL2 | 5' | ATCTCTGCTTCACAGT 2671 | A T AAAA | |
| | | | ACT GTG AG CAGAGAT | | |
| | | | | | |
| | | | TGA CAC TC GTCTCTA | | |
| | | | _ T _ | | |
| GAM258 | SFRS7 | 3' | TGCTTTCTACATTAGTTA 2529 | A | |
| | | | TAAGTAGTGTAGAAA CA | | |
| | | | | | |
| | | | ATTGATTACATCTTT GT | | |
| | | | C | | |
| GAM258 | SLC19A2 | 3' | GTCTTTCTACATAGTTA 2836 | G AAACA | |
| | | | TAAGTA TGTAGA GAGAT | | |
| | | | | | |
| | | | ATTGAT ACATCT TTCTG | | |
| | | | — — — | | |
| GAM258 | C20orf97 | 3' | ATCTCTGTCCTCTTGATTA 1946 | GT AA | |
| | | | TAGT AGA ACAGAGAT | | |
| | | | | | |
| | | | ATTA TCT TGTCTCTA | | |
| | | | GT CC | | |
| GAM258 | CYB5-M | 3' | TCTGTTTTTCTACCCTAG 2150 | T _ | |
| | | | CTAG GTAGAAA ACAGA | | |
| | | | | | |
| | | | GATC CATCTTT TGTCT | | |
| | | | C TT | | |
| GAM258 | CYB5-M | 3' | TCTGTTTTTCTACCCTAG 3658 | T _ | |
| | | | CTAG GTAGAAA ACAGA | | |
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| | | | GATC CATCTTT TGTCT | | |
| | | | C TT | | |
| GAM258 | FAM8A1 | 3' | TATCCCTGGGTTACACTA 1675 | AAAA | A |
| | | | TAGTGTAG CAG GATA | | |
| | | | | | |
| | | | ATCACATT GTC CTAT | | |
| | | | GG__ C | | |
| GAM258 | FLJ10853 | 5' | TCTGCCTACACTATTTA 1804 | C | AAAA |
| | | | TAA TAGTGTAG CAGA | | |
| | | | | | |
| | | | ATT ATCACATC GTCT | | |
| | | | T C__ | | |
| GAM258 | FLJ14327 | 3' | ATCTCTGTCTACAAACTAG 2111 | __ | AAA |
| | | | CTAGT GTAGA CAGAGAT | | |
| | | | | | |
| | | | GATCA CATCT GTCTCTA | | |
| | | | AAA __ | | |
| GAM258 | FLJ14681 | 5' | TATCTCTGCCTTCCAGGCAT 2285 | A__ | AA |
| | | | GTGT GAA CAGAGATA | | |
| | | | | | |
| | | | TACG CTT GTCTCTAT | | |
| | | | GAC CC | | |
| GAM258 | HNRPA3 | 3' | ATCTCTATTCTACATTTA 1245 | T | AAC |
| | | | C AGTGTAGAA AGAGAT | | |
| | | | | | |
| | | | A TTACATCTT TCTCTA | | |
| | | | T A__ | | |
| GAM258 | KIAA0426 | 3' | TATCTCTGTTTTGGGAGACAGG 1532 | A | GTAG__ |
| | T | | ACT GT AAAACAGAGATA | | |
| | | | | | |
| | | | TGG CA TTTTGTCTCTAT | | |
| | | | A GAGGG | | |
| GAM258 | KIAA0594 | 3' | TATCTCTAAGTTATACTAATTA 2707 | C | AAAAC |
| | | | TAA TAGTGTAG AGAGATA | | |
| | | | | | |
| | | | ATT ATCATATT TCTCTAT | | |
| | | | A GAA__ | | |
| GAM258 | KIAA0635 | 5' | ATCTCAATTTTACACTAG 1513 | | AAACA |
| | | | CTAGTGTAGA GAGAT | | |
| | | | | | |
| | | | GATCACATTT CTCTA | | |
| | | | AA__ | | |
| GAM258 | PDZD2 | 5' | ATCCCTGTTTTCGGGGACTA 3181 | GTA__ | A |
| | | | TAGT GAAAACAG GAT | | |
| | | | | | |
| | | | ATCA CTTTTGTC CTA | | |
| | | | GGGG C | | |
| GAM258 | PP1628 | 5' | ATCTCTGTTCCCATCCCCAGT 2145 | A__ | TA AA |
| | | | ACT GTG GA ACAGAGAT | | |
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| | | | TGA TAC CT TGTCTCTA | | |
| | | | CCCC CC _ | | |
| GAM258 | TIP120A | 3' | TATCCCTGTTGCGCACACTA | 1829 | AGAA A |
| | | | TAGTGT AACAG GATA | | |
| | | | | | |
| | | | ATCACA TTGTC CTAT | | |
| | | | CGCG C | | |
| GAM258 | LOC220988 | 3' | ATCTCTATTCTACATTTA | 3501 | T AAC |
| | | | C AGTGTAGAA AGAGAT | | |
| | | | | | |
| | | | A TTACATCTT TCTCTA | | |
| | | | T A_ | | |
| GAM258 | LOC221337 | 5' | ATCTCTGTTCTCTAAGCAC | 3555 | _ A |
| | | | GTGT AGA AACAGAGAT | | |
| | | | | | |
| | | | CACG TCT TTGTCTCTA | | |
| | | | AA C | | |
| GAM258 | LOC257017 | 5' | TATCTCTGTTTTGGCAT | 3737 | AG |
| | | | GTGT AAAACAGAGATA | | |
| | | | | | |
| | | | TACG TTTTGTCTCTAT | | |
| | | | G_ | | |
| GAM258 | LOC90829 | 5' | TATCTCTGTTTTGGTACCAGT | 2680 | A AG |
| | | | ACT GTGT AAAACAGAGATA | | |
| | | | | | |
| | | | TGA CATG TTTTGTCTCTAT | | |
| | | | C G_ | | |
| GAM259 | KIAA0268 | 3' | ACAAAACAATGCTGAAGTTAAT | 2874 | T A T |
| | AT | | ATATTA CT CG CATTGTTTTGT | | |
| | | | | | |
| | | | TATAAT GA GT GTAACAAAACA | | |
| | | | T A C | | |
| GAM259 | KIAA1255 | 3' | ACAAAACAACCTCTGAGATGA | 2783 | A TCA |
| | | | TTATCT CG TTGTTTTGT | | |
| | | | | | |
| | | | AGTAGA GT AACAAAACA | | |
| | | | _ CTC | | |
| GAM259 | MGC5370 | 3' | CAAAACATCAGATAATAT | 2275 | ACGTCAT |
| | | | ATATTATCT TGTTTTG | | |
| | | | | | |
| | | | TATAATAGA ACAAAC | | |
| | | | CT_ | | |
| GAM259 | UK114 | 3' | ACAAAATGTTATATAGATAATA | 1255 | CG CAT |
| | T | | ATATTATCTA T TGTTTTGT | | |
| | | | | | |
| | | | TATAATAGAT A GTAAAACA | | |
| | | | AT TT_ | | |
| GAM260 | OSBPL8 | 3' | CTACATATGAGTATAATA | 1927 | CC |
| | | | TATTATACTCATG TAG | | |
| | | | | | |

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| | | ATAATATGAGTAT ATC | |
| | | AC | |
| GAM260 | LOC147463 3' | CTATTACTATTGCAGGAATATA 3109 | C A C_ |
| | A | TTATA TC TGC TAGTAATAG | |
| | | | |
| | | AATAT AG ACG ATCATTATC | |
| | | A G TT | |
| GAM260 | LOC151201 5' | ATTAGTAGCATGAGTATAA 3340 | C G |
| | | TTATACTCATGC TA TAAT | |
| | | | |
| | | AATATGAGTACG AT ATTA | |
| | | _ G | |
| GAM261 | JJAZ1 3' | AGCACTGTGGTTGAGTAACATC 1621 | _ TT_ |
| | | GATGTTAC CAATCG TGCT | |
| | | | |
| | | CTACAATG GTTGGT ACGA | |
| | | A GTC | |
| GAM261 | SIAT1 3' | AGGGGATTGGAAACATCGT 986 | A G |
| | | ACGATGTT CCAATC TTT | |
| | | | |
| | | TGCTACAA GGTTAG GGA | |
| | | A G | |
| GAM261 | ATP6V0A1 3' | AGGGGACACTGGTAACAT 1191 | ATC G |
| | | ATGTTACCA GTTT CT | |
| | | | |
| | | TACAATGGT CAGG GA | |
| | | CA_ G | |
| GAM261 | FLJ21313 3' | AGCGAATTGGTTACATCGTT 2038 | T ATC |
| | | AACGATGT ACCA GTTTGCT | |
| | | | |
| | | TTGCTACA TGGT TAAGCGA | |
| | | T _ | |
| GAM261 | FLJ23548 3' | AGCAAATTTGGCTCGATAATAT 2068 | _____ TC |
| | CG | CGATGTTA CCAA GTTTGCT | |
| | | | |
| | | GCTATAAT GGTT TAAACGA | |
| | | AGCTC _ | |
| GAM261 | LOC196510 3' | GCAAAAGGCAACATTGTT 3414 | A AATCG |
| | | AACGATGTT CC TTTGC | |
| | | | |
| | | TTGTTACAA GG AAACG | |
| | | C A_____ | |
| GAM261 | LOC200220 3' | GCAAAAGGCAACATTGTT 3443 | A AATCG |
| | | AACGATGTT CC TTTGC | |
| | | | |
| | | TTGTTACAA GG AAACG | |
| | | C A_____ | |
| GAM261 | LOC222234 3' | AGCAAGATGGGTAACATC 3645 | A GT |
| | | GATGTTACC ATC TTGCT | |
| | | | |

CTACAATGG TAG AACGA
G _
GAM262 CDKN1B 3' GACAAAATTTTCTCATTCTT 1082 TGT____ C
TTCAC TGTAAAAGAA AAA TTTGTC
||||| |||
CACTTTTCTT TTT AAACAG
T TACTCT A
GAM262 CSPG3 3' ACAAAGGTCTTCTTTTCCT 1107 T TGTA
AG GAAAAGAA CTTTGT
|| |||||
TC CTTTCTT GAAACA
_ CTG_
GAM262 ITSN1 3' ACAAAGTTTACATTTTCACT 981 AAAA
AGTG GAATGTAACTTTGT
||| |||||
TCAT TTTACATTTGAAACA
AC_
GAM262 MBNL 5' GACATGCAACAGTCTTTTCACT 1937 A AAACCTT
AGTGAAAAGA TGT TGTC
||||| |||
TCACTTTTCT ACA ACAG
G ACGT_
GAM262 MEFV 3' GACAAAGTTTTGCTCTTGTCAC 719 A ATGT
GTGA AAGA AAACCTTGTC
||| ||| |||||
CACT TTCT TTTGAAACAG
G CGT_
GAM262 NR3C1 3' GACAAAGTAATTCCTCTCACT 716 AAA GTAA
AGTGA GAAT ACTTTGTC
|||| ||| |||||
TCACT CTTA TGAAACAG
CTC A_
GAM262 TIF1 3' ACAAAGACATTCTTCCCACT 2564 AA AAA
AGTG AAGAATGT CTTTGT
||| ||||| |||||
TCAC TTCTTACA GAAACA
CC _
GAM262 BZW1 3' ACAAATGGGTATTCTTTTCAT 1516 AAAC
GTGAAAAGAATGT TTTGT
||||| |||
TACTTTTCTTATG AAACA
GGT_
GAM262 FLJ10998 3' GACAAAGTCTCGCTCTGTCAC 1811 AA A TAA
GTGA AGA TG ACTTTGTC
||| ||| |||||
CACT TCT GC TGAAACAG
G_ C TC_
GAM262 FLJ12409 3' GACAAAGTGATGTTTCTTCCC 2137 AA TG A_
AT GTG AAGAA TA ACTTTGTC
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|--------|-----------|-----|-----------------------------|-----------|----|
| | | | TAC TTCTT GT TGAAACAG | | |
| | | | CC TT AG | | |
| GAM262 | FLJ32356 | 3' | ACAAAGCTTGATGTTTTCACT 2492 | GAATG | A |
| | | | AGTGAAAA TAA CTTTGT | | |
| | | | | | |
| | | | TCACTTTT GTT GAAACA | | |
| | | | GTA__ C | | |
| GAM262 | GRP3 | 3' | GTTTACATCCTTCCCACT 1624 | AA | A |
| | | | AGTG AAG ATGTAAAC | | |
| | | | | | |
| | | | TCAC TTC TACATTTG | | |
| | | | CC C | | |
| GAM262 | KIAA0210 | 3' | GACACTGTTTACGTCCCTCCCA 1538 | AAA A_ | TT |
| | | CT | AGTG AG ATGTAAAC TGTC | | |
| | | | | | |
| | | | TCAC TC TGCATTTG ACAG | | |
| | | | CC_ CC TC | | |
| GAM262 | MGC2477 | 3' | GACAAAAGCAAGGCCCTTTTC 2054 | AAT AAAC_ | |
| | | ACT | AGTGAAAAG GT TTTGTC | | |
| | | | | | |
| | | | TCACTTTTC CG AAACAG | | |
| | | | CC_ GAACGA | | |
| GAM262 | MGC2742 | 5' | ACAAAAGGGTATTTCTTTTCTC 2039 | T T AA _ | |
| | | T | AG GAAAAGAA GTA CTTT GT | | |
| | | | | | |
| | | | TC CTTTCTT TAT GAAA CA | | |
| | | | T _ GG A | | |
| GAM262 | MRF2 | 3' | GTTCTCATTCTTTTCACT 3056 | TA | |
| | | | AGTGAAAAGAATG AAC | | |
| | | | | | |
| | | | TCACTTTCTTAC TTG | | |
| | | | TC | | |
| GAM262 | P2RXL1 | 3' | GAGGGCCACACTCTTTTCAC 1213 | A AAA | |
| | | | GTGAAAAGA TGT CTTT | | |
| | | | | | |
| | | | CACTTTTCT ACA GGAG | | |
| | | | C CCG | | |
| GAM262 | STK38L | 3' | GACAAAGTTTAACACCTTCACT 2844 | AAGAATG | |
| | | | AGTGAA TAACTTTGTC | | |
| | | | | | |
| | | | TCACCT ATTTGAAACAG | | |
| | | | CCACA_ | | |
| GAM262 | LOC151579 | 3' | ACAAATGGGTATTCTTTTCAT 2859 | AAAC | |
| | | | GTGAAAAGAATGT TTTGT | | |
| | | | | | |
| | | | TACTTTTCTTATG AAACA | | |
| | | | GGT_ | | |
| GAM262 | LOC51312 | 5' | GACAAAATTCATTTTTTTCA 1849 | TAAAC | |
| | | | TGAAAAGAATG TTTGTC | | |
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|--------|---------------|----|-------------------------|--------|----------|
| | | | ACTTTTTTTAC | AAACAG | |
| | | | TTA__ | | |
| GAM262 | LOC91574 | 3' | GACAAAGTTCTGTTTCTTCAC | 2751 | AA TGTA |
| | | | GTGA AGAA AACTTTGTC | | |
| | | | | | |
| | | | CACT TCTT TTGAAACAG | | |
| | | | __ TGTC | | |
| GAM263 | MAB21L2 | 5' | CACTACAAACAAACAAACC | 1301 | CA_ C |
| | | | GGTTTGTT TTGT GTG | | |
| | | | | | |
| | | | CCAAACAA AACA CAC | | |
| | | | ACA T | | |
| GAM263 | LOC220672 | 3' | CACGAATAAACAAACTTAA | 2565 | CATTG |
| | | | TTAGGTTTGTT TCGTG | | |
| | | | | | |
| | | | AATTCAAACAA AGCAC | | |
| | | | ATA__ | | |
| GAM264 | FLRT2 | 3' | AACTTCACTCTACACTATA | 1437 | ACAC A C |
| | | | TATAGTGTA GA TG AGTT | | |
| | | | | | |
| | | | ATATCACAT CT AC TCAA | | |
| | | | __ C T | | |
| GAM264 | KDEL2 | 3' | AACTTGCAATCCACTATA | 1335 | TAACAC _ |
| | | | TATAGTG GAATGCA GTT | | |
| | | | | | |
| | | | ATATCAC CTTACGT CAA | | |
| | | | __ T | | |
| GAM264 | SMT3H2 | 3' | AAACTGCAATTTGGTTCCAC | 1341 | T A _ |
| | | | GTG AAC CGAAT GCAGTTT | | |
| | | | | | |
| | | | CAC TTG GTTTA CGTCAAA | | |
| | | | C _ A | | |
| GAM264 | LOC158997 | 3' | AAACTGCAATTTGGTTCCAC | 3230 | T A _ |
| | | | GTG AAC CGAAT GCAGTTT | | |
| | | | | | |
| | | | CAC TTG GTTTA CGTCAAA | | |
| | | | C _ A | | |
| GAM265 | APOC4 | 3' | GTTCATACTTCTCCAATAAATA | 841 | C AT T |
| | AA | | TTTAT TATTG GG GTATGAAC | | |
| | | | | | |
| | | | AAATA ATAAC CT CATACTTG | | |
| | | | A CT T | | |
| GAM265 | DKFZP434P0721 | 3' | TTCATACATATATAGATA | 2664 | TGATG |
| | | | TATCTAT GTGTATGAA | | |
| | | | | | |
| | | | ATAGATA TACATACTT | | |
| | | | TA__ | | |
| GAM265 | FLJ14082 | 3' | TCATACACACAGATAAA | 2129 | ATTGATG |
| | | | TTTATCT GTGTATGA | | |
| | | | | | |

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|--------|-----------|----|-----------------------------|--------|
| | | | AAATAGA CACATACT | |
| | | | CA_____ | |
| GAM266 | LMO7 | 3' | AATAAACTTGCTGATGCATTT 1202 | TAAT T |
| | | | AAATGC G CAAGTTTATT | |
| | | | | |
| | | | TTTACG C GTTCAAATAA | |
| | | | TAGT_ | |
| GAM266 | LMO7 | 3' | AATAAACTTGCTGATGCATTT 1643 | TAAT T |
| | | | AAATGC G CAAGTTTATT | |
| | | | | |
| | | | TTTACG C GTTCAAATAA | |
| | | | TAGT_ | |
| GAM266 | CDV-1 | 3' | AATAAACTTGGTACGTATTT 1466 | TAA GT |
| | | | AAATGC T CAAGTTTATT | |
| | | | | |
| | | | TTTATG A GTTCAAATAA | |
| | | | C__TG | |
| GAM266 | KIAA1671 | 3' | TTTGACATCAGCATTTTA 2726 | A _ |
| | | | TAAAATGCT ATGT CAAG | |
| | | | | |
| | | | ATTTTACGA TACA GTTT | |
| | | | C C | |
| GAM266 | SEMA5A | 3' | AAACCTTTGAAATTAGCATT 1075 | G _ |
| | | | AATGCTAAT TCAA GTTT | |
| | | | | |
| | | | TTACGATTA AGTT CAAA | |
| | | | A TC | |
| GAM266 | LOC127133 | 3' | AATAAATGGGAGTTAGCATTTT 3004 | G AA |
| | A | | TAAAATGCTAAT TC GTTTATT | |
| | | | | |
| | | | ATTTTACGATTG AG TAAATAA | |
| | | | _ GG | |
| GAM266 | LOC143154 | 3' | AATTTGACATCACATTTTA 3052 | CTA |
| | | | TAAAATG ATGTCAAGTT | |
| | | | | |
| | | | ATTTTAC TACAGTTTAA | |
| | | | AC_ | |
| GAM266 | LOC219294 | 3' | AATTTGACATCACATTTTA 3587 | CTA |
| | | | TAAAATG ATGTCAAGTT | |
| | | | | |
| | | | ATTTTAC TACAGTTTAA | |
| | | | AC_ | |
| GAM267 | GARP | 3' | TGGAGTTTGAGACTATGGAA 1221 | _ TGGA |
| | | | TTCCGTAGTC CA TCCA | |
| | | | | |
| | | | AAGGTATCAG GT AGGT | |
| | | | A TTG_ | |
| GAM267 | FLJ30213 | 3' | GATCATGGACCACAGAA 2507 | C A G |
| | | | TTC GT GTCCATG ATC | |
| | | | | |

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|--------|--------------|----|---------------------------|--------|--|
| | | | AAG CA CAGGTAC TAG | | |
| | | | A C _ | | |
| GAM267 | LOC196510 | 3' | GGTCCATGAACTAGGAA 3415 | G C | |
| | | | TTCC TAGT CATGGATC | | |
| | | | | | |
| | | | AAGG ATCA GTACCTGG | | |
| | | | _ A | | |
| GAM267 | LOC200220 | 3' | GGTCCATGAACTAGGAA 3444 | G C | |
| | | | TTCC TAGT CATGGATC | | |
| | | | | | |
| | | | AAGG ATCA GTACCTGG | | |
| | | | _ A | | |
| GAM267 | LOC220930 | 3' | GGTCATAGACTATGGAA 3591 | C AT | |
| | | | TTCCGTAGTC ATGG CC | | |
| | | | | | |
| | | | AAGGTATCAG TACT GG | | |
| | | | A _ | | |
| GAM268 | ZNF161 | 3' | ACTAGCAGAACTCTT 1359 | TAGT T | |
| | | | AAGAGTTT TG CTAGT | | |
| | | | | | |
| | | | TTCTCAAG AC GATCA | | |
| | | | _ _ | | |
| GAM268 | DKFZP566D193 | 3' | ACTGAATAACTAAAATCTC 3353 | _ C | |
| | | | GAG TTTTAGTTGT TAGT | | |
| | | | | | |
| | | | CTC AAAATCAATA GTCA | | |
| | | | T A | | |
| GAM268 | LOC200574 | 3' | GCTGACTACTAAACTC 3450 | T T | |
| | | | GAGTTTTAGT GTC AGT | | |
| | | | | | |
| | | | CTCAAATCA CAG TCG | | |
| | | | T _ | | |
| GAM269 | RAD50 | 3' | TGTTGATAAATCCATCA 1240 | A T | |
| | | | TGA TGGATTTATCA CA | | |
| | | | | | |
| | | | ACT ACCTAAATAGT GT | | |
| | | | _ T | | |
| GAM269 | RAD50 | 3' | TGTTGATAAATCCATCA 2420 | A T | |
| | | | TGA TGGATTTATCA CA | | |
| | | | | | |
| | | | ACT ACCTAAATAGT GT | | |
| | | | _ T | | |
| GAM269 | SMURF1 | 3' | ATGATGTAAATCCACCCA 3564 | AA T | |
| | | | TG TGGATTTA CATCAT | | |
| | | | | | |
| | | | AC ACCTAAAT GTAGTA | | |
| | | | CC _ | | |
| GAM269 | TRIM9 | 3' | ATGAATGAAAAATCCATCCA 1611 | A A _ | |
| | | | TG ATGGATTT TCAT CAT | | |
| | | | | | |

AC TACCTAAA AGTA GTA
 C A A
 GAM269 FLJ13902 3' AACGATGATGATGAACACA 2076 GA
 TG TTTATCATCATCGTT
 || |||||
 AC AAGTAGTAGTAGCAA
 AC
 GAM269 KIAA0650 3' AAACGATGATGATGTTAACC 3427 ATT_
 GG TATCATCATCGTTT
 || |||||
 CC GTAGTAGTAGCAAA
 AATT
 GAM269 MGC16075 3' AAACGATGATGCAGGCTATTCA 2277 ATTTAT
 TGAATGG CATCATCGTTT
 ||||| |||||
 ACTTATC GTAGTAGCAAA
 GGAC__
 GAM270 PAIP2 3' ACTGAAAATAGAATTGG 1687 TATA
 CCA TTTATTTTCAGT
 ||| |||||
 GGT AGATAAAAGTCA
 TA__
 GAM270 PIN4 3' CTGAAAATATTGGGCATC 1282 A ATATATT
 GATG CC TATTTTCAG
 ||| || |||||
 CTAC GG ATAAAAGTC
 _ GTT____
 GAM271 HLA-G 3' TCCTTCCCAATCACCTT 900 AAT
 AAGGTGATTGG GGGA
 ||||| |||
 TTCCACTAACC TCCT
 CCT
 GAM271 HRH2 5' TTCATTCCCAACACCTTA 1984 ATT
 TAAGGTG GGAATGGG
 ||||| |||||
 ATTCCAC CCTTACTT
 AAC
 GAM271 KCNJ15 3' ATTTATTTAACCAATGACCTTA 916 G AATG
 TAAGGT ATTGG GGATAAAT
 ||||| ||||| |||||
 ATTCCA TAACC TTTATTTA
 G AA__
 GAM271 C1orf8 5' ATCTCAGTCTCAATCACC 1161 _ A
 GGTGATTG GA TGGGAT
 ||||| || |||||
 CCACTAAC CT ACTCTA
 T G
 GAM271 FLJ10738 3' ATCCCATCTGGGTCACTT 1798 _TG A
 AGGTGA T GA TGGGAT
 ||||| | || |||||

TTCACT G CT ACCCTA
 G GT _
 GAM271 FLJ23511 3' ATCCACAATCCAATTACC 2239 A _
 GGTGATTGGA TG GGAT
 ||||| || ||||
 CCATTAACCT AC CCTA
 A A
 GAM271 GAB3 3' ATTCAGGGTTTCCAATCACC 2377 ____ GG
 GGTGATTGGAA TG AT
 ||||| || ||
 CCACTAACCTT AC TA
 TGGG TT
 GAM271 ITPK1 3' CTCACCCCATCACCTTG 1484 T AA
 TAAGGTGAT GG TGGG
 ||||| || ||||
 GTTCCACTA CC ACTC
 _ CC
 GAM271 TRIP-Br2 3' TCCCCCCCCATCACCTTA 1539 T AAT
 TAAGGTGAT GG GGA
 ||||| || ||||
 ATTCCACTA CC CCCT
 C CC_
 GAM271 LOC152313 3' ATCCCCCTGATCCAATCACCT 3355 AT____
 AGGTGATTGGA GGGAT
 ||||| || ||||
 TCCACTAACCT CCCTA
 AGTCC
 GAM271 LOC256642 3' TTTAGGCCCAATACCTTA 3701 A AAT GA
 TAAGGTG TTGG GG TAAA
 ||||| || || ||||
 ATTCCAT AACC CC ATTT
 _ ____ GG
 GAM272 C22orf2 3' TTTTTTATTAAACGATGT 3655 A
 ACGTC TTTAATAAAAAA
 |||| |||||
 TGTAG AAATTATTTTTT
 C
 GAM272 LOC153277 3' ATACTTAATAAATGACGT 3369 A AAAAA
 ACGTCATTTA TA AGTAT
 ||||| || ||||
 TGCAGTAAAT AT TCATA
 A ____
 GAM273 SH3BP4 3' CAGTGTGCAATTAGTCATTGAC 1506 G A AG
 A TG CAAT ACTAATTG ATATTG
 || |||| ||||| |||||
 AC GTTA TGATTAAC TGTGAC
 A C G_
 GAM273 UFD1L 3' CAACATCTTGGCTTTTAGTTAC 2973 G A ____ TG A
 TGGCA TG CA TAACTAA T AGAT TTG
 || || ||||| | |||||

AC GT ATTGATT G TCTA AAC
 G C TTC GT C
 GAM273 FLJ20081 3' CAATACTCTCAATTATTAACCA 1736 CAA C _
 TGG TAA TAATTGAGA TATTG
 ||| ||| ||||| |||||
 ACC ATT ATTA ACTCT ATAAC
 A _ _ C
 GAM273 KIAA1635 3' GTCCA ACTATTTATTGCCA 2804 C A A
 TGGCAATAA TA TTG GAT
 ||||| || ||| |||
 ACCGTTATT AT AAC CTG
 T C _
 GAM273 PRO1257 5' CAATATCTCATAAGACTACTGC 1848 A ACTAAT
 GCA TA TGAGATATTG
 ||| || ||||| |||
 CGT AT ACTCTATAAC
 C CAGAAT
 GAM273 LOC153020 3' CTCAATCAGTATTGCCA 3177 A A
 TGGCAATA CT ATTGAG
 ||||| || |||||
 ACCGTTAT GA TAACTC
 _ C
 GAM274 BNC 3' TGTTTCTGTTTCATATC 851 T
 GATATGA AACAGGAATA
 ||||| ||||| |||
 CTATACT TTGTCTTTGT
 _
 GAM274 PROS1 5' TGTCCTTGTTATCACTTC 3407 TA A
 GA TGATAACAGG ATA
 || ||||| |||
 CT ACTATTGTTT TGT
 TC C
 GAM274 FLJ20147 3' ATGTTGTAATTGTCATATC 1738 CAGGA
 GATATGATAA ATAACAT
 ||||| |||||
 CTATACTGTT TGTTGTA
 AA _
 GAM274 KIAA0737 3' ATGTTATTCCCCATTATCA 1562 CA_
 TGATAA GGAATAACAT
 |||| ||||| |||
 ACTATT CCTTATTGTA
 ACC
 GAM275 CA4 3' AGGCATGATTA AAAATATGGAC 769 T TGAG
 GTCCATATTTTA TC GCCT
 ||||| || |||
 CAGGTATA AAAAT AG CGGA
 T TA _
 GAM275 LU 3' AGGCCCCAGAATAGCTCCTGGA 1227 TATT A
 C GTCCA TTATTCTG GGCCT
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|--------|-----------|----|-----------------------------|----------|--------|
| | | | CAGGT GATAAGAC CCGGA | | |
| | | | CCTC C | | |
| GAM275 | FNBP3 | 5' | AGGAGTTACAAAATATGGAC 3155 | ATTC | GG |
| | | | GTCCATATTTT TGA CCT | | |
| | | | | | |
| | | | CAGGTATAAAA ATT GGA | | |
| | | | C__ GA | | |
| GAM275 | SAP18 | 3' | AGCCCTTCTGTAAAATATG 1258 | TCT | C |
| | | | CATATTTTAT GAGG CT | | |
| | | | | | |
| | | | GTATAAAATG TTCC GA | | |
| | | | TC_ C | | |
| GAM275 | SCYA4 | 3' | CTTTAAAATAAAATGCAGAC 978 | CA | C |
| | | | GTC TATTTTATT TGAGG | | |
| | | | | | |
| | | | CAG GTAAAATAA ATTTC | | |
| | | | AC A | | |
| GAM275 | SLC6A14 | 3' | CGTGATAAATATATGGAC 1368 | _ | C |
| | | | GTCCATAT TTTATT TG | | |
| | | | | | |
| | | | CAGGTATA AAATAG GC | | |
| | | | T T | | |
| GAM275 | LOC158629 | 5' | CCCAGGAAAACATGGAT 3393 | A TA | A |
| | | | GTCCAT TTT TTCTG GG | | |
| | | | | | |
| | | | TAGGTA AAA AGGAC CC | | |
| | | | C _ _ | | |
| GAM275 | LOC163115 | 5' | AGGCCTCAGTTTATATTGAC 3243 | C | TTTATT |
| | | | GTC ATAT CTGAGGCCT | | |
| | | | | | |
| | | | CAG TATA GACTCCGGA | | |
| | | | T TTT__ | | |
| GAM275 | LOC200339 | 3' | TCTTAGAAGAAAACATAGACG 3476 | C A | A |
| | | | CGTC AT TTTT TTCTGAGG | | |
| | | | | | |
| | | | GCAG TA AAAA AAGATTCT | | |
| | | | A C G | | |
| GAM275 | LOC200953 | 5' | AGGCCTCAGAGGGCCCTAGGGA 3481 | ATATTTTA | |
| | | | C GTCC TTCTGAGGCCT | | |
| | | | | | |
| | | | CAGG GAGACTCCGGA | | |
| | | | GATCCCGG | | |
| GAM275 | LOC255527 | 5' | AGGCCACATAAAATACCAAC 3718 | CCA | TC A |
| | | | GT TATTTTAT TG GGCCT | | |
| | | | | | |
| | | | CA ATAAAATA AC CCGGA | | |
| | | | ACC C_ _ | | |
| GAM275 | LOC51334 | 3' | CCTCAGAATGATGAAAAATATG 1706 | C | _____ |
| | | | AATG CGT CATATT TTATTCTGAGG | | |
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|--------|----------|----|-----------------------------|----------|
| | | | GTA GTATAA AGTAAGACTCC | |
| | | | A AAAGT | |
| GAM275 | LOC92710 | 3' | AGGCCTCAAAACAATGAAA 2884 | C___ |
| | | | TTTTATT TGAGGCCT | |
| | | | | |
| | | | AAAGTAA ACTCCGGA | |
| | | | CAAA | |
| GAM276 | TSN | 3' | TACACTTGGGGAGATTTGCCA 1136 | GCAA C_ |
| | | | TGGCAAATCT TCA TGTA | |
| | | | | |
| | | | ACCGTTTAGA GGT ACAT | |
| | | | GG__ TC | |
| GAM276 | FLJ20039 | 3' | TACAGTGATAGCAACTTTCCA 1734 | C TC A |
| | | | TGG AAA TGC ATCACTGTA | |
| | | | | |
| | | | ACC TTT ACG TAGTGACAT | |
| | | | _ CA A | |
| GAM276 | KIAA1204 | 3' | ACAGGGCCAGCTTGCCATA 2849 | AT CAA A |
| | | | TATGGCAA CTG TC CTGT | |
| | | | | |
| | | | ATACCGTT GAC GG GACA | |
| | | | C_ C_ _ | |
| GAM276 | OR2C3 | 3' | TACAGTGAGGCGAGATTCACCA 3023 | CA _ AA |
| | T | | ATGG AATCT GC TCACTGTA | |
| | | | | |
| | | | TACC TTAGA CG AGTGACAT | |
| | | | AC G G_ | |
| GAM276 | QKI | 3' | TACCTTGATGCAAATTTGCCA 2722 | C A CT |
| | | | TGGCAAAT TGCA TCA GTA | |
| | | | | |
| | | | ACCGTTTA ACGT AGT CAT | |
| | | | A _ TC | |
| GAM276 | TIP120A | 3' | ACAGTAACAATTTGCCA 1828 | C CAATC |
| | | | TGGCAAAT TG ACTGT | |
| | | | | |
| | | | ACCGTTTA AC TGACA | |
| | | | _ AA__ | |
| GAM276 | LOC90750 | 3' | CAGTGGTCCAGACTTGCCA 2673 | A CA |
| | | | TGGCAA TCTG ATCACTG | |
| | | | | |
| | | | ACCGTT AGAC TGGTGAC | |
| | | | C C_ | |
| GAM276 | LOC92912 | 3' | ACAGTAATTTTTGCCATG 2898 | TCTGC C |
| | | | TATGGCAAA AAT ACTGT | |
| | | | | |
| | | | GTACCGTTT TTA TGACA | |
| | | | _____ A | |
| GAM277 | BACH2 | 3' | ATTTCTGGTGAGTCAGTCCAC 1962 | AA TA_ |
| | | | GT ATT TCACCAGAAAT | |
| | | | | |

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|--------|----------|----|----------------------------|---------|-----|
| | | | CA TGA AGTGGTCTTTA | | |
| | | | CC CTG | | |
| GAM277 | DUSP11 | 3' | TTTGCTGATAAATTTGCAGT 1039 | C | C |
| | | | AC GTAAATTTATCA CAGA | | |
| | | | | | |
| | | | TG CGTTTAAATAGT GTTT | | |
| | | | A C | | |
| GAM277 | EPS8 | 3' | ATTTCTGGTAATAAGAAGC 1114 | AAA | C |
| | | | GT TTTAT ACCAGAAAT | | |
| | | | | | |
| | | | CG GAATA TGGTCTTTA | | |
| | | | AA_ A | | |
| GAM277 | TK1 | 3' | TCTGGTGATGGTTTCCACAGG 1005 | _ AAAT_ | |
| | | | CC GT TTATCACCAGA | | |
| | | | | | |
| | | | GG CA GGTAGTGGTCT | | |
| | | | A CCTTT | | |
| GAM277 | TRPC6 | 3' | ATTTCTGGGAGCATTTAC 1134 | TTA A | |
| | | | GTAAAT TC CCAGAAAT | | |
| | | | | | |
| | | | CATTTA AG GGTCTTTA | | |
| | | | CG_ _ | | |
| GAM277 | KIAA0924 | 3' | TTCTGAATAAATTTACAGT 1577 | C | CAC |
| | | | AC GTAAATTTAT CAGAA | | |
| | | | | | |
| | | | TG CATTTAAATA GTCTT | | |
| | | | A A_ | | |
| GAM277 | KIAA1946 | 3' | ATTTTGGGTGATGAATTTACA 3247 | C | _ |
| | | GT | AC GTAAATTTATCACC AGAAAT | | |
| | | | | | |
| | | | TG CATTTAAGTAGTGG TTTTTA | | |
| | | | A G | | |
| GAM277 | OSBPL3 | 3' | ATTTCTGGTGAATTAC 1635 | ATTTA | |
| | | | GTAA TCACCAGAAAT | | |
| | | | | | |
| | | | CATT AGTGGTCTTTA | | |
| | | | A_ | | |
| GAM277 | PSKH1 | 3' | TCTGGTGGAGGGCCATGG 2810 | AAA | A |
| | | | CCGT TTT TCACCAGA | | |
| | | | | | |
| | | | GGTA GGA GGTGGTCT | | |
| | | | CCG _ | | |
| GAM277 | URB | 5' | ATTTCTGGGACTGAATCCAGG 3162 | GTAA | _ A |
| | | | CC ATTTA TC CCAGAAAT | | |
| | | | | | |
| | | | GG TAAGT AG GGTCTTTA | | |
| | | | ACC_ C _ | | |
| GAM278 | PLS3 | 3' | TAGAAGAAAAATGTACCTTA 1174 | _ | CA |
| | | | TAAGGTAC TTTTCT TA | | |
| | | | | | |

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|--------|--------------|-----------------------------|-----------|
| | | ATTCCATG AAAAAGA AT | |
| | | T AG | |
| GAM278 | LOC121227 3' | TTATGCAAAAAAGTATCTTA 2989 | CT |
| | | TAAGGTACTTTTT CATAA | |
| | | | |
| | | ATTCTATGAAAAA GTATT | |
| | | AC | |
| GAM278 | LOC145786 3' | ATTATGAGAAAGGCC 3277 | ACT |
| | | GGT TTTTCTCATAAT | |
| | | | |
| | | CCG GAAAGAGTATTA | |
| | | — | |
| GAM278 | LOC149650 3' | TTAAGAGAAAAAAGTACC 3136 | _ A |
| | | GGTACTTTTT CTC TAA | |
| | | | |
| | | CCATGAAAAA GAG ATT | |
| | | A A | |
| GAM278 | LOC222223 3' | TTATCACATGGTCAAGTACCTT 3641 | TT TCATA |
| | G | TAAGGTACTT TC ATAA | |
| | | | |
| | | GTTCCATGAA GG TATT | |
| | | CT TACAC | |
| GAM279 | OGT 5' | GGTAATTTATAGAACAAA 1042 | C C |
| | | TTTGTTCCTAT AA TACC | |
| | | | |
| | | AAACAAGATA TT ATGG | |
| | | T A | |
| GAM279 | TNFRSF10B 3' | TTTATAGGTAGTTGTTTACA 1065 | TCTAT |
| | | TGT CAACTACCTATAAA | |
| | | | |
| | | ACA GTTGATGGATATTT | |
| | | TTT_ | |
| GAM279 | BA108L7.2 3' | TTATAGACACTAGTAGGACAAA 2180 | CAACTAC |
| | | TTTGTTCCTAT CTATAA | |
| | | | |
| | | AAACAGGATG GATATT | |
| | | ATCACA_ | |
| GAM279 | FLJ12598 5' | TTTACAGGTACCATGCAGAGAA 2086 | AT_ AC_ A |
| | CAAA | TTTGTTCCT CA TACCT TAAA | |
| | | | |
| | | AAACAAGA GT ATGGA ATTT | |
| | | GAC ACC C | |
| GAM279 | FLJ23071 3' | GGTAATTTATAGAACAAA 2144 | C C |
| | | TTTGTTCCTAT AA TACC | |
| | | | |
| | | AAACAAGATA TT ATGG | |
| | | T A | |
| GAM279 | LOC91266 5' | TATAGGTTAGGAACAAA 2720 | ATCAACT |
| | | TTTGTTCCT ACCTATA | |
| | | | |

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|--------|-----------|----|------------------------|---------|----------|------|
| | | | AAACAAGG | TGGATAT | | |
| | | | AT_____ | | | |
| GAM280 | CDH11 | 5' | CCGCTGACTTGTGAATGGGA | 2339 | A TG | AAAA |
| | | | TCC ATT TAA TCAGCGG | | | |
| | | | | | | |
| | | | AGG TAA GTT AGTCGCC | | | |
| | | | G GT C____ | | | |
| GAM280 | IGF1 | 3' | CCTGATGCAAATTGGA | 761 | AAAAA | C |
| | | | TCCAATTTGT ATCAG G | | | |
| | | | | | | |
| | | | AGGTAAACG TAGTC C | | | |
| | | | _____ A | | | |
| GAM280 | FKBP9 | 3' | CCGCTAATTTTTGTATTTTTGG | 3632 | TTTGTA | C |
| | | | CCAA AAAAAT AGCGG | | | |
| | | | | | | |
| | | | GGTT TTTTTCGCGC | | | |
| | | | TTTATG A | | | |
| GAM280 | FLJ23045 | 3' | TGCTTGACAAATTGGAT | 2082 | AAAAAATC | |
| | | | ATCCAATTTGT AGCG | | | |
| | | | | | | |
| | | | TAGGTAAACA TCGT | | | |
| | | | GT_____ | | | |
| GAM280 | FLJ30567 | 3' | CCTGATTTGAATTGG | 2510 | GTAAA | C |
| | | | CCAATTT AAATCAG G | | | |
| | | | | | | |
| | | | GGTTAAG TTTAGTC C | | | |
| | | | _____ A | | | |
| GAM280 | FLJ30678 | 5' | CCGCTGATTCCTTTCGTAA | 2490 | TA | __ |
| | | | TTG AAA AATCAGCGG | | | |
| | | | | | | |
| | | | AAT TTT TTAGTCGCC | | | |
| | | | GC CC | | | |
| GAM280 | KIAA1676 | 3' | CCACTGTGGGAACCAAATTGGA | 3590 | TAAAAAAT | C |
| | T | | ATCCAATTTG CAG GG | | | |
| | | | | | | |
| | | | TAGGTAAAC GTC CC | | | |
| | | | CAAGGGT_ A | | | |
| GAM280 | KLF3 | 3' | CCGCCAATTTTTTACAAAT | 1693 | CA | |
| | | | ATTTGTAAAAAAT GCGG | | | |
| | | | | | | |
| | | | TAAACATTTTTTA CGCC | | | |
| | | | AC | | | |
| GAM280 | LOC146952 | 5' | CCACTGATTTTTTTTTCTGGA | 3286 | ATTTGT | C |
| | | | TCCA AAAAATCAG GG | | | |
| | | | | | | |
| | | | AGGT TTTTTTAGTC CC | | | |
| | | | CTTTT_ A | | | |
| GAM280 | LOC81569 | 3' | CCACTGATTTTTCATTGG | 2616 | TTGTA | C |
| | | | CCAAT AAAAATCAG GG | | | |
| | | | | | | |

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|--------|----------|----|------------------------|------------|------------|-------|--|
| | | | GGTTA | TTTTTAGTC | CC | | |
| | | | C_____ | A | | | |
| GAM280 | LOC83690 | 3' | CCACTGATTTTTTTTTTAAAT | 2204 | T_ | C | |
| | | | ATTTG | AAAAAATCAG | GG | | |
| | | | | | | | |
| | | | TAAAT | TTTTTTAGTC | CC | | |
| | | | TT | A | | | |
| GAM281 | ASPH | 3' | AAAAAAGCATGGAAAATG | 1896 | C | A | |
| | | | CATTT | CCATGT | TTTTT | | |
| | | | | | | | |
| | | | GTAAA | GGTACG | AAAAA | | |
| | | | A | A | | | |
| GAM281 | ASPH | 3' | AAAAAAGCATGGAAAATG | 2252 | C | A | |
| | | | CATTT | CCATGT | TTTTT | | |
| | | | | | | | |
| | | | GTAAA | GGTACG | AAAAA | | |
| | | | A | A | | | |
| GAM281 | CABC1 | 3' | ATAAAAATGCTCATGGGAAGTG | 1908 | | TATTT | |
| | A | | TCATTTCCCATG | TTTTTAT | | | |
| | | | | | | | |
| | | | AGTGAAGGGTAC | AAAAATA | | | |
| | | | TCGT_ | | | | |
| GAM281 | SLC6A12 | 5' | ATAAAAAGGGACATGAAAATGA | 987 | CC | A | |
| | | | TCATTT | CATGT | TTTTTTTTAT | | |
| | | | | | | | |
| | | | AGTAAA | GTACA | GGGAAAAATA | | |
| | | | A_ | _ | | | |
| GAM281 | CSAD | 3' | AAAATACATAGGAAAAGA | 1654 | A | C | |
| | | | TC | TTTCC | ATGTATTTT | | |
| | | | | | | | |
| | | | AG | AAAGG | TACATAAAA | | |
| | | | A | A | | | |
| GAM281 | DICER1 | 3' | AAAAAAAATTAAGGGGAAA | 2151 | ATGT | | |
| | | | TTTCCC | ATTTTTTTT | | | |
| | | | | | | | |
| | | | AAAGGG | TAAAAAAA | | | |
| | | | GAAT | | | | |
| GAM281 | KIAA1025 | 3' | AAAAAAAGGGGAAATGG | 2675 | ATGTA | | |
| | | | TCATTTCCC | TTTTTTTTT | | | |
| | | | | | | | |
| | | | GGTAAAGGG | GAAAAAAA | | | |
| | | | _____ | | | | |
| GAM281 | KLF12 | 3' | AAAAAAAATACATGGGAA | 1372 | | | |
| | | | TTCCCATGTATTTTTTTT | | | | |
| | | | | | | | |
| | | | AAGGGTACATAAAAAAAA | | | | |
| GAM281 | NFAT5 | 3' | AAAAAGTGTCAAAGGAAATGA | 2451 | CA | _ | |
| | | | TCATTTCC | TG | TATTTTTT | | |
| | | | | | | | |

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|--------|-----------|----|------------------------------|-----------|
| | | | AGTAAAGG AC GTGAAAAA | |
| | | | AA T | |
| GAM281 | LOC170261 | 3' | ATAAAAAAGGTACAAAAAGTGA 3256 | CCCA |
| | | | TCATTT TGTATTTTTTTTAT | |
| | | | | |
| | | | AGTGAA ACATGGAAAAAATA | |
| | | | AA__ | |
| GAM281 | LOC222602 | 3' | ATAAAAAACAAAAATGGAAAT 3583 | CATGTAT |
| | | | GA TCATTTC TTTTTTAT | |
| | | | | |
| | | | AGTAAAGG AAAAAAATA | |
| | | | TAAAAAC | |
| GAM281 | LOC257051 | 3' | ATAAAAAAGGTACAAAAAGTGA 3703 | CCCA |
| | | | TCATTT TGTATTTTTTTTAT | |
| | | | | |
| | | | AGTGAA ACATGGAAAAAATA | |
| | | | AA__ | |
| GAM282 | FGF7 | 3' | TATAAGAACCCAGTTCCA 886 | C C |
| | | | TGGAATTGGG TC TTATA | |
| | | | | |
| | | | ACCTTGACCC AG AATAT | |
| | | | A A | |
| GAM282 | MTNR1B | 3' | TGGGGCAGAAGAGCCCAACTCC 1262 | A C ATA_ |
| | | | GGA TTGGGCTC TT CCA | |
| | | | | |
| | | | CCT AACCCGAG AG GGT | |
| | | | C A ACGG | |
| GAM282 | SEPX1 | 3' | TGTGAGGCCCAATTCCA 1681 | TC |
| | | | TGGAATTGGGC CTTATA | |
| | | | | |
| | | | ACCTTAACCCG GAGTGT | |
| | | | — | |
| GAM282 | PPFIA4 | 3' | TGGCATAAGCTGAATCCCA 2883 | A G CCT A |
| | | | TGG ATT GGCT TAT CCA | |
| | | | | |
| | | | ACC TAA TCGA ATA GGT | |
| | | | C G _ C | |
| GAM282 | LOC145231 | 3' | CTTGACACGAGACTAGTCCCAA 3274 | _ C_ ATAC |
| | | | TTCCA TGGAATTGGG CT CTT CAAG | |
| | | | | |
| | | | ACCTTAACCC GA GAG GTTC | |
| | | | T TCA CACA | |
| GAM283 | CAV3 | 3' | AATGCCCAGTACTGCCATTTGA 2329 | ATCC |
| | | | TCAAATG TGTTGGGCATT | |
| | | | | |
| | | | AGTTTAC ATGACCCGTAA | |
| | | | CGTC | |
| GAM283 | HOXC4 | 5' | AATGACGTCAGAATCATTTG 1509 | C T GG |
| | | | CAAATGAT CTG TG CATT | |
| | | | | |

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|--------|---------------|----|-----------------------------|----------|
| | | | GTTTACTA GAC GC GTAA | |
| | | | A T A_ | |
| GAM283 | MYCL1 | 3' | CTTTTACACGACCATTTGATA 1203 | A C T_ |
| | | | TATCAAATG TC TGT GGG | |
| | | | | |
| | | | ATAGTTTAC AG ACA TTC | |
| | | | C C TT | |
| GAM283 | FLJ20666 | 5' | AACAGGAGAATCACTTGATG 1762 | A ____ |
| | | | TATCAA TGA TCCTGTT | |
| | | | | |
| | | | GTAGTT ACT AGGACAA | |
| | | | C AAG | |
| GAM283 | KIAA1001 | 3' | AATGCCTGGCAAATTACCTGA 1599 | AA CC TG |
| | | | TCA TGAT TGT GGCATT | |
| | | | | |
| | | | AGT ATTA ACG CCGTAA | |
| | | | CC A_ GT | |
| GAM283 | PGRMC2 | 3' | AACAGAAAGATCATTTGA 1286 | ____ |
| | | | TCAAATGATC CTGTT | |
| | | | | |
| | | | AGTTTACTAG GACAA | |
| | | | AAA | |
| GAM283 | LOC152286 | 3' | AATGCAGGGAGACATTTGATA 3354 | A_ GTTGG |
| | | | TATCAAATG TCCT GCATT | |
| | | | | |
| | | | ATAGTTTAC AGGG CGTAA | |
| | | | AG A____ | |
| GAM283 | LOC158549 | 3' | AATGCTTAGGAATCATTTTATA 3392 | C _ TTG |
| | | | TAT AAATGAT CCTG GGCATT | |
| | | | | |
| | | | ATA TTTACTA GGAT TCGTAA | |
| | | | T A ____ | |
| GAM284 | DKFZp761G0313 | 3' | AAGATAAGCTATTATTAA 2731 | TA |
| | | | TTAATAAT CTTATCTT | |
| | | | | |
| | | | AATTATTA GAATAGAA | |
| | | | TC | |
| GAM285 | NRCAM | 3' | CAGCATGCCAACAGTAATA 1170 | A T__ |
| | | | TATTATT TTGGC CTG | |
| | | | | |
| | | | ATAATGA AACCG GAC | |
| | | | C TAC | |
| GAM285 | C22orf23 | 3' | TGATTAAGTGGCCAATAA 2259 | C__ |
| | | | TTATTGGCT TGATCA | |
| | | | | |
| | | | AATAACCGG ATTAGT | |
| | | | TCA | |
| GAM285 | SARM | 3' | GACAGCGCCAATAACAATA 1609 | A T A |
| | | | TATT TTATTGGC CTG TC | |
| | | | | |

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|--------|-----------|----|-----------------------------|--------|--------|
| | | | ATAA AATAACCG GAC AG | | |
| | | | C C _ | | |
| GAM285 | LOC219918 | 3' | CGGTGGTTAAACAACAATAAT 3529 | A | GCTC |
| | A | | TATTATT TTG TGATCACCG | | |
| | | | | | |
| | | | ATAATAA AAC ATTGGTGGC | | |
| | | | C AAA_ | | |
| GAM286 | FABP5 | 3' | TTTATCATAAACATTTTACA 828 | T | C |
| | | | TGTAAAAT TTTGT GATAAA | | |
| | | | | | |
| | | | ACATTTTA AAATA CTATTT | | |
| | | | C _ | | |
| GAM286 | ZHX1 | 3' | TTGACCAAAAATTTTACA 1367 | _ | |
| | | | TGTAAAATTTTGT TCGA | | |
| | | | | | |
| | | | ACATTTTAAAAAC AGTT | | |
| | | | C | | |
| GAM286 | KIAA0981 | 3' | TTTGTGGCAAAAATTTTCA 2599 | T | G |
| | | | TG AAAATTTTGTGTC ATAAA | | |
| | | | | | |
| | | | AC TTTTAAAAACGG TGTTT | | |
| | | | _ _ | | |
| GAM286 | KIAA1615 | 3' | ATTTTATAAGAAAATTTTAC 2829 | | GTCG |
| | | | GTAAAATTTT ATAAAAAT | | |
| | | | | | |
| | | | CATTTTAAAAG TATTTTA | | |
| | | | AA_ | | |
| GAM286 | SGP28 | 3' | TTTTTATCTGCATAAATTTTAC 1271 | T | C |
| | A | | TGTAAAATTT TGT GATAAAAA | | |
| | | | | | |
| | | | ACATTTTAAA ACG CTATTTT | | |
| | | | T T | | |
| GAM286 | LOC201973 | 3' | TTTTTTGAGAAAAATTTTGCA 3456 | G | T |
| | | | TGTAAAATTTT TCGA AAA | | |
| | | | | | |
| | | | ACGTTTAAAAA AGTT TTT | | |
| | | | G T | | |
| GAM287 | LOC146237 | 3' | CGCACGCTCAGCAGGCATGA 3283 | A | CACCGA |
| | | | TCGT CC GAGCGTGTG | | |
| | | | | | |
| | | | AGTA GG CTCGCACGC | | |
| | | | C ACGA_ | | |
| GAM287 | LOC255146 | 5' | CACACGCTCCCGCCAGCGA 3679 | ACCCAC | A |
| | | | TCGT CG GAGCGTGTG | | |
| | | | | | |
| | | | AGCG GC CTCGCACAC | | |
| | | | ACC_ C | | |
| GAM288 | ATBF1 | 5' | CGTACTGGGTGCAATGAA 1336 | A | |
| | | | TTCGTTGTAT TAGTACG | | |
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|--------|-----------|----|-----------------------------|----------|--|
| | | | AAGTAACGTG GTCATGC | | |
| | | | G | | |
| GAM289 | FMR2 | 3' | GCATCAGTGTTTTTCAACTCC 889 | ATT _ C | |
| | | | GGAG AAAAATA TGA GC | | |
| | | | | | |
| | | | CCTC TTTTGT ACT CG | | |
| | | | AAC G A | | |
| GAM289 | SF1 | 3' | GCGTGGGGTTTTTTAATCTCTG 1138 | TATG_ | |
| | | | CGGAGATTAAAAA ACGC | | |
| | | | | | |
| | | | GTCTCTAATTTT TGCG | | |
| | | | TGGGG | | |
| GAM289 | BAL | 3' | GCAGTTGTTCTTTAATCTCC 2201 | AAT TG _ | |
| | | | GGAGATTAAA A AC GC | | |
| | | | | | |
| | | | CCTCTAATTT T TG CG | | |
| | | | CT_ GT A | | |
| GAM289 | BTN3A1 | 3' | ATATTTTAAATCCCGTTA 1355 | A | |
| | | | TAACGG GATTAAAAATAT | | |
| | | | | | |
| | | | ATTGCC CTAATTTTATA | | |
| | | | — | | |
| GAM289 | PDE4DIP | 3' | CGTCATATTCTCAACAGTTTCT 1512 | AAA__ | |
| | | | GGAGATT AATATGACG | | |
| | | | | | |
| | | | TCTTTGA TTATACTGC | | |
| | | | CAACTC | | |
| GAM289 | LOC200251 | 3' | GCGAGTGCCTGTAATCTCCG 3447 | AAAA GA | |
| | | | CGGAGATTA TAT CGC | | |
| | | | | | |
| | | | GCCTCTAAT GTG GCG | | |
| | | | GTCC A_ | | |
| GAM290 | CDK10 | 3' | CGGAAGCAGCCCTACAACAAC 2354 | TTGCGA | |
| | | | GTTGTTGT CTGCTTCCG | | |
| | | | | | |
| | | | CAACAACA GACGAAGGC | | |
| | | | TCCC__ | | |
| GAM290 | COL1A1 | 3' | CGGAAACAGACAAGCAAC 704 | CGA C | |
| | | | GTTGTTTG CTG TTCCG | | |
| | | | | | |
| | | | CAACGAAC GAC AAGGC | | |
| | | | A__ A | | |
| GAM290 | ESPN | 3' | AAGCTGCTGACGCAAACAACAA 2210 | ACT__ | |
| | C | | GTTGTTGTTTGCG GCTT | | |
| | | | | | |
| | | | CAACAACAAACGC CGAA | | |
| | | | AGTCGT | | |
| GAM290 | GRIA1 | 3' | CAGTGCCAAAAACAACAAC 779 | __ G | |
| | | | GTTGTTGTTT GC ACTG | | |
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CAACAACAAA CG TGAC
AAC _
GAM290 PLAG1 3' AAGCAGAAAACAAAAACAAC 942 G CGA_
GTTGTT TTTG CTGCTT
||||| ||| |||||
CAACAA AAAC GACGAA
_ AAAA
GAM290 SORCS1 3' TCAGAAGTTCCAAACAGCAAC 2345 C CT C
GTTGTTGTTTGA GCTTC GA
||||||| || ||||| ||
CAACGACAAAC CT TGAAG CT
_ _ A
GAM290 BM046 3' AAGCAAGACAACAAC 1830 GCGAC
GTTGTTGTTT TGCTT
||||||| |||||
CAACAACAGA ACGAA

GAM290 KLF12 3' AAGCAGTTGAGTAACAGCAAC 1373 TG_
GTTGTTGTT CGACTGCTT
||||||| |||||
CAACGACAA GTTGACGAA
TGA
GAM290 PSMA6 5' CGGAAGCAGTCGCTGCAAC 2880 TT
GTTGT GCGACTGCTTCCG
||||| |||||
CAACG CGCTGACGAAGGC
T_
GAM290 LOC157292 5' CAGCTCAAAAACAACAAC 3377 GC _
GTTGTTGTTT GA CTG
||||||| || |||
CAACAACAAA CT GAC
AA C
GAM291 CELSR3 3' TCCCCAGTGGTGGGTG 825 T T A
CACCCAT CA CTGG GA
||||| || ||||| ||
GTGGGTG GT GACC CT
_ _ C
GAM291 CMAR 5' CTCCACTTGGAAATGGGTACCAC 1195 AC ATC_
A TGTG ACCCATTC TGGAG
||||| ||||| |||||
ACAC TGGGTAAG ACCTC
CA GTTC
GAM291 FCER2 3' TCTCCAGATGAGAGTACAC 881 _ ACCCA
GTG AC TTCATCTGGAGA
||| || |||||
CAC TG GAGTAGACCTCT
A A____
GAM291 FCER2 3' TCTCCAGATGAGAGTACAC 882 _ ACCCA
GTG AC TTCATCTGGAGA
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| | | | CAC TG | GAGTAGACCTCT | | |
| | | | A A | _____ | | |
| GAM291 | FCER2 | 3' | TCTCCAGATGAGAGTACAC | 883 | _ | ACCCA |
| | | | GTG AC | TTCATCTGGAGA | | |
| | | | | | | |
| | | | CAC TG | GAGTAGACCTCT | | |
| | | | A A | _____ | | |
| GAM291 | MEN1 | 3' | CTCCAGAGTGGGTGTCCA | 3601 | T | TCA |
| | | | TG GACACCCAT | TCTGGAG | | |
| | | | | | | |
| | | | AC CTGTGGGTG | AGACCTC | | |
| | | | — | — | | |
| GAM291 | NCSTN | 3' | TTCTCCAGGCCCTCAGATGGCA | 2979 | ACAC | CA_____ |
| | CA | | GTG CCATT | TCTGGAGAA | | |
| | | | | | | |
| | | | CAC GGTAG | GGACCTCTT | | |
| | | | — | ACTCCC | | |
| GAM291 | RBM10 | 3' | TTCTCCACATGTTGGGTGTCCA | 1235 | T | TT C |
| | | | TG GACACCCA | CAT TGGAGAA | | |
| | | | | | | |
| | | | AC CTGTGGGT | GTA ACCTCTT | | |
| | | | — | T_ C | | |
| GAM291 | TNFSF8 | 3' | GGATGAATGGATGTCCCA | 812 | T | C |
| | | | TG GACA CCATTCATCT | | | |
| | | | | | | |
| | | | AC CTGT GGTAAGTAGG | | | |
| | | | C A | | | |
| GAM291 | YES1 | 3' | TCCTTATGGGGATGGGTGCCAC | 1210 | A | ATCT__ |
| | A | | TGTG CACCCATTC | GGA | | |
| | | | | | | |
| | | | ACAC GTGGGTAGG | CCT | | |
| | | | C | GGTATT | | |
| GAM291 | ZNF256 | 5' | TTCTCCACAGCGGGTGTGACA | 1247 | | ATTCATC |
| | | | TGTGACACCC | TGGAGAA | | |
| | | | | | | |
| | | | ACACTGTGGG | ACCTCTT | | |
| | | | CGAC | _____ | | |
| GAM291 | BAT8 | 3' | TCCCCAGCATGGATGGCCACA | 1325 | ACAC | _ A |
| | | | TGTG CCATTCAT | CTGG GA | | |
| | | | | | | |
| | | | ACAC GGTAGGTA | GACC CT | | |
| | | | C_____ | C C | | |
| GAM291 | CPLX1 | 3' | TCTCCGGATGGAATCACA | 1318 | | CACCCA |
| | | | TGTGA | TTCATCTGGAGA | | |
| | | | | | | |
| | | | ACACT | AGGTAGGCCTCT | | |
| | | | A | _____ | | |
| GAM291 | DKFZP566K0524 | 3' | TTCCAGTGAAACAGATGTTACA | 2855 | | CCCA_ T |
| | | | TGTGACA | TTCA CTGGAG | | |
| | | | | | | |

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|--------|-----------|----|-----------------------------------|------|----------|
| | | | ACATTGT AAGT GACCTT | | |
| | | | AGACA _ | | |
| GAM291 | FLJ12891 | 3' | TCTCCAGGGCCACAAC TGTGACA TCTGGAGA | 2117 | CCCATTCA |
| | A | | | | |
| | | | ACACTGT GGACCTCT | | |
| | | | CAACACCG | | |
| GAM291 | GR6 | 3' | CCTGAATGAATGGGTGTCAC | 1396 | _ T |
| | | | GTGACACCCATTCAT C GG | | |
| | | | | | |
| | | | CACTGTGGGTAAGTA G CC | | |
| | | | A T | | |
| GAM291 | KIAA0455 | 3' | CAGATGAATAGTATCACA | 2947 | C CC |
| | | | TGTGA AC ATTCATCTG | | |
| | | | | | |
| | | | ACACT TG TAAGTAGAC | | |
| | | | A A_ | | |
| GAM291 | KIAA0513 | 3' | TTCCCTGCAATGGGTGCACA | 1536 | A _ TCT |
| | | | TGTG CACCCATT CA GGAG | | |
| | | | | | |
| | | | ACAC GTGGGTAA GT CCTT | | |
| | | | _ C C__ | | |
| GAM291 | KIAA1655 | 5' | CTCTGAGAAGAGTGTGACA | 2753 | CCA A T |
| | | | TGTGACAC TTC TC GGAG | | |
| | | | | | |
| | | | ACACTGTG AAG AG TCTC | | |
| | | | AG_ _ _ | | |
| GAM291 | SCAND2 | 3' | TTCCCCAGCCAGATGGGGTGCAC | 2338 | A CAT A |
| | A | | TGTGAC CCCATT CTGG GAA | | |
| | | | | | |
| | | | ACACTG GGGTAG GACC CTT | | |
| | | | _ ACC C | | |
| GAM291 | WDR5B | 3' | TCTCCACGTCCAGGTGTACACA | 1878 | _ CATT C |
| | | | TGTG ACACC AT TGGAGA | | |
| | | | | | |
| | | | ACAC TGTGG TG ACCTCT | | |
| | | | A ACC_ C | | |
| GAM291 | LOC146330 | 5' | TCTCCAAGAAGGGTGTCA | 3088 | A ATC |
| | | | TGACACCC TTC TGGAGA | | |
| | | | | | |
| | | | ACTGTGGG AAG ACCTCT | | |
| | | | _ A_ | | |
| GAM291 | LOC148181 | 5' | CTCCAGACCCAGATGGTGTCTC | 3117 | T C CA_ |
| | A | | TG GACACC ATT TCTGGAG | | |
| | | | | | |
| | | | AC CTGTGG TAG AGACCTC | | |
| | | | T _ ACCC | | |
| GAM291 | LOC150271 | 5' | TCTCCAGACTGGTGACACA | 3326 | A CATTCA |
| | | | TGTG CACC TCTGGAGA | | |
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| | | ACAC GTGG AGACCTCT | |
| | | A TC_____ | |
| GAM291 | LOC150605 5' | TCTCCGGTGGAACCAAGTGTAC 3331 | CCA_ T |
| | A | TGTGACAC TTCA CTGGAGA | |
| | | | |
| | | ACACTGTG AGGT GGCCTCT | |
| | | ACCA _ | |
| GAM291 | LOC153277 3' | AGATAAATGTGTGTCACA 3368 | C C |
| | | TGTGACAC CATT ATCT | |
| | | | |
| | | ACACTGTG GTAA TAGA | |
| | | T A | |
| GAM291 | LOC154990 5' | CTCCAGACCCAGATGGTGTCTC 3196 | T C CA__ |
| | A | TG GACACC ATT TCTGGAG | |
| | | | |
| | | AC CTGTGG TAG AGACCTC | |
| | | T _ ACCC | |
| GAM291 | LOC158014 5' | TTCTCCAGATAAGAAAATCACA 3209 | CACCCA C |
| | | TGTGA TT ATCTGGAGAA | |
| | | | |
| | | ACACT AA TAGACCTCTT | |
| | | AAAAG_ _ | |
| GAM291 | LOC158056 5' | TCTCCAGGCCCCAGGTGCCAGC 3210 | GA_ CATTCA |
| | A | TGT CACC TCTGGAGA | |
| | | | |
| | | ACG GTGG GGACCTCT | |
| | | ACC ACCC_ | |
| GAM291 | LOC202908 3' | CTCCAGACCCAGATGGTGTCTC 3462 | T C CA__ |
| | A | TG GACACC ATT TCTGGAG | |
| | | | |
| | | AC CTGTGG TAG AGACCTC | |
| | | T _ ACCC | |
| GAM291 | LOC220143 5' | CTCCCGAGATGGTGTACACA 3610 | CAT A T |
| | | TGTGACACC TC TC GGAG | |
| | | | |
| | | ACACTGTGG AG AG CCTC | |
| | | T_ _ C | |
| GAM291 | LOC220143 5' | CTCCCGAGATGGTGTACACA 3611 | CAT A T |
| | | TGTGACACC TC TC GGAG | |
| | | | |
| | | ACACTGTGG AG AG CCTC | |
| | | T_ _ C | |
| GAM291 | LOC222057 3' | CTCCAGACCCAGATGGTGTCTC 3576 | T C CA__ |
| | A | TG GACACC ATT TCTGGAG | |
| | | | |
| | | AC CTGTGG TAG AGACCTC | |
| | | T _ ACCC | |
| GAM291 | LOC255096 3' | CTCATGGATGAGTACCACA 3744 | AC C CTG |
| | | TGTG AC CATTCA GAG | |
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| | | | ACAC TG GTAGGTA CTC | | |
| | | | CA A ____ | | |
| GAM291 | LOC255975 5' | | CTCCAGACCCAGATGGTGTCTC 3686 | T | C CA__ |
| | A | | TG GACACC ATT TCTGGAG | | |
| | | | | | |
| | | | AC CTGTGG TAG AGACCTC | | |
| | | | T _ ACCC | | |
| GAM291 | LOC256878 3' | | CTCCAGACCCAGATGGTGTCTC 3720 | T | C CA__ |
| | A | | TG GACACC ATT TCTGGAG | | |
| | | | | | |
| | | | AC CTGTGG TAG AGACCTC | | |
| | | | T _ ACCC | | |
| GAM291 | LOC51333 3' | | TTCTCCAGGCTCAGGTGCCA 1705 | A | CATTCA |
| | | | TG CACC TCTGGAGAA | | |
| | | | | | |
| | | | AC GTGG GGACCTCTT | | |
| | | | C ACTC__ | | |
| GAM291 | LOC89919 3' | | TCAGAACAGATGGATGTCACA 2580 | C | CA_ |
| | | | TGTGACA CCATT TCTGG | | |
| | | | | | |
| | | | ACACTGT GGTAG AGACT | | |
| | | | A ACA | | |
| GAM292 | IL2RA 3' | | TCCACCCTATATGTAGTATAAA 739 | _ | CA CAA |
| | GA | | TCTTT TAC ACA AGGGTGGA | | |
| | | | | | |
| | | | AGAAA ATG TGT TCCCACCT | | |
| | | | T A_ ATA | | |
| GAM292 | INPP5D 3' | | CCATCGTGCTGGTAGAAGA 3263 | A | AAAG |
| | | | TCTTTTACCA CAC GGTGG | | |
| | | | | | |
| | | | AGAAGATGGT GTG CTACC | | |
| | | | C ____ | | |
| GAM292 | PLXNA1 3' | | TCCACCCTTGCCCTCAGCAAGA 2941 | | ACCAACACA |
| | GA | | TCTTTT AAGGGTGGA | | |
| | | | | | |
| | | | AGAGAA TTCCCACCT | | |
| | | | C GACTCCCG | | |
| GAM292 | PRKCN 3' | | TCTTTAAGTCGTGTTTGTA AAA 1253 | C | AAAGGGT |
| | GA | | TCTTTTAC AACAC GGA | | |
| | | | | | |
| | | | AGAAAATG TTGTG TCT | | |
| | | | T CTGAATT | | |
| GAM292 | BHMT 3' | | CCACTTTTCTACCAGTAAAAGA 849 | | CAACACA |
| | | | TCTTTTAC AAGGGTGG | | |
| | | | | | |
| | | | AGAAAATG TTTTCACC | | |
| | | | ACCATC_ | | |
| GAM292 | DKFZP434B044 3' | | CCACCCCTTTAAGGAGTTGGTA 2211 | AC__ | _ |
| | AAA | | TTTTACCAAC AAAGGG TGG | | |
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| | | AAAATGGTTG TTTCCC ACC | |
| | | AGGAA C | |
| GAM292 | FLJ10458 3' | CCCCGTGTTGGTAAGAGA 1777 | AAA |
| | | TCTTTTACCAACAC GGG | |
| | | | |
| | | AGAGAATGGTTGTG CCC | |
| | | C__ | |
| GAM292 | FLJ20272 3' | CACCTGCTGGTAAAAGA 1744 | ACACAAA |
| | | TCTTTTACCA GGGTG | |
| | | | |
| | | AGAAAATGGT TCCAC | |
| | | CG_____ | |
| GAM292 | FLJ23598 3' | TCCACCCTGGGTAATAAAAGA 3665 | CCAAC AA |
| | | TCTTTTA AC AGGGTGGA | |
| | | | |
| | | AGAAAAT TG TCCCACCT | |
| | | AA__ GG | |
| GAM292 | KIAA1755 3' | CCACCCTTCATACTGGCCAGAG 2595 | TA ACACA |
| | | CTTT CCA AAGGGTGG | |
| | | | |
| | | GAGA GGT TTCCCACC | |
| | | CC CATA C | |
| GAM292 | MGC21621 3' | CCCTAGGCTGGTTGGTAAAAGA 2508 | A A__ |
| | | TCTTTTACCAAC CA AGGG | |
| | | | |
| | | AGAAAATGGTTG GT TCCC | |
| | | _ CGGA | |
| GAM292 | MGC3077 3' | TCCTTGCTCTGGTAAAAGA 2048 | ACACA |
| | | TCTTTTACCA AAGGG | |
| | | | |
| | | AGAAAATGGT TTCCT | |
| | | CTCG_ | |
| GAM292 | MGC4707 3' | CCCTCATGTCTGGTAAAA 2055 | _ CAA |
| | | TTTTACCA ACA AGGG | |
| | | | |
| | | AAAATGGT TGT TCCC | |
| | | C AC_ | |
| GAM292 | MGC5149 3' | TCCTCATTGGTAAAAGA 2940 | CACAA |
| | | TCTTTTACCAA AGGG | |
| | | | |
| | | AGAAAATGGTT TCCT | |
| | | AC__ | |
| GAM292 | RAB3IL1 3' | CAGGCTTTGTTGGTAAAA 1448 | CA GG |
| | | TTTTACCAACA AAG TG | |
| | | | |
| | | AAAATGGTTGT TTC AC | |
| | | _ GG | |
| GAM292 | LOC119369 5' | TCCACCCTATTTCTGGAAAAA 3026 | A ACACAA |
| | | TTTT CCA AGGGTGGA | |
| | | | |

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|--------|--------------|---------------------------|--------|---------|
| | | AAAA GGT TCCCACCT | | |
| | | A CTTTA_ | | |
| GAM292 | LOC150035 5' | TTGTAGTACTGGTAAAAGA 3321 | — | — |
| | | TCTTTTACCA AC ACAA | | |
| | | | | |
| | | AGAAAATGGT TG TGTT | | |
| | | CA A | | |
| GAM292 | LOC219649 5' | TCCACCCTTTGTGCTTTGGT 3586 | — | |
| | | ACCAA CACAAAGGGTGGA | | |
| | | | | |
| | | TGGTT GTGTTTCCACCT | | |
| | | TC | | |
| GAM292 | LOC221688 5' | TCCAACCACATTGGTAAAA 3617 | CACAAA | G |
| | | TTTTACCAA GG TGGA | | |
| | | | | |
| | | AAAATGGTT CC ACCT | | |
| | | ACA__ A | | |
| GAM293 | RLBP1 5' | CAGGTACCAGGTAGCCCCA 729 | A | CGACA G |
| | | TG GGCTACCT TAC TG | | |
| | | | | |
| | | AC CCGATGGA ATG AC | | |
| | | C CC__ G | | |
| GAM293 | MGC23280 3' | GCTGGTATCGAGGTGCCCA 2493 | A T | CA GT |
| | | TG GGC ACCTCGA TAC GT | | |
| | | | | |
| | | AC CCG TGGAGCT ATG CG | | |
| | | C _ _ GT | | |
| GAM293 | LOC113523 3' | TATGCCGAAATAGCTTCA 2966 | CC | A |
| | | TGAGGCTA TCG CATA | | |
| | | | | |
| | | ACTTCGAT AGC GTAT | | |
| | | AA C | | |
| GAM293 | LOC150157 3' | CACACGTATGCCATGGCC 3325 | CCTCGA | |
| | | GGCTA CACACGTGTG | | |
| | | | | |
| | | CCGGT GTATGCACAC | | |
| | | ACC__ | | |
| GAM293 | LOC196890 3' | CACACGTATGCCATGGCC 3468 | CCTCGA | |
| | | GGCTA CACACGTGTG | | |
| | | | | |
| | | CCGGT GTATGCACAC | | |
| | | ACC__ | | |
| GAM294 | ARHGAP6 3' | TGTATTCTGTAACAGATTA 807 | CA | |
| | | TAA TGTTACAGAATATA | | |
| | | | | |
| | | ATT ACAATGTCTTATGT | | |
| | | AG | | |
| GAM294 | ARHGAP6 3' | TGTATTCTGTAACAGATTA 1450 | CA | |
| | | TAA TGTTACAGAATATA | | |
| | | | | |

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|--------|-----------|----|-----------------------------|-------|-------|
| | | | ATT ACAATGTCTTATGT | | |
| | | | AG | | |
| GAM294 | ATP11B | 3' | TAATTTGAATCTGAACATGTTA 3158 | A | ATA |
| | | | TAACATGTT CAGA TAAATTA | | |
| | | | | | |
| | | | ATTGTACAA GTCT GTTTAAT | | |
| | | | _ AA_ | | |
| GAM294 | BNC | 3' | TAATTCTTGTTCTGTAACATG 850 | TA | |
| | | | CATGTTACAGAATA AATTA | | |
| | | | | | |
| | | | GTACAATGTCTTGT TTAAT | | |
| | | | TC | | |
| GAM294 | CREBL2 | 3' | TAATTTATATTCTTTCCATGT 817 | TTAC | |
| | | | ACATG AGAATATAAATTA | | |
| | | | | | |
| | | | TGTAC TCTTATATTTAAT | | |
| | | | CTT_ | | |
| GAM294 | GCNT1 | 3' | TAATTTATATTCTGCTCTAATA 830 | ___ | |
| | | | TGTTA CAGAATATAAATTA | | |
| | | | | | |
| | | | ATAAT GTCTTATATTTAAT | | |
| | | | CTC | | |
| GAM294 | MBNL | 3' | TATACTGTATAACATGTTA 1938 | ___ | A |
| | | | TAACATGT TACAG ATA | | |
| | | | | | |
| | | | ATTGTACA ATGTC TAT | | |
| | | | AT A | | |
| GAM294 | AFAP | 3' | TAATTTATATCTGTACATATTA 1952 | C T A | |
| | | | TAA ATGT ACAGA TATAAATTA | | |
| | | | | | |
| | | | ATT TACA TGTCT ATATTTAAT | | |
| | | | A _ _ | | |
| GAM294 | LOC148195 | 3' | TAATTTATCTGTTAACATGTT 3299 | _ | ATA |
| | | | AACATGTTA CAGA TAAATTA | | |
| | | | | | |
| | | | TTGTACAAT GTCT ATTTAAT | | |
| | | | T ___ | | |
| GAM295 | ATP6V1A1 | 3' | GAGGTTTCTCAGAATATCT 847 | CGCT | |
| | | | AGATATTCTGAG AACCTT | | |
| | | | | | |
| | | | TCTATAAGACTC TTGGAG | | |
| | | | T___ | | |
| GAM295 | DAP | 3' | AGGTTAGGAGAAAACCTCA 2954 | ATA | GAGCG |
| | | | TGAG TTCT CTAACCT | | |
| | | | | | |
| | | | ACTC AAGA GATTGGA | | |
| | | | CAA G___ | | |
| GAM295 | LIFR | 3' | AAGTATAGTGACTCAGAATCCT 919 | AT | _ AC |
| | CA | | TGAG ATTCTGAG CGCTA CTT | | |
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|--------|--------------|----|-----------------------------|-----|-----------|
| | | | ACTC TAAGACTC GTGAT GAA | | |
| | | | C_ A AT | | |
| GAM295 | RECK | 3' | AGCTTTCAGAATATGTCA 1941 | G | C |
| | | | TGA ATATTCTGAG GCT | | |
| | | | | | |
| | | | ACT TATAAGACTT CGA | | |
| | | | G T | | |
| GAM295 | SLC13A3 | 3' | AAGGCCAGGGTAAAATGTCTCA 2570 | | CTGA G AA |
| | | | TGAGATATT GC CT CCTT | | |
| | | | | | |
| | | | ACTCTGTAA TG GA GGAA | | |
| | | | AA_ G CC | | |
| GAM295 | TEM8 | 3' | GGGGCCAGAATATCTCA 2236 | A | G |
| | | | TGAGATATTCTG GC CT | | |
| | | | | | |
| | | | ACTCTATAAGAC CG GG | | |
| | | | _ G | | |
| GAM295 | DKFZp5471224 | 3' | GTTAGCAAGGATATCCA 1903 | A | GAGC |
| | | | TG GATATTCT GCTAAC | | |
| | | | | | |
| | | | AC CTATAGGA CGATTG | | |
| | | | _ A_ | | |
| GAM295 | OLFM3 | 3' | AGCATCATCCTCAAATATCTCA 3232 | C | C_ |
| | | | TGAGATATT TGAG GCT | | |
| | | | | | |
| | | | ACTCTATAA ACTC CGA | | |
| | | | _ C TACTA | | |
| GAM295 | TSARG1 | 3' | AGATGTTTCAGAATATCTCA 2470 | | _ |
| | | | TGAGATATTCTGAGCG CT | | |
| | | | | | |
| | | | ACTCTATAAGACTTGT GA | | |
| | | | A | | |
| GAM295 | LOC114987 | 3' | AGGCCAAAAATATCTCA 2517 | C_ | A G |
| | | | TGAGATATT TG GC CT | | |
| | | | | | |
| | | | ACTCTATAA AC CG GA | | |
| | | | AA _ _ | | |
| GAM295 | LOC152445 | 5' | AGGCTCCGCAAATATCTCA 3360 | | CT_ G |
| | | | TGAGATATT GAGC CT | | |
| | | | | | |
| | | | ACTCTATAA CTCG GA | | |
| | | | ACGC _ | | |
| GAM296 | FLJ20139 | 5' | ACCATATCAATCCATATA 1737 | CAA | |
| | | | TGTA ATTGATATGGT | | |
| | | | | | |
| | | | ATAT TAACTATACCA | | |
| | | | ACC | | |
| GAM296 | LOC91796 | 3' | ACGTTTTACAATCAATTTGTAC 2785 | A | GTCGT |
| | A | | TGTACAAATTGAT TG CGT | | |
| | | | | | |

ACATGTTTAACTA AC GCA
 _ ATTTT
 GAM297 CMAR 3' CCCCATCGCCTACTCCATG 1194 A AGA
 CATGGAGTAG TGAT GGGG
 ||||| ||| |||
 GTACCTCATC GCTA CCCC
 C ____
 GAM297 CRHR1 3' TTCCCCTCACTTAACCACCCCA 1105 A AGA TA
 T ATGG GT TGA GAGGGGAA
 ||| || ||| |||||
 TACC CA ATT CTCCCCTT
 C CCA CA
 GAM297 DTR 3' TTCCCCTCCACCAAACCCCA 874 A AGA ATA
 TGG GT TG GAGGGGAA
 ||| || ||| |||||
 ACC CA AC CTCCCCTT
 C A__ CAC
 GAM297 FGF5 3' TCCCCTCTCCACCCACCCCA 1117 A AGA AT
 TGG GT TG AGAGGGGA
 ||| || ||| |||||
 ACC CA AC TCTCCCCT
 C CCC C_
 GAM297 FGF5 3' TCCCCTCTCCACCCACCCCA 2315 A AGA AT
 TGG GT TG AGAGGGGA
 ||| || ||| |||||
 ACC CA AC TCTCCCCT
 C CCC C_
 GAM297 GAA 3' CCCCTCCATCTGTTCC 713 ATA
 GGAGTAGATG GAGGGG
 ||||| |||||
 CCTTGTCTAC CTCCCC

 GAM297 GNL1 3' TCCCCTCTGCCACCCCA 3550 A AGAT A
 TGG GT G TAGAGGGGA
 ||| || | |||||
 ACC CA C GTCTCCCCT
 C ____ C
 GAM297 GNL1 3' TCCCCTCTGCCACCCCA 3748 A AGAT A
 TGG GT G TAGAGGGGA
 ||| || | |||||
 ACC CA C GTCTCCCCT
 C ____ C
 GAM297 KCNA6 3' TCCCCTCCCTACCTCATG 915 GA ATGATA
 CATG GTAG GAGGGGA
 ||| ||| |||||
 GTAC CATC CTCCCCT
 TC C____
 GAM297 LDHB 5' CCCCATACACCATCTATTCCAT 918 ATAGA_
 ATGGAGTAGATG GGGG
 ||||| |||

TACCTTATCTAC CCCC
 CACATA
 GAM297 LTBP2 3' TTCCCCTCCACTCAGAAACCCC 740 A AGA TA_
 GG GT TGA GAGGGGAA
 || || || |||||
 CC CA ACT CTCCCCTT
 C AAG CAC
 GAM297 MARK1 5' CCCCTCCTCTTACTCCG 1856 AT TA
 TGGAGTAG GA GAGGGG
 ||||| || |||||
 GCCTCATT CT CTCCCC
 _ C_
 GAM297 PLAT 3' TTCCCCTTTCCCCACTCCCTG 2306 T AGAT TA
 CA GGAGT GA GAGGGGAA
 || |||| || |||||
 GT CCTCA CT TTCCCCTT
 C CCC_ _
 GAM297 PLAT 3' TTCCCCTTTCCCCACTCCCTG 788 T AGAT TA
 CA GGAGT GA GAGGGGAA
 || |||| || |||||
 GT CCTCA CT TTCCCCTT
 C CCC_ _
 GAM297 PTGIR 3' CCCCTCTACCAAGCCACTCCA 791 AGA_ A
 TGGAGT TG TAGAGGGG
 |||| || |||||
 ACCTCA AC ATCTCCCC
 CCGA C
 GAM297 PXN 3' CCCCTCTTTCACTTCAT 965 AGAT T
 ATGGAGT GA AGAGGGG
 |||| || |||||
 TACTTCA CT TCTCCCC
 _ T
 GAM297 RNH 5' TCCCCTCTACCAAGGGTTCC 2536 AGA A
 GGAGT TG TAGAGGGGA
 |||| || |||||
 CCTTG AC ATCTCCCCT
 GGA C
 GAM297 SCN4A 3' TCCCTTCTCATCTCCCCA 730 AGT TA
 TGG AGATGA GAGGGGA
 || |||| |||||
 ACC TCTACT CTTCCCT
 CC_ _
 GAM297 SH3GL1 3' TCCCTTCCCCACTCCATG 982 AGATGATA
 CATGGAGT GAGGGGA
 ||||| |||||
 GTACCTCA CTTCCCT
 CCC____
 GAM297 ZNF261 3' TTCCCCTCTATTGTTCCCC 1184 AGTA TG
 GG GA ATAGAGGGGAA
 || || |||||

CC TT TATCTCCCCTT
 CC__ GT
 GAM297 AKAP3 3' CCCCTCTATATCCTC 1300 TA A
 GAG GATG TAGAGGGG
 ||| ||| |||||
 CTC CTAT ATCTCCCC

— —
 GAM297 C3F 3' TCCCCTCTGATTCCCCCATG 1246 AGTA TGA
 CATGG GA TAGAGGGGA
 |||| || |||||
 GTACC CT GTCTCCCCT
 CC__ TA_

GAM297 CL24751 5' CTCCTTCATCTACTCC 2698 TAG
 GGAGTAGATGA AGGGG
 ||||| ||||
 CCTCATCTACT TCCTC

—
 GAM297 DIS3 3' TTCCCCTAAGTTCTATTCCAT 1597 TGATAG
 ATGGAGTAGA AGGGGAA
 ||||| |||||
 TACCTTATCT TCCCCTT
 TGAA__

GAM297 FLJ10700 3' CCTTCATCCACTCCATG 1794 A TAG
 CATGGAGT GATGA AGG
 ||||| |||| ||
 GTACCTCA CTA CTACT TCC
 C —

GAM297 FLJ13102 3' TCCCCTCTACCAATCCCTG 2104 T GTAGA A
 CA GGA TG TAGAGGGGA
 || ||| || |||||
 GT CCT AC ATCTCCCCT
 C A__ C

GAM297 FLJ32978 3' TCCCATTGGTCACCTTACTCCA 2488 A_ AGAG
 TGGAGTAG TGAT GGA
 ||||| |||| ||||
 ACCTCATT ACTG CCCT
 CC GTTA

GAM297 HSPB7 3' TTCCCCTCTACCAGCCTCCA 1499 TAGA A
 TGGAG TG TAGAGGGGAA
 |||| || |||||
 ACCTC AC ATCTCCCCTT
 CG__ C

GAM297 HTCD37 3' TTCCCCTTTTTCCTACCCCA 2796 A AT T
 TGG GTAG GA AGAGGGGAA
 ||| ||| || |||||
 ACC CATC CT TTTCCCCTT
 C __ T

GAM297 KIAA0280 3' TTCCCCTCCATCTGATCC 3537 G ATA
 GGA TAGATG GAGGGGAA
 ||| |||| |||||

CCT GTCTAC CTCCCCTT
 A ____
 GAM297 KIAA0450 5' TCCCCTCTACTACCCC 1511 A ATGA
 GG GTAG TAGAGGGGA
 || ||| |||||
 CC CATC ATCTCCCCT
 C ____
 GAM297 KIAA0731 3' CCCCTCCTCTCTCCATG 2767 T TGATA
 CATGGAG AGA GAGGGG
 ||||| || |||||
 GTACCTC TCT CTCCCC
 _ C ____
 GAM297 KIAA1462 3' TCCCCTCTGTGTCTCCATG 3523 TAGATG
 CATGGAG ATAGAGGGGA
 ||||| |||||
 GTACCTC TGTCTCCCCT
 TG ____
 GAM297 LIMK2 3' CCCCTTTCTACTCCA 1710 TGATA
 TGGAGTAGA GAGGGG
 ||||| |||||
 ACCTCATCT TTCCCC

 GAM297 LIMK2 3' CCCCTTTCTACTCCA 1225 TGATA
 TGGAGTAGA GAGGGG
 ||||| |||||
 ACCTCATCT TTCCCC

 GAM297 MGC2541 5' TCCCCTTCCTAGCTCCATG 2385 _ ATGATA
 CATGGAGT AG GAGGGGA
 ||||| || |||||
 GTACCTCG TC TTCCCCT
 A C ____
 GAM297 MGC3101 3' CCCTTCTTCTACTCCA 2046 TGAT
 TGGAGTAGA AGAGGGG
 ||||| |||||
 ACCTCATCT TCTTCCC

 GAM297 NCOA2 3' TTCCCCTCTCTCATTCCCCAT 1307 AGTA T
 ATGG GATGA AGAGGGGAA
 ||| ||| |||||
 TACC TTACT TCTCCCCTT
 CC__ C
 GAM297 RBM14 3' TTCCCCTCTACCCTGCCTCC 1289 _ ATGA
 GGAG TAG TAGAGGGGAA
 ||| ||| |||||
 CCTC GTC ATCTCCCCTT
 C CC__
 GAM297 SCYA5 3' TTCCCCTCACTATCCTACCCCA 979 A AT ____
 TGG GTAG GATA GAGGGGAA
 ||| ||| ||| |||||

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|--------|-----------|----|----------------------------|----------|
| | | | ACC CATC CTAT CTCCCCTT | |
| | | | C _ CA | |
| GAM297 | U5-116KD | 3' | CCCCTTGCTCCCACTCCATG 1095 | AGAT TA |
| | | | CATGGAGT GA GAGGGG | |
| | | | | |
| | | | GTACCTCA CT TTCCCC | |
| | | | CC_ CG | |
| GAM297 | WSB1 | 3' | TCCCCCACCTACTCCA 2429 | A ATAGA |
| | | | TGGAGTAG TG GGGGA | |
| | | | | |
| | | | ACCTCATC AC CCCCT | |
| | | | C _ | |
| GAM297 | LOC144501 | 3' | TCCCCTTCCTCCCTCCATG 3268 | TAGAT TA |
| | | | CATGGAG GA GAGGGGA | |
| | | | | |
| | | | GTACCTC CT TTCCCCT | |
| | | | C_ CC | |
| GAM297 | LOC146940 | 3' | TCCCTTCCCCACTCCATG 3101 | AGATGATA |
| | | | CATGGAGT GAGGGGA | |
| | | | | |
| | | | GTACCTCA CTTCCCT | |
| | | | CCC_ | |
| GAM297 | LOC197003 | 3' | TCCCCTTCTCCACTCC 3418 | A T TAG |
| | | | GGAGT GA GA AGGGGA | |
| | | | | |
| | | | CCTCA CT CT TCCCCT | |
| | | | C _ | |
| GAM297 | LOC200953 | 5' | CCCCTCCACCTGCTCCA 3482 | A ATA |
| | | | TGGAGTAG TG GAGGGG | |
| | | | | |
| | | | ACCTCGTC AC CTCCCC | |
| | | | C _ | |
| GAM297 | LOC257541 | 3' | TCCCCTCTGCCACCCCA 3746 | A AGAT A |
| | | | TGG GT G TAGAGGGGA | |
| | | | | |
| | | | ACC CA C GTCTCCCCT | |
| | | | C _ C | |
| GAM298 | G2 | 5' | TGGGACAGCCGACTT 2756 | ATCTTA |
| | | | AAGTTGGCTGTC CCA | |
| | | | | |
| | | | TTCAGCCGACAG GGT | |
| | | | | |
| GAM298 | REM | 5' | ATTGGCTGACAGCCAATT 1462 | TCTTA |
| | | | AGTTGGCTGTCA CCAAT | |
| | | | | |
| | | | TTAACCGACAGT GGTTA | |
| | | | C_ | |
| GAM298 | LOC90321 | 3' | GTAAGATGACAGGGCTGACTT 2631 | TG _ |
| | | | AAGT GCT GTCATCTTAC | |
| | | | | |

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|--------|----------|----|-----------------------------|---------|------|
| | | | TTCA CGG CAGTAGAATG | | |
| | | | GT GA | | |
| GAM298 | LOC91650 | 5' | ATTGGTAAACAACCAAT 2766 | C | CATC |
| | | | GTTGG TGT TTACCAAT | | |
| | | | | | |
| | | | TAACC ACA AATGGTTA | | |
| | | | A ____ | | |
| GAM299 | CD28 | 3' | ATAATTAATGGTACTCCTATAA 1274 | ATAC | |
| | TT | | AATTATAG GCTATTAATTAT | | |
| | | | | | |
| | | | TTAATATC TGGTAATTAATA | | |
| | | | CTCA | | |
| GAM299 | ABCA6 | 3' | ATAATTAATAGTATGTTTA 2374 | CG | |
| | | | TAGATA CTATTAATTAT | | |
| | | | | | |
| | | | ATTTGT GATAATTAATA | | |
| | | | AT | | |
| GAM299 | FLJ21302 | 3' | GTAGCACAATCTATAATT 2021 | AC_ | |
| | | | AATTATAGAT GCTAT | | |
| | | | | | |
| | | | TTAATATCTA CGATG | | |
| | | | ACA | | |
| GAM299 | SLC7A11 | 3' | TAATAGTCCCATATCTGTAAT 1492 | C__ | |
| | | | ATTATAGATA GCTATTA | | |
| | | | | | |
| | | | TAATGTCTAT TGATAAT | | |
| | | | ACCC | | |
| GAM300 | AP2B1 | 3' | AGTGTTACACTGTTTGA 814 | TCC | |
| | | | TTAGATA GTAACACT | | |
| | | | | | |
| | | | AGTTTGT CATTGTGA | | |
| | | | CA_ | | |
| GAM300 | GOT1 | 3' | TGGTAAGAAGGATATTTAA 897 | GTAACAC | |
| | | | TTAGATATCC TACCA | | |
| | | | | | |
| | | | AATTTATAGG ATGGT | | |
| | | | AAGA__ | | |
| GAM300 | ZNF14 | 3' | TGGTAGTGCATGCCTCTAA 1934 | TATC AA | |
| | | | TTAGA CGT CACTACCA | | |
| | | | | | |
| | | | AATCT GTA GTGATGGT | | |
| | | | CC_ C_ | | |
| GAM300 | FLJ11827 | 3' | TAGTGTTTAGAATATCTAA 2136 | CCGT | |
| | | | TTAGATAT AACACTA | | |
| | | | | | |
| | | | AATCTATA TTGTGAT | | |
| | | | AGAT | | |
| GAM300 | HEYL | 3' | TGGGTTGTTGCGGACATC 1507 | A | CTA |
| | | | GAT TCCGTAACA CCA | | |
| | | | | | |

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|--------|--------------|-----------------------------|--------|--------|
| | | CTA AGGCGTTGT GGT | | |
| | | C TG_ | | |
| GAM300 | LOC158722 5' | TGGTAGTGCAGCTCATCTGA 3226 | ATCC | AA |
| | | TTAGAT GT CACTACCA | | |
| | | | | |
| | | AGTCTA CG GTGATGGT | | |
| | | CT__ AC | | |
| GAM301 | ADAMTS5 3' | AAAATTCATAGTAATCCTGCCA 1350 | A | GCTC |
| | | TGGTA GATTACTG GTTTT | | |
| | | | | |
| | | ACCGT CTAATGAT TAAAA | | |
| | | C ACT_ | | |
| GAM301 | SLC38A4 3' | GACGTTTACCAGTAATATCACC 1774 | AAG | CT__ |
| | A | TGGT ATTACTGG CGTT | | |
| | | | | |
| | | ACCA TAATGACC GCAG | | |
| | | CTA ATTT | | |
| GAM302 | SLC19A2 3' | ATGGAATGTGGTACAAATTGTT 2835 | G | A AAAT |
| | | AA AATTT TAT CATTCCAT | | |
| | | | | |
| | | TT TTAATG ATG GTAAGGTA | | |
| | | G C GT__ | | |
| GAM302 | COLEC12 3' | ATGGACTGAATCACATAGATTC 2165 | ATAAA | T |
| | T | AGAATTTAT TCA TCCAT | | |
| | | | | |
| | | TCTTAGATA AGT AGGTA | | |
| | | CACTA C | | |
| GAM302 | COLEC12 3' | ATGGACTGAATCACATAGATTC 2395 | ATAAA | T |
| | T | AGAATTTAT TCA TCCAT | | |
| | | | | |
| | | TCTTAGATA AGT AGGTA | | |
| | | CACTA C | | |
| GAM302 | SH3BGRL 3' | ATGGAATGATATATCCAAGTTC 2615 | AT | A |
| | | GAATTT ATA ATCATTCCAT | | |
| | | | | |
| | | CTTGAA TAT TAGTAAGGTA | | |
| | | CC A | | |
| GAM302 | LOC150848 5' | GAATGATTTGGAGTTCTT 3334 | ATA | |
| | | AAGAATTT TAAATCATTC | | |
| | | | | |
| | | TTCTTGAG GTTTAGTAAG | | |
| | | — | | |
| GAM302 | LOC219846 3' | ATGAAATGATTTTATAATTCT 3504 | T T | C |
| | | AGAATT ATA AAATCATT CAT | | |
| | | | | |
| | | TCTTAA TAT TTTAGTAA GTA | | |
| | | _ T A | | |
| GAM303 | DRD1 3' | ATTAACCTCCGTTTCCAAATACA 774 | GCTCCT | |
| | | TGTAT AGCGGAGTTAAT | | |
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|--------|-----------|----|------------------------|--------------------------|---------|--------|
| | | | ACATA | TTGCCTCAATTA | | |
| | | | AACCT_ | | | |
| GAM303 | KIAA0182 | 3' | AAGTCCTAGGAGCACACA | 2931 | A | GC G |
| | | | TGT TGCTCCTA | GGA TT | | |
| | | | | | | |
| | | | ACA ACGAGGAT | CCT AA | | |
| | | | C | _ G | | |
| GAM303 | SSH2 | 3' | AGCCCCAGGAGCATACA | 2626 | | AGC A |
| | | | TGTATGCTCCT | GG GTT | | |
| | | | | | | |
| | | | ACATACGAGGA | CC CGA | | |
| | | | C | _ _ | | |
| GAM303 | LOC90918 | 5' | ATTAAATCCAGGAACATATA | 2687 | C | AGC G |
| | | | TGTATG TCCT | GGA TTAAT | | |
| | | | | | | |
| | | | ATATAC AGGA | CCT AATTA | | |
| | | | A | _ A | | |
| GAM304 | PAFAH1B2 | 3' | ACATTCATTGAATTATTATCAC | 937 | A | _ |
| | | | TG | CAGT ATAATAATTCAGT AATGT | | |
| | | | | | | |
| | | | GTCA TATTATTAAGTTA | TTACA | | |
| | | | C | C | | |
| GAM305 | GL004 | 3' | CGACAGAATAAGGTACAAATGT | 2736 | A | G C_ A |
| | | | AG | CTACATTT TAT TT TCT TCG | | |
| | | | | | | |
| | | | GATGTAAA ATG AA | AGA AGC | | |
| | | | C | G TA C | | |
| GAM305 | KIAA1336 | 3' | CGATTTTCATATAAATGTATGA | 2942 | _ | TTCTCT |
| | | | TC TACATTTATATG | ATCG | | |
| | | | | | | |
| | | | AG ATGTAAATATAC | TAGC | | |
| | | | T | TTT_ | | |
| GAM305 | LOC147711 | 3' | GAGAAAAACCATATAAATG | 3112 | _____ | |
| | | | CATTTATATG | TTCTC | | |
| | | | | | | |
| | | | GTAAATATAC | AAGAG | | |
| | | | CAAA | | | |
| GAM306 | B3GALT3 | 3' | TACTACACTGCCAGTTGTA | 1058 | ATA | |
| | | | TACAA GCAGTGTAGTG | | | |
| | | | | | | |
| | | | ATGTT CGTCACATCAT | | | |
| | | | GAC | | | |
| GAM306 | CSNK1G3 | 3' | TACTGATGGTACTGTTATT | 1106 | TA | G |
| | | | AATAGCAGTG | GT CAGTA | | |
| | | | | | | |
| | | | TTATTGTCAT | TA GTCAT | | |
| | | | GG | _ | | |
| GAM306 | DSC3 | 3' | TACTGCACTACCAAATTCATTT | 2061 | AGCAGT_ | |
| | | | G | CAAAT GTAGTGCAGTA | | |
| | | | | | | |

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|--------|---------|----|----------------------------|---------|
| | | | GTTTA CATCACGTCAT | |
| | | | CTTAAAC | |
| GAM306 | DSC3 | 3' | TACTGCACTACCAAATTCATTT 872 | AGCAGT_ |
| | G | | CAAAT GTAGTGCAGTA | |
| | | | | |
| | | | GTTTA CATCACGTCAT | |
| | | | CTTAAAC | |
| GAM306 | STK24 | 3' | CAGAACA CTCTATTTGTA 1037 | C AG |
| | | | TACAAATAG AGTGT TG | |
| | | | | |
| | | | ATGTTTATC TCACA AC | |
| | | | C AG | |
| GAM306 | SUV39H2 | 3' | TACTCACTGTACTTGTA 2080 | ATA T |
| | | | TACAA GCAGTG AGTG | |
| | | | | |
| | | | ATGTT TGTCAC TCAT | |
| | | | CA_ _ | |
| GAM306 | TAC1 | 3' | TATTACACTGTATTTGTA 1456 | G |
| | | | TACAAATA CAGTGTAGTG | |
| | | | | |
| | | | ATGTTTAT GTCACATTAT | |
| | | | — | |
| GAM306 | TAC1 | 3' | TATTACACTGTATTTGTA 1457 | G |
| | | | TACAAATA CAGTGTAGTG | |
| | | | | |
| | | | ATGTTTAT GTCACATTAT | |
| | | | — | |
| GAM306 | TAC1 | 3' | TATTACACTGTATTTGTA 1458 | G |
| | | | TACAAATA CAGTGTAGTG | |
| | | | | |
| | | | ATGTTTAT GTCACATTAT | |
| | | | — | |
| GAM306 | TAC1 | 3' | TATTACACTGTATTTGTA 996 | G |
| | | | TACAAATA CAGTGTAGTG | |
| | | | | |
| | | | ATGTTTAT GTCACATTAT | |
| | | | — | |
| GAM306 | UBQLN1 | 3' | TACTGCATGCATCACTTCTG 1452 | C TA__ |
| | | | TAG AGTG GTGCAGTA | |
| | | | | |
| | | | GTC TCAC TACGTCAT | |
| | | | T TACG | |
| GAM306 | ZNF207 | 3' | GCTTACATTGCTATTTGTA 1023 | T |
| | | | TACAAATAGCAGTGTAG GC | |
| | | | | |
| | | | ATGTTTATCGTTACATT CG | |
| | | | — | |
| GAM306 | AKAP12 | 3' | TACTACATGCTTTTTGTA 1185 | T G |
| | | | TACAAA AGCA TGTAGTG | |
| | | | | |

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|--------|----------|----|------------------------------|----------|--|
| | | | ATGTTT TCGT ACATCAT | | |
| | | | T _ | | |
| GAM306 | AKAP12 | 3' | TACTACATGCTTTTGTGTA 2481 | T G | |
| | | | TACAAA AGCA TGTAGTG | | |
| | | | | | |
| | | | ATGTTT TCGT ACATCAT | | |
| | | | T _ | | |
| GAM306 | FLJ10352 | 3' | CACTACAATTATGCTTTTGTGTA 2232 | T G__ | |
| | | | TACAAA AGCA TGTAGTG | | |
| | | | | | |
| | | | ATGTTT TCGT ACATCAC | | |
| | | | _ ATTA | | |
| GAM306 | FLJ11222 | 3' | CACTACAGAGCACTGTTTG 1819 | _ AG | |
| | | | CAAATA GC TGTAGTG | | |
| | | | | | |
| | | | GTTTGT CG ACATCAC | | |
| | | | CA AG | | |
| GAM306 | FLJ14641 | 3' | TACTGCCTGTGCTGCTA 2284 | TG T | |
| | | | TAGCAG TAG GCAGTA | | |
| | | | | | |
| | | | ATCGTC GTC CGTCAT | | |
| | | | GT _ | | |
| GAM306 | FLJ23537 | 3' | ACTGCAGTACTGTTTGTA 2105 | GCAGT G | |
| | | | TACAAATA GTA TGCAGT | | |
| | | | | | |
| | | | ATGTTTGT CAT ACGTCA | | |
| | | | _____ G | | |
| GAM306 | KIAA1161 | 5' | ACTGCACTAACCCATTTGTG 3212 | AGCA G | |
| | | | TACAAAT GT TAGTGCACT | | |
| | | | | | |
| | | | GTGTTTA CA ATCACGTCA | | |
| | | | CC__ _ | | |
| GAM306 | MGC10646 | 3' | CACTACGCTGCCATTTTA 2270 | C A | |
| | | | A AAAT GCAGTGTAGTG | | |
| | | | | | |
| | | | A TTTA CGTCGCATCAC | | |
| | | | T C | | |
| GAM306 | MLL5 | 3' | TACAGTCTCACACTGCTATCGT 3644 | AA _ T A | |
| | A | | TAC ATAGCAGTGT AG GC GTA | | |
| | | | | | |
| | | | ATG TATCGTCACA TC TG CAT | | |
| | | | C_ C _ A | | |
| GAM306 | ZAK | 3' | ACTGCACATATTGCTTTTG 2426 | T A | |
| | | | CAAA AGCAGTGT GTGCAGT | | |
| | | | | | |
| | | | GTTT TCGTTATA CACGTCA | | |
| | | | _ _ | | |
| GAM306 | ZNF387 | 3' | ACTGTTATTACTGTTACCTG 1520 | AA TAGT | |
| | | | CA TAGCAGTG GCAGT | | |
| | | | | | |

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|--------|--------------|-----------------------------|-----------|--|
| | | GT ATTGTCAT TGTCA | | |
| | | CC TAT_ | | |
| GAM306 | LOC126661 3' | ACTGCAGCCTCCGCTTCCTGT 3000 | C_ T _ | |
| | | ATAG AGTG AG TGCAGT | | |
| | | | | |
| | | TGTC TCGC TC ACGTCA | | |
| | | CT C CG | | |
| GAM306 | LOC139770 3' | CACTACCGCTGTATCTGTA 3022 | A G _ | |
| | | TACA ATA CAGTG TAGTG | | |
| | | | | |
| | | ATGT TAT GTCGC ATCAC | | |
| | | C _ C | | |
| GAM306 | LOC150577 3' | ACCGCATTGCTGCTATCTGTG 3329 | A T A | |
| | | TACA ATAGCAGTG AGTGC GT | | |
| | | | | |
| | | GTGT TATCGTCGT TTACG CA | | |
| | | C _ C | | |
| GAM306 | LOC89919 5' | TACTACACACATTGCTATTTG 2579 | A C | |
| | | CAAATAGCAGTGT GTG AGTA | | |
| | | | | |
| | | GTTTATCGTTACA CAC TCAT | | |
| | | _ A | | |
| GAM306 | LOC92573 5' | ACCGCAGGCTATGCTCTTTGTA 2869 | T GT AG A | |
| | | TACAAA AGCA GT TGC GT | | |
| | | | | |
| | | ATGTTT TCGT CG ACG CA | | |
| | | C AT G_ C | | |
| GAM307 | NTRK2 3' | GATGGCTTCCGTGAGACA 1275 | C GA | |
| | | TGTC CACGGAAGT ATC | | |
| | | | | |
| | | ACAG GTGCCTTCG TAG | | |
| | | A G_ | | |
| GAM307 | ING3 3' | AGGATTACATAGACAAT 1879 | CCACGGAA | |
| | | ATTGTC GTGAATCCT | | |
| | | | | |
| | | TAACAG CATTAGGA | | |
| | | ATA_____ | | |
| GAM307 | KIAA1164 5' | AAGGAACGCTTCCCGGGACAAT 2861 | AC AA | |
| | | ATTGTCCC GGAAGTG TCCTT | | |
| | | | | |
| | | TAACAGGG CCTTCGC AGGAA | | |
| | | C_ A_ | | |
| GAM307 | LOC150577 5' | AAGGAATTATTTCCACGAGACA 3328 | CCAC A | |
| | A | TTGTC GGAAGTGA TCCTT | | |
| | | | | |
| | | AACAG CCTTTATT AGGAA | | |
| | | AGCA A | | |
| GAM307 | LOC199936 3' | AAGGGGCCCCCATGGGACAA 3474 | C AA GAA | |
| | | TTGTCCCA GG GT TCCTT | | |
| | | | | |

AACAGGGT CC CG GGGAA
A CC ____
GAM307 LOC257235 3' AAGGATTTCAGTATTCATGGGA 3727 C AG_ _
CAA TTGTCCCA GGA TGAA TCCTT
||||||| ||| ||| |||||
AACAGGGT CTT ACTT AGGAA
A ATG T
GAM308 COL19A1 3' ATCCACATGGTACAAGCCTTTC 863 ACCA G _
TCA TGAGAAAG GTA TAT TGGAT
||||||| ||| ||| |||||
ACTCTTTC CAT GTA ACCTA
CGAA G C
GAM308 EFEMP1 3' ATCCACTAAACTGGTCTTCTTC 1089 GA AG T
A TGA AAGACCAGT TA TGGAT
||| ||||||| || |||||
ACT TTCTGGTCA AT ACCTA
TC A_ C
GAM308 EFEMP1 3' ATCCACTAAACTGGTCTTCTTC 1864 GA AG T
A TGA AAGACCAGT TA TGGAT
||| ||||||| || |||||
ACT TTCTGGTCA AT ACCTA
TC A_ C
GAM308 FACL2 3' ATCCCTGCTACTGTCCCTTCTC 1943 A_ C TT
A TGAGAA GAC AGTAGTA GGAT
||||| ||| ||||||| |||||
ACTCTT CTG TCATCGT CCTA
CC _ C_
GAM308 HDGF 3' CCTCTTCCTACTGGTCTCTCT 1120 A TATT_
AGA AGACCAGTAG GG
||| ||||||| ||
TCT TCTGGTCATC CC
C CTTCT
GAM308 HGF 3' ATCCAAGTAGTTGCTGGTCTCT 3642 GAA _ _
ATCA TGA AGACCAGTAG TA TTGGAT
||| ||||||| || |||||||
ACT TCTGGTCGTT AT AACCTA
ATC G C
GAM308 NFE2L1 3' CCAATATATCTTCTCA 999 A CCAGTA
TGAGAA GA GTATTGG
||||| || |||||||
ACTCTT CT TATAACC
_ A____
GAM308 NLGN1 5' CCATTATACAGTCTTTCTCA 1592 CA GTAT
TGAGAAAGAC GTA TGG
||||||||| ||| |||
ACTCTTTCTG CAT ACC
A_ ATT_
GAM308 SLC21A2 3' ACTAACCCTGGTCTTTCCCA 1232 A ____
TG GAAAGACCAG TAGT
|| ||||||||| |||||

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|--------|-----------|----|-----------------------------|-----------|
| | | | AC CTTTCTGGTC ATCA | |
| | | | C CCA | |
| GAM308 | FHR5 | 3' | ATCCAATACTAAATACCCCTTA 2166 | AAAGACCAG |
| | | | TGAG TAGTATTGGAT | |
| | | | | |
| | | | ATTC ATCATAACCTA | |
| | | | CCCATAA__ | |
| GAM308 | FLJ13710 | 3' | CTGGTGCTACTGGTCTTTCT 2091 | TG |
| | | | AGAAAGACCAGTAGTAT G | |
| | | | | |
| | | | TCTTTCTGGTCATCGTG C | |
| | | | GT | |
| GAM308 | KIAA1155 | 3' | ATCACGGGCTAATAATCTTTCT 2628 | CCAG ATTG |
| | | | CA TGAGAAAGA TAGT GAT | |
| | | | | |
| | | | ACTCTTTCT ATCG CTA | |
| | | | AATA GGCA | |
| GAM308 | SEF | 3' | TCTCTCACTACCTTTCTCA 2860 | ACCA ATT |
| | | | TGAGAAAG GTAGT GGA | |
| | | | | |
| | | | ACTCTTTC CATCA TCT | |
| | | | ____ CTC | |
| GAM308 | TREX1 | 5' | ATCCAGTAATCCAGTCTCCCTC 2337 | AA CAGTAG |
| | | | A TGAG AGAC TATTGGAT | |
| | | | | |
| | | | ACTC TCTG ATGACCTA | |
| | | | CC ACCTA_ | |
| GAM308 | TRIM6 | 3' | ATCCAATACATATTTTTCTC 2366 | CCA A |
| | | | GAGAAAGA GT GTATTGGAT | |
| | | | | |
| | | | CTCTTTTT TA CATAACCTA | |
| | | | A__ _ | |
| GAM308 | VEST1 | 3' | ATTCTCTACCACTGCTCTTTCT 2349 | C A TT |
| | | | CA TGAGAAAGA CAGT GTA GGAT | |
| | | | | |
| | | | ACTCTTTCT GTCA CAT CTTA | |
| | | | C C CT | |
| GAM308 | LOC149076 | 5' | ATGCCCACTGACCTTTTTCA 3128 | AC A_ |
| | | | TGAGAAAG CAGT GTAT | |
| | | | | |
| | | | ACTTTTTC GTCA CGTA | |
| | | | CA CC | |
| GAM308 | LOC254043 | 3' | ATCTTTCTCTAGTCTTTCTC 3667 | C T TATT |
| | | | A TGAGAAAGAC AG AG GGAT | |
| | | | | |
| | | | ACTCTTTCTG TC TC TCTA | |
| | | | A _ TCTT | |
| GAM309 | BUB3 | 3' | AAAGGTATTTGGGCAAAC 1149 | A_ T |
| | | | GTTT TCA ATACCTTT | |
| | | | | |

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|--------|-----------|----|-----------------------------|-------|-----|
| | | | CAAA GGT TATGGAAA | | |
| | | | CG T | | |
| GAM309 | CLCN6 | 3' | TAAAGGTATGTGCTATGATAAA 815 | _____ | III |
| | | | TTTATCATA TACCTTT A | | |
| | | | | | |
| | | | AAATAGTAT ATGGAAA T | | |
| | | | CGTGT III | | |
| GAM309 | CLCN6 | 3' | TAAAGGTATGTGCTATGATAAA 1957 | _____ | III |
| | | | TTTATCATA TACCTTT A | | |
| | | | | | |
| | | | AAATAGTAT ATGGAAA T | | |
| | | | CGTGT III | | |
| GAM309 | CLCN6 | 3' | TAAAGGTATGTGCTATGATAAA 1958 | _____ | III |
| | | | TTTATCATA TACCTTT A | | |
| | | | | | |
| | | | AAATAGTAT ATGGAAA T | | |
| | | | CGTGT III | | |
| GAM309 | CMAR | 3' | AAAGGAAGTGATAAACTA 1193 | ATA | |
| | | | TAGTTTATCAT CCTTT | | |
| | | | | | |
| | | | ATCAAATAGTG GGAAA | | |
| | | | AA_ | | |
| GAM309 | CTPS | 3' | AAAGGTATTTGGGAAACT 3441 | AT T | |
| | | | AGTTT CA ATACCTTT | | |
| | | | | | |
| | | | TCAA GT TATGGAAA | | |
| | | | GG T | | |
| GAM309 | RB1 | 3' | AAAGGTGTATTTAAACTA 3505 | TC | |
| | | | TAGTTTA ATATACCTTT | | |
| | | | | | |
| | | | ATCAAAT TATGTGGAAA | | |
| | | | T_ | | |
| GAM309 | RP2 | 3' | AAAGGTATATGCAATGCTA 1339 | TTAT | |
| | | | TAGT CATATACCTTT | | |
| | | | | | |
| | | | ATCG GTATATGGAAA | | |
| | | | TAAC | | |
| GAM309 | WHSC1 | 3' | AAAGGTATATGTGATAAAT 1394 | — | |
| | | | GTTTATCAT ATACCTTT | | |
| | | | | | |
| | | | TAAATAGTG TATGGAAA | | |
| | | | TA | | |
| GAM309 | ARHGAP11A | 3' | AAGGGTAGAGATAAACT 1546 | ATA | |
| | | | AGTTTATC TACCTTT | | |
| | | | | | |
| | | | TCAAATAG ATGGGAA | | |
| | | | AG_ | | |
| GAM309 | FLJ20533 | 3' | AAAGGTATGTGAATAAAT 1758 | — | |
| | | | GTTTAT CATATACCTTT | | |
| | | | | | |

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|--------|-----------|----|------------------------|------|----------|
| | | | TAAATA GTGTATGGAAA | | |
| | | | A | | |
| GAM309 | MGC16063 | 3' | AAAGGCTTACTGATAAACT | 2356 | _ TA |
| | | | AGTTTATCA TA CCTTT | | |
| | | | | | |
| | | | TCAAATAGT AT GGAAA | | |
| | | | C TC | | |
| GAM309 | SEMA3C | 3' | AAAGGTATAATTAAACT | 1293 | TCA |
| | | | AGTTTA TATACCTTT | | |
| | | | | | |
| | | | TCAAAT ATATGGAAA | | |
| | | | TA_ | | |
| GAM309 | LOC135293 | 3' | AAGGTATAATAAACTG | 3047 | CA |
| | | | TAGTTTAT TATACCTT | | |
| | | | | | |
| | | | GTCAAATA ATATGGAA | | |
| | | | — | | |
| GAM309 | LOC153883 | 3' | AAAGGTATATTTGACTA | 3182 | TATC |
| | | | TAGTT ATATACCTTT | | |
| | | | | | |
| | | | ATCAG TATATGGAAA | | |
| | | | TT_ | | |
| GAM309 | LOC199692 | 3' | GAGGGTGTAATAAACTG | 2521 | CA |
| | | | TAGTTTAT TATACCTTT | | |
| | | | | | |
| | | | GTCAAATA ATGTGGGAG | | |
| | | | — | | |
| GAM310 | MGC5242 | 5' | CCTTACAATCCGAGACTA | 2042 | — |
| | | | TGGTCTCGGATT AGG | | |
| | | | | | |
| | | | ATCAGAGCCTAA TCC | | |
| | | | CAT | | |
| GAM310 | LOC197259 | 3' | GCCAATCAAGACCAGAA | 3422 | CG A |
| | | | TTCTGGTCT GATT GGC | | |
| | | | | | |
| | | | AAGACCAGA CTAA CCG | | |
| | | | A_ _ | | |
| GAM311 | CRYBA4 | 3' | AAACTCAAACGAATAAAAAAG | 865 | _ ATC |
| | | | CTTTTTTAT CGTT GGTTTT | | |
| | | | | | |
| | | | GAAAAAATA GCAA TCAAAA | | |
| | | | A AC_ | | |
| GAM311 | UCLH1 | 3' | GCTGATAAGATAAAAAA | 1093 | G |
| | | | TTTTTTATC TTATCGGT | | |
| | | | | | |
| | | | AAAAAATAG AATAGTCG | | |
| | | | — | | |
| GAM311 | BDG-29 | 3' | GAAAACCGTCTCATAACAAAAG | 2944 | _ CGTTAT |
| | G | | CCTTTT TTAT CGGTTTTC | | |
| | | | | | |

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|--------|---------------|----|-----------------------------|---|------------|
| | | | GGAAAA AATA GCCAAAAG | | |
| | | | C CTCT__ | | |
| GAM311 | ERG-1 | 5' | GAAATTTCAATGATAAAAAAGG 1972 | | ATC |
| | | | CCTTTTTTATCGTT GGTTTT | | |
| | | | | | |
| | | | GGAAAAAATAGTAA TTAAAG | | |
| | | | CT_ | | |
| GAM311 | LOC199837 | 5' | GAAAGAAGAAACAATAGAAAAG 3434 | | C A GG |
| | G | | CCTTTTTTAT GTT TC TTTC | | |
| | | | | | |
| | | | GGAAAAGATA CAA AG GAAAG | | |
| | | | A _ AA | | |
| GAM312 | BHLHB3 | 3' | AAGTCCAAACTGATATATCCTA 2160 | A | TTAAA |
| | | | TAG ATATATT GGACTT | | |
| | | | | | |
| | | | ATC TATATAG CCTGAA | | |
| | | | C TCAA | | |
| GAM312 | CLN2 | 3' | AAGTCCTTCCAATTATATTT 735 | T | TA |
| | | | GAATATA TT AAGGACTT | | |
| | | | | | |
| | | | TTTATAT AA TTCCTGAA | | |
| | | | T CC | | |
| GAM312 | ZFP36L1 | 3' | TCCATAGAATATATTCT 1165 | | AA |
| | | | AGAATATATTTTA GGA | | |
| | | | | | |
| | | | TCTTATATAAGAT CCT | | |
| | | | A_ | | |
| GAM312 | C8orf2 | 3' | TCCATTTAAAATACATTC 1361 | A | _ |
| | | | GAAT TATTTTAAA GGA | | |
| | | | | | |
| | | | CTTA ATAAAATTT CCT | | |
| | | | C A | | |
| GAM312 | DKFZP566K0524 | 3' | AAGGATTTAAAATATATTC 2854 | | GGA |
| | | | GAATATATTTTAAA CTT | | |
| | | | | | |
| | | | CTTATATAAAATTT GAA | | |
| | | | AG_ | | |
| GAM312 | FIGNL1 | 3' | TTTTTAAGAATATATTCTA 1980 | | A |
| | | | TAGAATATATTTT AAGGA | | |
| | | | | | |
| | | | ATCTTATATAAGA TTTTT | | |
| | | | A | | |
| GAM312 | FLJ10704 | 3' | TTTTTTAAAATATATTTTA 1796 | | |
| | | | TAGAATATATTTTAAAGGA | | |
| | | | | | |
| | | | ATTTTATATAAAATTTTTT | | |
| GAM312 | HDAC9-PENDING | 3' | TCTTTTAAAATACATTTTA 1528 | | A |
| | | | TAGAAT TATTTTAAAGGA | | |
| | | | | | |

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|--------|-----------|----|-----------------------------|-------|--------|
| | | | ATTTTA ATAAAATTTTCT | | |
| | | | C | | |
| GAM312 | KIAA1384 | 3' | AAGCCTAAAATATATTTTA 2695 | AA | A |
| | | | TAGAATATATTTT AGG CTT | | |
| | | | | | |
| | | | ATTTTATATAAAA TCC GAA | | |
| | | | — — | | |
| GAM312 | SOX30 | 3' | TTTCTTAAAATATATTCTG 1346 | AG | |
| | | | TAGAATATATTTTAA GA | | |
| | | | | | |
| | | | GTCTTATATAAAATT TT | | |
| | | | CT | | |
| GAM312 | LOC221810 | 3' | AGTCTTTAAAATATATTCTG 3625 | G | |
| | | | TAGAATATATTTTAAAG ACT | | |
| | | | | | |
| | | | GTCTTATATAAAATTC TGA | | |
| | | | — | | |
| GAM312 | LOC255177 | 3' | AGTTCTTTAAAATATTCTA 3712 | A | |
| | | | TAGAATAT TTTTAAAGGACT | | |
| | | | | | |
| | | | ATCTTATA AAAATTTCTTGA | | |
| | | | — | | |
| GAM313 | ADRA1A | 3' | TTCCCATAGACACCCAGCCCAT 2327 | CCA__ | A |
| | AG | | CTATGGGT TCTATG GAA | | |
| | | | | | |
| | | | GATACCCG AGATAC CTT | | |
| | | | ACCCAC C | | |
| GAM313 | ARF3 | 3' | TTCTCATAAATGGATCTG 845 | C | |
| | | | TGGGTCCAT TATGAGAA | | |
| | | | | | |
| | | | GTCTAGGTA ATACTCTT | | |
| | | | A | | |
| GAM313 | C14orf1 | 3' | TCTCTGCTGCTGGACCCAAGA 1362 | A | TCTAT_ |
| | | | TCT TGGGTCCA GAGA | | |
| | | | | | |
| | | | AGA ACCCAGGT CTCT | | |
| | | | — CGTCGT | | |
| GAM313 | CTNNA2 | 3' | TTCTCATAAAATTGGGCACA 1108 | G | TC__ |
| | | | TG GTCCA TATGAGAA | | |
| | | | | | |
| | | | AC CGGGT ATACTCTT | | |
| | | | A TAAA | | |
| GAM313 | FAT2 | 3' | TTCTCATACCTGCCCACAG 829 | A | CCATC |
| | | | CT TGGGT TATGAGAA | | |
| | | | | | |
| | | | GA ACCCG ATACTCTT | | |
| | | | C TCC__ | | |
| GAM313 | GALNT3 | 3' | TTCAATGGACCCACAGG 1118 | A | CTA |
| | | | TCT TGGGTCCAT TGAG | | |
| | | | | | |

GGA ACCCAGGTA ACTT
 C ____
 GAM313 HMG20A 3' TCTCATAGTATGCCCATA 1801 CCAT
 TATGGGT CTATGAGA
 ||||| |||||
 ATACCCG GATACTCT
 TAT_
 GAM313 HPCA 3' TCTCACACACACAGGCCCAT 903 CATCTA____
 AGA TCTATGGGTC TGAGA
 ||||| ||||
 AGATACCCGG ACTCT
 ACACACACAC
 GAM313 MTMR3 3' CTCACAGATGGATAAATG 1939 GG A
 TAT GTCCATCT TGAG
 || ||||| ||||
 GTA TAGGTAGA ACTC
 AA C
 GAM313 PIGR 3' CTCACATGGACCCAAGA 2955 A CTA
 TCT TGGGTCCAT TGAG
 || ||||| ||||
 AGA ACCCAGGTA ACTC
 _ C_
 GAM313 PIWIL1 3' TTCTCATAGATATTTTGTG 2959 GG TCC
 TAT G ATCTATGAGAA
 || | |||||
 GTG T TAGATACTCTT
 TT TA_
 GAM313 SORBS1 3' TTCTCATAGAACACCA 1625 _ CCA
 TGG GT TCTATGAGAA
 || || |||||
 ACC CA AGATACTCTT
 A ____
 GAM313 TOP3A 3' TTCTCATAGACGTCCTGAGA 1132 A TCCA
 TCT TGGG TCTATGAGAA
 || || |||||
 AGA GTCC AGATACTCTT
 _ TGC_
 GAM313 UC28 3' TTCTCAATCTTGAACATCATAGA 1951 C TCTA
 TCTATGGGT CA TGAGAA
 ||||| || |||||
 AGATACTCA GT ACTCTT
 A TCTA
 GAM313 ARL5 3' TTCTCATAGATTTTGTA 1406 GG TCC
 TAT G ATCTATGAGAA
 || | |||||
 ATG T TAGATACTCTT
 TT ____
 GAM313 DDM36 3' TCTCATAGGAGCATAGA 1932 GG ATC
 TCTATG TCC TATGAGA
 ||||| || |||||

AGATAC AGG ATACTCT
 G_ _
 GAM313 FLJ21596 3' TCTCAGGGTGGGACCCATA 2093 _ A
 TATGGGTCC ATCT TGAGA
 ||||| ||| |||||
 ATACCCAGG TGGG ACTCT
 G _
 GAM313 FLJ22202 5' TCCAGGAGATGGACCAACAGA 2102 ATG A_ A
 TCT GGTCCATCT TG GA
 || ||||| || ||
 AGA CCAGGTAGA AC CT
 CAA GG _
 GAM313 GPNMB 3' TCTCATAAATGGGTGGGA 935 ATGGG C
 TCT TCCAT TATGAGA
 || |||| |||||
 AGG GGGTA ATACTCT
 GT_ A
 GAM313 HSZFP36 3' CAGGAGATGGACCCCA 2659 AT A_
 TCT GGTCCATCT TG
 || ||||| ||
 AGA CCCAGGTAGA AC
 C_ GG
 GAM313 IPLA2(GAMMA) 3' TTCTCATAAATGAAGGTCTGT 2577 GT _ C
 ATGG C CAT TATGAGAA
 ||| | ||| |||||
 TGTC G GTA ATACTCTT
 TG AA A
 GAM313 KIAA0648 3' TTCTCATAGATAATCAAGA 3258 A GTCC
 TCT TGG ATCTATGAGAA
 ||| ||| |||||
 AGA ACT TAGATACTCTT
 _ AA_
 GAM313 KIAA1239 3' TTCATGTAACCCATAGA 2915 CCATC
 TCTATGGGT TATGAG
 ||||| |||||
 AGATACCCA GTACTT
 AT_
 GAM313 KIAA1577 5' TTCTCATGGGTACCCCA 2691 AT CC
 TCT GGGT ATCTATGAGAA
 || ||| |||||
 AGA CCA TGGGTACTCTT
 C_ _
 GAM313 KIAA1821 3' CTCATCCTGTACCTATAGA 2926 C TCT
 TCTATGGGT CA ATGAG
 ||||| || |||||
 AGATATCCA GT TACTC
 T CC_
 GAM313 KIAA1853 5' CTCAGGATGGACCCTCAGA 2857 AT A
 TCT GGTCCATCT TGAG
 || ||||| |||||

AGA CCCAGGTAGG ACTC
 CT _
 GAM313 MGC3169 3' TCTCTGCCAGGACCCCATAGA 2051 _ ATCTAT
 TCTATGGG TCC GAGA
 ||||| ||| |||
 AGATACCC AGG CTCT
 C ACCGT_
 GAM313 MST4 3' TTCATATGGACCCAGAGA 1696 A TC
 TCT TGGGTCCA TATGAG
 ||| ||||| |||||
 AGA ACCCAGGT ATAATT
 G _
 GAM313 PDE10A 3' ATTCTCACAGATCAGATCACTC 1321 ____ C_ A |||
 CATAGA TGG GTC ATCT TGAGAA T
 ||| ||| ||||| ||||| |
 ACC TAG TAGA ACTCTT A
 TCAC AC C |||
 GAM313 SKD3 3' TTCTAAGGGGAAGGGACCCATA 2170 A_ ATG_
 GA TCTATGGGTCC TCT AGAA
 ||||| ||| |||
 AGATACCCAGG AGG TCTT
 GA GGAA
 GAM313 STX18 3' CTCATGGGCACTCACAGA 1714 A CCA
 TCT TGGGT TCTATGAG
 ||| ||||| |||||
 AGA ACTCA GGGTACTC
 C C_
 GAM313 LOC115811 5' CTCTGTGGACCTACAGA 2441 A CTAT
 TCT TGGGTCCAT GAG
 ||| ||||| |||
 AGA ATCCAGGTG CTC
 C T_
 GAM313 LOC131308 3' TTCCAGCCTGAACCCATGGA 3013 C TCTA A
 TCTATGGGT CA TG GAA
 ||||| || |||
 AGGTACCCA GT AC CTT
 A CCG_ _
 GAM313 LOC139221 3' TCTCATAGATACTAGTTGA 3036 TATG CC
 TC GGT ATCTATGAGA
 || ||| |||||
 AG TCA TAGATACTCT
 TTGA _
 GAM313 LOC158490 5' TCTCATAGGACTGTCCTAGA 3220 T TCCA
 TCTA GGG TCTATGAGA
 ||| ||| |||||
 AGAT CCT GGATACTCT
 _ GTCA
 GAM313 LOC221466 5' CTCAGGATCCATAGA 3618 ATCTA
 TCTATGGGTCC TGAG
 ||||| |||

AGATACCTAGG ACTC

GAM313 LOC221540 3' TTCTCATAAATCCCCGCCCA 3621 CC__ C
TGGGT AT TATGAGAA
|||| |||||||
ACCCG TA ATACTCTT
CCCC A

GAM313 LOC222233 5' CTCAGCAGAGACAGACCCCAGA 3648 AT CA__ A_
TCT GGGTC TCT TGAG
||| |||| ||| ||||
AGA CCCAG AGA ACTC
C_ ACAG CG

GAM313 LOC255042 3' TTCTCACAGATGGGCAGCA 3671 G_ A
TG GTCCATCT TGAGAA
|| ||||||| |||||
AC CGGGTAGA ACTCTT
GA C

GAM313 LOC256117 3' CTCATTGAGACCCCATAGA 3705 _ CATCT
TCTATGGG TC ATGAG
||||||| || |||||
AGATACCC AG TACTC
C AGCT_

GAM313 LOC257545 3' TTCTCATAAATCCCCGCCCA 3747 CC__ C
TGGGT AT TATGAGAA
|||| |||||||
ACCCG TA ATACTCTT
CCCC A

GAM313 LOC257598 3' TTCTCATAAATCCCCGCCCA 3750 CC__ C
TGGGT AT TATGAGAA
|||| |||||||
ACCCG TA ATACTCTT
CCCC A

GAM314 CHAC 3' TGCCCATATGTCCATTTAT 1612 AGAT
ATAAGTGGACATAT GCA
||||||||||| |||
TATTTACCTGTATA CGT
CC__

GAM314 GGCX 3' CTGCACCCTGCCACTTGT 778 A TATAGA
ATAAGTGG CA TGCAG
||||||| || |||||
TGTTACCC GT ACGTC
_ CCC__

GAM314 ITPKB 3' TCTGCATCTGTCCAC 911 TATA
GTGGACA GATGCAGA
||||||| |||||||
CACCTGT CTACGTCT

GAM314 KCNAB1 3' TCTAATGTTATGTCCACTTA 2584 ____
TAAGTGGACATA TAGA
||||||||||| |||||

ATTCACCTGTAT ATCT
 TGTA
 GAM314 KLRC4 5' CTGTCAAAATATACACCACTTA 1451 ACA GA_ _
 T ATAAGTGG TATA TG CAG
 ||||| ||| ||||
 TATTCACC ATAT AC GTC
 AC_ AAA T
 GAM314 MLF2 3' TCTGCATCTACTGACTTG 1212 _ ACATA
 TAAGT GG TAGATGCAGA
 ||||| || |||||
 GTTCA TC ATCTACGTCT
 G _
 GAM314 NR1I2 3' TCTGCATCCATTTGAACAC 1971 GA T A
 GTG CA AT GATGCAGA
 ||| ||| |||||
 CAC GT TA CTACGTCT
 AA T C
 GAM314 NR1I2 3' TCTGCATCCATTTGAACAC 1067 GA T A
 GTG CA AT GATGCAGA
 ||| ||| |||||
 CAC GT TA CTACGTCT
 AA T C
 GAM314 CEP3 3' TTCTACATCAGATGTTGTCACT 1304 _ ATA C
 TAT ATAAGTGG GACAT GATG AGAA
 ||||| |||| ||| ||||
 TATTCAC TTGTA CTAC TCTT
 TG GA_ A
 GAM314 FHX 3' TCATGGATCATGTCCAC 1825 ATA G _
 GTGGACAT GAT CA GA
 ||||| ||| |||
 CACCTGTA CTA GT CT
 _ G A
 GAM314 FLJ10352 3' TTCTGCATCTACAACCAACAT 2233 GACATA_
 TTA TAAGTG TAGATGCAGAA
 ||||| |||||
 ATTTAC ATCTACGTCTT
 AACTCAAC
 GAM314 FLJ22127 3' TCGAGTCCATATGTCCAC 2008 A GCA
 GTGGACATAT GAT GA
 ||||| ||| |||
 CACCTGTATA CTG CT
 C AG_
 GAM314 GDAP1L1 3' TCTGCATCCATGCCAC 2043 A ATA
 GTGG CAT GATGCAGA
 ||| ||| |||||
 CACC GTA CTACGTCT
 _ C_
 GAM314 H-L(3)MBT 3' TCTGCTCTCTACCCACT 2230 ACA T T
 AGTGG TA AGA GCAGA
 ||||| ||| ||| |||||

TCACC AT TCT CGTCT
 C__ C _
 GAM314 KIAA1340 3' TCTAAGCTATGCCCATTTAT 2846 A ____
 ATAAGTGG CATA TAGA
 ||||| ||| |||
 TATTTACC GTAT ATCT
 C CGA
 GAM314 KNSL7 3' TTCTGCATCCATATACACCCT 1905 T AC_ A
 AG GG ATAT GATGCAGAA
 || || ||| |||||
 TC CC TATA CTACGTCTT
 _ ACA C
 GAM314 P5-1 3' CTCCATTTATGTACCCAC 1322 AC C
 GTGG ATATAGATG AG
 ||| ||||| ||
 CACC TGTATTTAC TC
 CA C
 GAM314 PP1044 5' CTGCATCTTTACCTATATCCAT 1956 C T____
 TTA TAAGTGGA ATA AGATGCAG
 ||||| || |||||
 ATTTACCT TAT TCTACGTC
 A CCATT
 GAM314 SIRPB1 3' TGCATGTGTCCACTTA 1272 ATAG
 TAAGTGGACAT ATGCA
 ||||| |||
 ATTCACCTGTG TACGT

 GAM314 LOC148811 3' CTGCATCTCTCCCCTTA 3126 T CATAT
 TAAG GGA AGATGCAG
 ||| || |||||
 ATTC CCT TCTACGTC
 C C____
 GAM314 LOC149711 3' TCCATATGTCTATCCACTTA 3315 ____ A
 TAAGTGA CATAT GA
 ||||| ||| ||
 ATTCACCT GTATA CT
 ATCT C
 GAM314 LOC150630 5' CTGCATCTTCTGCCACT 3332 A TAT
 AGTGG CA AGATGCAG
 |||| || |||||
 TCACC GT TCTACGTC
 _ CT_
 GAM314 LOC150819 5' CTGCATTTTAGTCCAACCT 3333 _ ATAT
 AGT GGAC AGATGCAG
 || ||| |||||
 TCA CCTG TTTACGTC
 A AT_
 GAM314 LOC154877 3' TCTGCATCCATTCCACT 3373 CAT A
 AGTGGA AT GATGCAGA
 |||| || |||||

TCACCT TA CTACGTCT
 ____ C
 GAM314 LOC158327 3' TTCTGCAGGGACACCACTTAT 3216 ACATATAGA
 ATAAGTGG TGCAGAA
 ||||| |||||
 TATTCACC ACGTCTT
 ACAGGG____
 GAM314 LOC196540 3' TCTGCATCCATGTACTCC 3467 C_ A
 GGA ATAT GATGCAGA
 || ||| |||||
 CCT TGTA CTACGTCT
 CA C
 GAM314 LOC220394 5' TCTCAGAATATGTCCAT 3581 AGA C
 GTGGACATAT TG AGA
 ||||| || |||
 TACCTGTATA AC TCT
 AG_ _
 GAM314 LOC254428 3' CTGTTGACCCATGTCCACCTAT 3677 A ATAGAT
 ATA GTGGACAT GCAG
 || ||||| |||
 TAT CACCTGTA TGTC
 C CCCAGT
 GAM314 LOC92405 3' TTCTGTTACACATGTCTACTTA 2848 ATAGAT
 TAAGTGGACAT GCAGAA
 ||||| |||||
 ATTCATCTGTA TGTCTT
 CACAT_
 GAM315 PIGH 3' CAAGATCATAGTATTTTCAGTCA 1126 T _ GTA
 TG CT AAAT ATTATGATCTTG
 || ||| |||||
 AC GA TTTA TGATACTAGAAC
 T C ____
 GAM315 PRSC 3' CAAGATCATAATTTTATAGA 1313 AATGT
 TCTA AATTATGATCTTG
 ||| |||||
 AGAT TTAATACTAGAAC
 ATT_
 GAM315 PXMP4 3' CAAGATCATAGGCCTCAGAC 1370 AAATGTAA
 GTCT TTATGATCTTG
 ||| |||||
 CAGA GATACTAGAAC
 CTCCG____
 GAM316 C1orf1 5' TATGCTGACAGAAGAACCA 809 CC A A
 TGGTTCTTT GT CA CATA
 ||||| || |||
 ACCAAGAAG CA GT GTAT
 A_ _ C
 GAM316 LRAT 3' AGTATGCATACATAAAAGCAAC 2556 _ CC_ CAA
 CA
 TGGTTCTTT GTA CATACT
 ||||| ||| |||||

ACCAA GAAA CAT GTATGA
 C ATA AC_
 GAM316 MYBL1 3' AGTATGTTATACAAATGCCA 2679 TCTTTCC C
 TGGT GTA AACATACT
 |||| ||| |||||
 ACCG CAT TTGTATGA
 TAAA__ A
 GAM316 KIAA1028 3' TATGTCTGCATTGAAAAGAACC 3547 C TA_ _
 A TGGTTCTTT CG CA ACATA
 ||||| || |||
 ACCAAGAAA GT GT TGTAT
 A TAC C
 GAM316 MGC2488 3' TGTAGTGGAAAGAAGCAT 2045 G _
 ATG TTCTTTCCG TACA
 ||| ||||| |||
 TAC AAGAAAGGT ATGT
 G G
 GAM317 CX3CR1 3' ACTGCCTACTGCATCGAGTCA 2891 TCCCTTAA
 TGACTCG TAGGCAGT
 ||||| |||||
 ACTGAGC ATCCGTCA
 TACGTC__
 GAM317 WNT14 3' CTGCAAGGGACGAGTC 1014 AATAG
 GACTCGTCCCTT GCAG
 ||||| |||
 CTGAGCAGGGAA CGTC

 GAM317 FLJ20275 3' TACTGCCTTCATAAGATCAAGT 1745 CGTCC AT_
 CA TGACT CTTA AGGCAGTA
 |||| ||| |||||
 ACTGA GAAT TCCGTCAT
 ACTA_ ACT
 GAM317 FLJ22390 5' TACTGCCTATCAAACG 2002 CCC A
 CGT TT ATAGGCAGTA
 || ||| |||||
 GCA AA TATCCGTCAT
 _ C
 GAM318 LOC120864 5' CAAGGTCCAAACTGATATAA 2986 CGTAG
 TTGTATCAGTTT TCTTG
 ||||| |||
 AATATAGTCAAA GGAAC
 CCT__
 GAM319 KIAA0626 3' AACATCAGGGTGCAGAATTGAT 1954 C_ A_
 ATCGATTG CAT TGATGTT
 ||||| ||| |||||
 TAGTTAAG GTG ACTACAA
 AC GG
 GAM319 KIAA1239 3' AACATCATGATTATTGATG 2914 TCCCA
 CATCGAT TATGATGTT
 ||||| |||||

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|--------|-----------|----|------------------------|---------------|-----|--------|
| | | | GTAGTTA | GTACTACAA | | |
| | | | TTA__ | | | |
| GAM319 | LOC201475 | 5' | AACATCATATATTTTGATGTTA | 3428 | | TTCCC |
| | | | TAACATCGA | ATATGATGTT | | |
| | | | | | | |
| | | | ATTGTAGTT | TATACTACAA | | |
| | | | TTA__ | | | |
| GAM320 | CAPN2 | 3' | AAAACTTTATGAACTTCACCA | 855 | A _ | AAA |
| | | | TG TGGAGT | CGTAA AGTTTT | | |
| | | | | | | |
| | | | AC ACTTCA | GTATT TCAAAA | | |
| | | | C A | __ | | |
| GAM320 | DAAM2 | 3' | AAAATTTTTCTAAAACTCCATC | 3559 | | CG A |
| | A | | TGATGGAGT | TA AAAAGTTTT | | |
| | | | | | | |
| | | | ACTACCTCA | AT TTTTAAAA | | |
| | | | AA C | | | |
| GAM320 | SELE | 3' | AAAACTCTCCTACACTTCCATT | 747 | _ C | AAAA |
| | A | | TGATGGA | GT GTA AGTTTT | | |
| | | | | | | |
| | | | ATTACCT | CA CAT TCAAAA | | |
| | | | T _ | CCTC | | |
| GAM320 | KIAA0475 | 3' | AAAACCTTGCATTCCATCA | 1570 | | C AAAA |
| | | | TGATGGAGT | GTAA GTTTT | | |
| | | | | | | |
| | | | ACTACCTTA | CGTT CAAAA | | |
| | | | _ C__ | | | |
| GAM320 | LOC222671 | 5' | GCTTCTACGACTCCGCCA | 3582 | A | AAA |
| | | | TG TGGAGTCGTA | AAGT | | |
| | | | | | | |
| | | | AC GCCTCAGCAT | TTCG | | |
| | | | C C__ | | | |
| GAM320 | LOC254901 | 5' | AATTTCTTCACTGACTCCACCA | 3699 | A _ | A A |
| | | | TG TGGAGTC | GT AA AAGTT | | |
| | | | | | | |
| | | | AC ACCTCAG | CA TT TTTAA | | |
| | | | C T C C | | | |
| GAM320 | LOC257615 | 5' | GCTTCTACGACTCCGCCA | 3749 | A | AAA |
| | | | TG TGGAGTCGTA | AAGT | | |
| | | | | | | |
| | | | AC GCCTCAGCAT | TTCG | | |
| | | | C C__ | | | |
| GAM321 | CAPN2 | 3' | AAAACTTTATGAACTTCACCA | 855 | A _ | AAA |
| | | | TG TGGAGT | CGTAA AGTTTT | | |
| | | | | | | |
| | | | AC ACTTCA | GTATT TCAAAA | | |
| | | | C A | __ | | |
| GAM321 | DAAM2 | 3' | AAAATTTTTCTAAAACTCCATC | 3559 | | CG A |
| | A | | TGATGGAGT | TA AAAAGTTTT | | |
| | | | | | | |

| | | | | | |
|--------|-----------|----|-----------------------------|---------|------|
| | | | ACTACCTCA AT TTTTAAAA | | |
| | | | AA C | | |
| GAM321 | SELE | 3' | AAAACCTCTCCTACACTTCCATT 747 | _ C | AAAA |
| | A | | TGATGGA GT GTA AGTTTT | | |
| | | | | | |
| | | | ATTACCT CA CAT TCAAAA | | |
| | | | T _ CCTC | | |
| GAM321 | KIAA0475 | 3' | AAAACCTTGCATTCCATCA 1570 | C | AAAA |
| | | | TGATGGAGT GTAA GTTTT | | |
| | | | | | |
| | | | ACTACCTTA CGTT CAAAA | | |
| | | | _ C__ | | |
| GAM321 | LOC222671 | 5' | GCTTCTACGACTCCGCCA 3582 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C__ | | |
| GAM321 | LOC254901 | 5' | AATTTCTTCACTGACTCCACCA 3699 | A _ A A | |
| | | | TG TGGAGTC GT AA AAGTT | | |
| | | | | | |
| | | | AC ACCTCAG CA TT TTAA | | |
| | | | C T C C | | |
| GAM321 | LOC257615 | 5' | GCTTCTACGACTCCGCCA 3749 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C__ | | |
| GAM322 | CAPN2 | 3' | AAAACCTTTATGAACTTCACCA 855 | A _ | AAA |
| | | | TG TGGAGT CGTAA AGTTTT | | |
| | | | | | |
| | | | AC ACTTCA GTATT TCAAAA | | |
| | | | C A _ | | |
| GAM322 | DAAM2 | 3' | AAAATTTTTCTAAAACTCCATC 3559 | CG A | |
| | A | | TGATGGAGT TA AAAAGTTTT | | |
| | | | | | |
| | | | ACTACCTCA AT TTTTAAAA | | |
| | | | AA C | | |
| GAM322 | SELE | 3' | AAAACCTCTCCTACACTTCCATT 747 | _ C | AAAA |
| | A | | TGATGGA GT GTA AGTTTT | | |
| | | | | | |
| | | | ATTACCT CA CAT TCAAAA | | |
| | | | T _ CCTC | | |
| GAM322 | KIAA0475 | 3' | AAAACCTTGCATTCCATCA 1570 | C | AAAA |
| | | | TGATGGAGT GTAA GTTTT | | |
| | | | | | |
| | | | ACTACCTTA CGTT CAAAA | | |
| | | | _ C__ | | |
| GAM322 | LOC222671 | 5' | GCTTCTACGACTCCGCCA 3582 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |

| | | | | | |
|--------|-----------|----|-----------------------------|-----|-------|
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C__ | | |
| GAM322 | LOC254901 | 5' | AATTTCTTCACTGACTCCACCA 3699 | A | _ A A |
| | | | TG TGGAGTC GT AA AAGTT | | |
| | | | | | |
| | | | AC ACCTCAG CA TT TTAA | | |
| | | | C T C C | | |
| GAM322 | LOC257615 | 5' | GCTTCTACGACTCCGCCA 3749 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C__ | | |
| GAM323 | CAPN2 | 3' | AAAACTTTATGAACTTCACCA 855 | A | _ AAA |
| | | | TG TGGAGT CGTAA AGTTTT | | |
| | | | | | |
| | | | AC ACTTCA GTATT TCAAAA | | |
| | | | C A _ | | |
| GAM323 | DAAM2 | 3' | AAAATTTTTCTAAACTCCATC 3559 | CG | A |
| | A | | TGATGGAGT TA AAAAGTTTT | | |
| | | | | | |
| | | | ACTACCTCA AT TTTTAAAA | | |
| | | | AA C | | |
| GAM323 | SELE | 3' | AAAACTCTCCTACACTTCCATT 747 | _ C | AAAA |
| | A | | TGATGGA GT GTA AGTTTT | | |
| | | | | | |
| | | | ATTACCT CA CAT TCAAAA | | |
| | | | T _ CCTC | | |
| GAM323 | KIAA0475 | 3' | AAAACCTTGCAATTCCATCA 1570 | C | AAAA |
| | | | TGATGGAGT GTAA GTTTT | | |
| | | | | | |
| | | | ACTACCTTA CGTT CAAAA | | |
| | | | _ C__ | | |
| GAM323 | LOC222671 | 5' | GCTTCTACGACTCCGCCA 3582 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C__ | | |
| GAM323 | LOC254901 | 5' | AATTTCTTCACTGACTCCACCA 3699 | A | _ A A |
| | | | TG TGGAGTC GT AA AAGTT | | |
| | | | | | |
| | | | AC ACCTCAG CA TT TTAA | | |
| | | | C T C C | | |
| GAM323 | LOC257615 | 5' | GCTTCTACGACTCCGCCA 3749 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C__ | | |
| GAM324 | CAPN2 | 3' | AAAACTTTATGAACTTCACCA 855 | A | _ AAA |
| | | | TG TGGAGT CGTAA AGTTTT | | |
| | | | | | |

| | | | | | |
|--------|-----------|----|-----------------------------|-----|-------|
| | | | AC ACTTCA GTATT TCAAAA | | |
| | | | C A _ | | |
| GAM324 | DAAM2 | 3' | AAAATTTTCTAAACTCCATC 3559 | CG | A |
| | A | | TGATGGAGT TA AAAAGTTTT | | |
| | | | | | |
| | | | ACTACCTCA AT TTTTAAAA | | |
| | | | AA C | | |
| GAM324 | SELE | 3' | AAACTCTCCTACACTTCCATT 747 | _ C | AAAA |
| | A | | TGATGGA GT GTA AGTTTT | | |
| | | | | | |
| | | | ATTACCT CA CAT TCAAAA | | |
| | | | T _ CCTC | | |
| GAM324 | KIAA0475 | 3' | AAAACCTTGCATTCCATCA 1570 | C | AAAA |
| | | | TGATGGAGT GTAA GTTTT | | |
| | | | | | |
| | | | ACTACCTTA CGTT CAAAA | | |
| | | | _ C _ | | |
| GAM324 | LOC222671 | 5' | GCTTCTACGACTCCGCCA 3582 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C _ | | |
| GAM324 | LOC254901 | 5' | AATTTCTTCACTGACTCCACCA 3699 | A | _ A A |
| | | | TG TGGAGTC GT AA AAGTT | | |
| | | | | | |
| | | | AC ACCTCAG CA TT TTAA | | |
| | | | C T C C | | |
| GAM324 | LOC257615 | 5' | GCTTCTACGACTCCGCCA 3749 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C _ | | |
| GAM325 | CAPN2 | 3' | AAACTTTATGAACTTCACCA 855 | A | _ AAA |
| | | | TG TGGAGT CGTAA AGTTTT | | |
| | | | | | |
| | | | AC ACTTCA GTATT TCAAAA | | |
| | | | C A _ | | |
| GAM325 | DAAM2 | 3' | AAAATTTTCTAAACTCCATC 3559 | CG | A |
| | A | | TGATGGAGT TA AAAAGTTTT | | |
| | | | | | |
| | | | ACTACCTCA AT TTTTAAAA | | |
| | | | AA C | | |
| GAM325 | SELE | 3' | AAACTCTCCTACACTTCCATT 747 | _ C | AAAA |
| | A | | TGATGGA GT GTA AGTTTT | | |
| | | | | | |
| | | | ATTACCT CA CAT TCAAAA | | |
| | | | T _ CCTC | | |
| GAM325 | KIAA0475 | 3' | AAAACCTTGCATTCCATCA 1570 | C | AAAA |
| | | | TGATGGAGT GTAA GTTTT | | |
| | | | | | |

| | | | | | |
|--------|-----------|----|-----------------------------|---|----------|
| | | | ACTACCTTA CGTT CAAAA | | |
| | | | _ C_ | | |
| GAM325 | LOC222671 | 5' | GCTTCTACGACTCCGCCA 3582 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C_ | | |
| GAM325 | LOC254901 | 5' | AATTTCTTCACTGACTCCACCA 3699 | A | _ A A |
| | | | TG TGGAGTC GT AA AAGTT | | |
| | | | | | |
| | | | AC ACCTCAG CA TT TTTAA | | |
| | | | C T C C | | |
| GAM325 | LOC257615 | 5' | GCTTCTACGACTCCGCCA 3749 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C_ | | |
| GAM326 | CAPN2 | 3' | AAAACTTTATGAACTTCACCA 855 | A | _ AAA |
| | | | TG TGGAGT CGTAA AGTTTT | | |
| | | | | | |
| | | | AC ACTTCA GTATT TCAAAA | | |
| | | | C A _ | | |
| GAM326 | DAAM2 | 3' | AAAATTTTTCTAAAACTCCATC 3559 | | CG A |
| | A | | TGATGGAGT TA AAAAGTTTT | | |
| | | | | | |
| | | | ACTACCTCA AT TTTTAAAA | | |
| | | | AA C | | |
| GAM326 | SELE | 3' | AAAACTCTCCTACACTTCCATT 747 | | _ C AAAA |
| | A | | TGATGGA GT GTA AGTTTT | | |
| | | | | | |
| | | | ATTACCT CA CAT TCAAAA | | |
| | | | T _ CCTC | | |
| GAM326 | KIAA0475 | 3' | AAAACCTTGCATTCCATCA 1570 | C | AAAA |
| | | | TGATGGAGT GTAA GTTTT | | |
| | | | | | |
| | | | ACTACCTTA CGTT CAAAA | | |
| | | | _ C_ | | |
| GAM326 | LOC222671 | 5' | GCTTCTACGACTCCGCCA 3582 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C_ | | |
| GAM326 | LOC254901 | 5' | AATTTCTTCACTGACTCCACCA 3699 | A | _ A A |
| | | | TG TGGAGTC GT AA AAGTT | | |
| | | | | | |
| | | | AC ACCTCAG CA TT TTTAA | | |
| | | | C T C C | | |
| GAM326 | LOC257615 | 5' | GCTTCTACGACTCCGCCA 3749 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |

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|--------|-----------|----|------------------------|------------------------|------|----------|
| | | | AC GCCTCAGCAT | TTCG | | |
| | | | C | C__ | | |
| GAM327 | CAPN2 | 3' | AAAAC | TTTATGAACTTCACCA | 855 | A _ AAA |
| | | | | TG TGGAGT CGTAA AGTTTT | | |
| | | | | | | |
| | | | | AC ACTTCA GTATT TCAAAA | | |
| | | | C | A | | |
| GAM327 | DAAM2 | 3' | AAAAT | TTTTTCTAAAACTCCATC | 3559 | CG A |
| | A | | | TGATGGAGT TA AAAAGTTTT | | |
| | | | | | | |
| | | | | ACTACCTCA AT TTTTAAAA | | |
| | | | | AA C | | |
| GAM327 | SELE | 3' | AAAAC | TCTCCTACACTTCCATT | 747 | _ C AAAA |
| | A | | | TGATGGA GT GTA AGTTTT | | |
| | | | | | | |
| | | | | ATTACCT CA CAT TCAAAA | | |
| | | | | T _ CCTC | | |
| GAM327 | KIAA0475 | 3' | AAAAC | CTTGCATTCCATCA | 1570 | C AAAA |
| | | | | TGATGGAGT GTAA GTTTT | | |
| | | | | | | |
| | | | | ACTACCTTA CGTT CAAAA | | |
| | | | | _ C__ | | |
| GAM327 | LOC222671 | 5' | GCTTCTACGACTCCGCCA | 3582 | A | AAA |
| | | | | TG TGGAGTCGTA AAGT | | |
| | | | | | | |
| | | | | AC GCCTCAGCAT TTCG | | |
| | | | C | C__ | | |
| GAM327 | LOC254901 | 5' | AATTTCTTCACTGACTCCACCA | 3699 | A | _ A A |
| | | | | TG TGGAGTC GT AA AAGTT | | |
| | | | | | | |
| | | | | AC ACCTCAG CA TT TTTAA | | |
| | | | C | T C C | | |
| GAM327 | LOC257615 | 5' | GCTTCTACGACTCCGCCA | 3749 | A | AAA |
| | | | | TG TGGAGTCGTA AAGT | | |
| | | | | | | |
| | | | | AC GCCTCAGCAT TTCG | | |
| | | | C | C__ | | |
| GAM328 | CAPN2 | 3' | AAAAC | TTTATGAACTTCACCA | 855 | A _ AAA |
| | | | | TG TGGAGT CGTAA AGTTTT | | |
| | | | | | | |
| | | | | AC ACTTCA GTATT TCAAAA | | |
| | | | C | A | | |
| GAM328 | DAAM2 | 3' | AAAAT | TTTTTCTAAAACTCCATC | 3559 | CG A |
| | A | | | TGATGGAGT TA AAAAGTTTT | | |
| | | | | | | |
| | | | | ACTACCTCA AT TTTTAAAA | | |
| | | | | AA C | | |
| GAM328 | SELE | 3' | AAAAC | TCTCCTACACTTCCATT | 747 | _ C AAAA |
| | A | | | TGATGGA GT GTA AGTTTT | | |
| | | | | | | |

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|--------|-----------|----|-------------------------|------|----------|
| | | | ATTACCT CA CAT TCAAAA | | |
| | | | T _ CCTC | | |
| GAM328 | KIAA0475 | 3' | AAAACCTTGCATTCCATCA | 1570 | C AAAA |
| | | | TGATGGAGT GTAA GTTTT | | |
| | | | | | |
| | | | ACTACCTTA CGTT CAAAA | | |
| | | | _ C__ | | |
| GAM328 | LOC222671 | 5' | GCTTCTACGACTCCGCCA | 3582 | A AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C__ | | |
| GAM328 | LOC254901 | 5' | AATTTCTTCACTGACTCCACCA | 3699 | A _ A A |
| | | | TG TGGAGTC GT AA AAGTT | | |
| | | | | | |
| | | | AC ACCTCAG CA TT TTTAA | | |
| | | | C T C C | | |
| GAM328 | LOC257615 | 5' | GCTTCTACGACTCCGCCA | 3749 | A AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C__ | | |
| GAM329 | CAPN2 | 3' | AAAACCTTTATGAACTTCACCA | 855 | A _ AAA |
| | | | TG TGGAGT CGTAA AGTTTT | | |
| | | | | | |
| | | | AC ACTTCA GTATT TCAAAA | | |
| | | | C A _ | | |
| GAM329 | DAAM2 | 3' | AAAATTTTTTCTAAAACTCCATC | 3559 | CG A |
| | A | | TGATGGAGT TA AAAAGTTTT | | |
| | | | | | |
| | | | ACTACCTCA AT TTTTAAAA | | |
| | | | AA C | | |
| GAM329 | SELE | 3' | AAAACCTCTCCTACACTTCCATT | 747 | _ C AAAA |
| | A | | TGATGGA GT GTA AGTTTT | | |
| | | | | | |
| | | | ATTACCT CA CAT TCAAAA | | |
| | | | T _ CCTC | | |
| GAM329 | KIAA0475 | 3' | AAAACCTTGCATTCCATCA | 1570 | C AAAA |
| | | | TGATGGAGT GTAA GTTTT | | |
| | | | | | |
| | | | ACTACCTTA CGTT CAAAA | | |
| | | | _ C__ | | |
| GAM329 | LOC222671 | 5' | GCTTCTACGACTCCGCCA | 3582 | A AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C__ | | |
| GAM329 | LOC254901 | 5' | AATTTCTTCACTGACTCCACCA | 3699 | A _ A A |
| | | | TG TGGAGTC GT AA AAGTT | | |
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|--------|-----------|----|-----------------------------|-------|-------|
| | | | AC ACCTCAG CA TT TTTAA | | |
| | | | C T C C | | |
| GAM329 | LOC257615 | 5' | GCTTCTACGACTCCGCCA 3749 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C__ | | |
| GAM330 | CAPN2 | 3' | AAAACCTTTATGAACTTCACCA 855 | A | _ AAA |
| | | | TG TGGAGT CGTAA AGTTTT | | |
| | | | | | |
| | | | AC ACTTCA GTATT TCAAAA | | |
| | | | C A ____ | | |
| GAM330 | DAAM2 | 3' | AAAATTTTTCTAAACTCCATC 3559 | | CG A |
| | A | | TGATGGAGT TA AAAAGTTTT | | |
| | | | | | |
| | | | ACTACCTCA AT TTTTAAAA | | |
| | | | AA C | | |
| GAM330 | SELE | 3' | AAAACCTCTCCTACACTTCCATT 747 | _ C | AAAA |
| | A | | TGATGGA GT GTA AGTTTT | | |
| | | | | | |
| | | | ATTACCT CA CAT TCAAAA | | |
| | | | T _ CCTC | | |
| GAM330 | KIAA0475 | 3' | AAAACCTTGCATTCCATCA 1570 | C | AAAA |
| | | | TGATGGAGT GTAA GTTTT | | |
| | | | | | |
| | | | ACTACCTTA CGTT CAAAA | | |
| | | | _ C__ | | |
| GAM330 | LOC222671 | 5' | GCTTCTACGACTCCGCCA 3582 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C__ | | |
| GAM330 | LOC254901 | 5' | AATTTCTTCACTGACTCCACCA 3699 | A | _ A A |
| | | | TG TGGAGTC GT AA AAGTT | | |
| | | | | | |
| | | | AC ACCTCAG CA TT TTTAA | | |
| | | | C T C C | | |
| GAM330 | LOC257615 | 5' | GCTTCTACGACTCCGCCA 3749 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C__ | | |
| GAM331 | ITGB7 | 5' | AGAGAAAGTCTGACTTGCCCCA 783 | AAAA_ | TTAT |
| | C | | GT AAGTT CTTTCTCT | | |
| | | | | | |
| | | | CA TTCAG GAAAGAGA | | |
| | | | CCCCG TCT_ | | |
| GAM331 | RPP30 | 3' | AGAGAAAGACAACTGTTCTGCG 1297 | A A | TTA |
| | | | CGTA AA AGTT TCTTTCTCT | | |
| | | | | | |

GCGT TT TCAA AGAAAGAGA
 C G C__
 GAM331 FLJ13263 3' AGAGAAAGATTTTAGCTTTT 2139 TT_
 AAAAGTT ATCTTTCTCT
 ||||| |||||
 TTTTCGA TAGAAAGAGA
 TTT
 GAM331 FLJ23074 5' AGAGAAAGACAAGGGTTT 2133 G A
 AAA TTTT TCTTTCTCT
 ||| ||| |||||
 TTT GGAA AGAAAGAGA
 G C
 GAM331 GTF2A2 3' AGAAAAAATATGACTTTTTTAC 1119 T C_
 GTAAAAAAGTT TAT TTTCT
 ||||| ||| |||||
 CATTTTTTCAG ATA AAAGA
 T AA
 GAM331 IMP-2 3' AGAGAAAGCAGGCTTTTCTA 1308 A TAT
 TA AAAAGTTT CTTTCTCT
 || ||||| |||||
 AT TTTTCGGA GAAAGAGA
 C C_
 GAM331 KIAA0212 3' AGAAAGGTAAATCTTTTTAC 1518 A T
 GTAAAAA G TTTATCTTTCT
 ||||| |||||
 CATTTTT C AAATGGAAAGA
 _T
 GAM331 OSBPL2 5' AGAGAAAGTTTGTAATAATTCCT 1566 AAA ____
 TAC GTAA AGTTTTAT CTTTCTCT
 ||| ||||| |||||
 CATT TAAAAATG GAAAGAGA
 CC_ TTT
 GAM331 OSBPL2 5' AGAGAAAGTTTGTAATAATTCCT 2482 AAA ____
 TAC GTAA AGTTTTAT CTTTCTCT
 ||| ||||| |||||
 CATT TAAAAATG GAAAGAGA
 CC_ TTT
 GAM331 RBM9 3' AGAAAGAATACTTTTTTAT 1489 TTTA
 GTAAAAAAGT TCTTTCT
 ||||| |||||
 TATTTTTTCA AGAAAGA
 TA_
 GAM331 LOC254826 3' AGAGAAAGTCTTGCTTTTT 3732 TTTAT
 AAAAAGT CTTTCTCT
 ||||| |||||
 TTTTTCG GAAAGAGA
 TTCT_
 GAM332 DSC3 3' TAAAATCTATGTGTTTTAGACT 871 AGT A
 TA TAAGTT AATACATA ATTTTA
 ||||| ||||| |||||

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|--------|-----------|----|------------------------------|----------|---|
| | | | ATTCAG TTGTGTAT TAAAAT | | |
| | | | ATT C | | |
| GAM332 | DSC3 | 3' | TAAAATCTATGTGTTTTAGACT 2060 | AGT | A |
| | TA | | TAAGTT AATACATA ATTTTA | | |
| | | | | | |
| | | | ATTCAG TTGTGTAT TAAAAT | | |
| | | | ATT C | | |
| GAM332 | FLJ20366 | 3' | AAGTTTACATGTACTAACTTA 1751 | ATACA | |
| | | | TAAGTTAGTA TAAATTT | | |
| | | | | | |
| | | | ATTCAATCAT ATTTGAA | | |
| | | | GTAC_ | | |
| GAM333 | CAPN2 | 3' | AAAACCTTTATGAACTTCACCA 855 | A _ AAA | |
| | | | TG TGGAGT CGTAA AGTTTT | | |
| | | | | | |
| | | | AC ACTTCA GTATT TCAAAA | | |
| | | | C A _ | | |
| GAM333 | DAAM2 | 3' | AAAATTTTTCTAAAACCTCCATC 3559 | CG A | |
| | A | | TGATGGAGT TA AAAAGTTTT | | |
| | | | | | |
| | | | ACTACCTCA AT TTTTAAAA | | |
| | | | AA C | | |
| GAM333 | SELE | 3' | AAAACCTCTCCTACACTTCCATT 747 | _ C AAAA | |
| | A | | TGATGGA GT GTA AGTTTT | | |
| | | | | | |
| | | | ATTACCT CA CAT TCAAAA | | |
| | | | T _ CCTC | | |
| GAM333 | KIAA0475 | 3' | AAAACCTTGCAATTCCATCA 1570 | C AAAA | |
| | | | TGATGGAGT GTAA GTTTT | | |
| | | | | | |
| | | | ACTACCTTA CGTT CAAAA | | |
| | | | _ C_ | | |
| GAM333 | LOC222671 | 5' | GCTTCTACGACTCCGCCA 3582 | A AAA | |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C_ | | |
| GAM333 | LOC254901 | 5' | AATTTCTTCACTGACTCCACCA 3699 | A _ A A | |
| | | | TG TGGAGTC GT AA AAGTT | | |
| | | | | | |
| | | | AC ACCTCAG CA TT TTTAA | | |
| | | | C T C C | | |
| GAM333 | LOC257615 | 5' | GCTTCTACGACTCCGCCA 3749 | A AAA | |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C_ | | |
| GAM334 | CAPN2 | 3' | AAAACCTTTATGAACTTCACCA 855 | A _ AAA | |
| | | | TG TGGAGT CGTAA AGTTTT | | |
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|--------|-----------|----|-----------------------------|-----|-------|
| | | | AC ACTTCA GTATT TCAAAA | | |
| | | | C A _ | | |
| GAM334 | DAAM2 | 3' | AAAATTTTCTAAACTCCATC 3559 | CG | A |
| | A | | TGATGGAGT TA AAAAGTTTT | | |
| | | | | | |
| | | | ACTACCTCA AT TTTTAAAA | | |
| | | | AA C | | |
| GAM334 | SELE | 3' | AAACTCTCCTACACTTCCATT 747 | _ C | AAAA |
| | A | | TGATGGA GT GTA AGTTTT | | |
| | | | | | |
| | | | ATTACCT CA CAT TCAAAA | | |
| | | | T _ CCTC | | |
| GAM334 | KIAA0475 | 3' | AAAACCTTGCATTCCATCA 1570 | C | AAAA |
| | | | TGATGGAGT GTAA GTTTT | | |
| | | | | | |
| | | | ACTACCTTA CGTT CAAAA | | |
| | | | _ C _ | | |
| GAM334 | LOC222671 | 5' | GCTTCTACGACTCCGCCA 3582 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C _ | | |
| GAM334 | LOC254901 | 5' | AATTTCTTCACTGACTCCACCA 3699 | A | _ A A |
| | | | TG TGGAGTC GT AA AAGTT | | |
| | | | | | |
| | | | AC ACCTCAG CA TT TTAA | | |
| | | | C T C C | | |
| GAM334 | LOC257615 | 5' | GCTTCTACGACTCCGCCA 3749 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C _ | | |
| GAM335 | CAPN2 | 3' | AAACTTTATGAACTTCACCA 855 | A | _ AAA |
| | | | TG TGGAGT CGTAA AGTTTT | | |
| | | | | | |
| | | | AC ACTTCA GTATT TCAAAA | | |
| | | | C A _ | | |
| GAM335 | DAAM2 | 3' | AAAATTTTCTAAACTCCATC 3559 | CG | A |
| | A | | TGATGGAGT TA AAAAGTTTT | | |
| | | | | | |
| | | | ACTACCTCA AT TTTTAAAA | | |
| | | | AA C | | |
| GAM335 | SELE | 3' | AAACTCTCCTACACTTCCATT 747 | _ C | AAAA |
| | A | | TGATGGA GT GTA AGTTTT | | |
| | | | | | |
| | | | ATTACCT CA CAT TCAAAA | | |
| | | | T _ CCTC | | |
| GAM335 | KIAA0475 | 3' | AAAACCTTGCATTCCATCA 1570 | C | AAAA |
| | | | TGATGGAGT GTAA GTTTT | | |
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|--------|-----------|----|-----------------------------|---|----------|
| | | | ACTACCTTA CGTT CAAAA | | |
| | | | _ C_ | | |
| GAM335 | LOC222671 | 5' | GCTTCTACGACTCCGCCA 3582 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C_ | | |
| GAM335 | LOC254901 | 5' | AATTTCTTCACTGACTCCACCA 3699 | A | _ A A |
| | | | TG TGGAGTC GT AA AAGTT | | |
| | | | | | |
| | | | AC ACCTCAG CA TT TTTAA | | |
| | | | C T C C | | |
| GAM335 | LOC257615 | 5' | GCTTCTACGACTCCGCCA 3749 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C_ | | |
| GAM336 | CAPN2 | 3' | AAAACTTTATGAACTTCACCA 855 | A | _ AAA |
| | | | TG TGGAGT CGTAA AGTTTT | | |
| | | | | | |
| | | | AC ACTTCA GTATT TCAAAA | | |
| | | | C A _ | | |
| GAM336 | DAAM2 | 3' | AAAATTTTTCTAAAACTCCATC 3559 | | CG A |
| | A | | TGATGGAGT TA AAAAGTTTT | | |
| | | | | | |
| | | | ACTACCTCA AT TTTTAAAA | | |
| | | | AA C | | |
| GAM336 | SELE | 3' | AAAACTCTCCTACACTTCCATT 747 | | _ C AAAA |
| | A | | TGATGGA GT GTA AGTTTT | | |
| | | | | | |
| | | | ATTACCT CA CAT TCAAAA | | |
| | | | T _ CCTC | | |
| GAM336 | KIAA0475 | 3' | AAAACCTTGCATTCCATCA 1570 | C | AAAA |
| | | | TGATGGAGT GTAA GTTTT | | |
| | | | | | |
| | | | ACTACCTTA CGTT CAAAA | | |
| | | | _ C_ | | |
| GAM336 | LOC222671 | 5' | GCTTCTACGACTCCGCCA 3582 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C_ | | |
| GAM336 | LOC254901 | 5' | AATTTCTTCACTGACTCCACCA 3699 | A | _ A A |
| | | | TG TGGAGTC GT AA AAGTT | | |
| | | | | | |
| | | | AC ACCTCAG CA TT TTTAA | | |
| | | | C T C C | | |
| GAM336 | LOC257615 | 5' | GCTTCTACGACTCCGCCA 3749 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |

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|--------|-----------|----|-----------------------------|-------|
| | | | AC GCCTCAGCAT TTCG | |
| | | | C C__ | |
| GAM337 | FGF2 | 3' | ATATTTTTGTGGCTGCTTTTT 884 | T_ |
| | | | AAAAAGT TTACAAAATAT | |
| | | | | |
| | | | TTTTTCG GGTGTTTTTATA | |
| | | | TC | |
| GAM337 | MPHOSPH1 | 3' | ATATTTTTATAAGGCTTTTTT 1670 | C |
| | | | AAAAAGTTTTTA AAAAATAT | |
| | | | | |
| | | | TTTTTTCGGAAT TTTTATA | |
| | | | A | |
| GAM337 | FLJ11274 | 3' | ATATCTTTGTAGTAGCTTTTTT 1820 | _ A |
| | | | TA TAAAAAAGTT TTACAAA ATAT | |
| | | | | |
| | | | ATTTTTTTCGA GATGTTT TATA | |
| | | | T C | |
| GAM337 | FLJ31101 | 3' | ATATTTTTGTAAATGTATTTG 1771 | AAAA |
| | | | T ATAA GTTTTACAAAAATAT | |
| | | | | |
| | | | TGTTT TAAATGTTTTTATA | |
| | | | ATG_ | |
| GAM337 | GPT2 | 3' | ATATTTTTGTAACAATTGCTTT 2417 | T____ |
| | | | TTT AAAAAAGT TTACAAAATAT | |
| | | | | |
| | | | TTTTTTCG AATGTTTTTATA | |
| | | | TTAAC | |
| GAM337 | RMP | 3' | TTTTGTAAACTTTTTTTTC 2430 | T |
| | | | A AAAAAAAGTTTTACAAAA | |
| | | | | |
| | | | C TTTTTTTCAAAATGTTTT | |
| | | | T | |
| GAM337 | RMP | 3' | TTTTGTAAACTTTTTTTTC 1059 | T |
| | | | A AAAAAAAGTTTTACAAAA | |
| | | | | |
| | | | C TTTTTTTCAAAATGTTTT | |
| | | | T | |
| GAM337 | SOX6 | 3' | ATATTTTGTCTTACTTTTTTT 2328 | TTT |
| | | | AAAAAAAGT ACAAAAATAT | |
| | | | | |
| | | | TTTTTTTCA TGTTTTTATA | |
| | | | TTC | |
| GAM337 | LOC136288 | 3' | ATATTTCTGAGGCTTTTTTTGT 3018 | CAA |
| | | | ATAAAAAAAGTTTTTA AAATAT | |
| | | | | |
| | | | TGTTTTTTTCGGAGT TTTATA | |
| | | | C__ | |
| GAM338 | AICDA | 3' | AGAAAGAGAACAATATTT 1922 | TTTA |
| | | | AAATATT TTCTCTTTCT | |
| | | | | |

| | | | | | |
|--------|--------------|----|-----------------------------|--------|--|
| | | | TTTATAA AAGAGAAAGA | | |
| | | | C__ | | |
| GAM338 | AS3 | 3' | AGAAAGATTTAAAGTATTTTA 1652 | TATTC | |
| | | | TAAAATATTTT TCTTTCT | | |
| | | | | | |
| | | | ATTTTATGAAA AGAAAGA | | |
| | | | TTT__ | | |
| GAM338 | EPM2A | 3' | AGAAAGAGAAGTGTTTT 1234 | TTTTA | |
| | | | AAAATAT TTCTCTTCT | | |
| | | | | | |
| | | | TTTTGTG AAGAGAAAGA | | |
| | | | _____ | | |
| GAM338 | HRH1 | 3' | AGAAAGAGAAATGAAATATTTT 780 | TA | |
| | | | AAAATATTTT TTCTCTTCT | | |
| | | | | | |
| | | | TTTTATAAAG AAGAGAAAGA | | |
| | | | TA | | |
| GAM338 | MAPK14 | 3' | GAGAAAGGGCAAATTATTTTA 818 | T TATT | |
| | | | TAAAATA TTT CTCTTTCTC | | |
| | | | | | |
| | | | ATTTTAT AAA GGGAAAGAG | | |
| | | | T C__ | | |
| GAM338 | MAPK14 | 3' | GAGAAAGGGCAAATTATTTTA 2465 | T TATT | |
| | | | TAAAATA TTT CTCTTTCTC | | |
| | | | | | |
| | | | ATTTTAT AAA GGGAAAGAG | | |
| | | | T C__ | | |
| GAM338 | MAPK14 | 3' | GAGAAAGGGCAAATTATTTTA 2466 | T TATT | |
| | | | TAAAATA TTT CTCTTTCTC | | |
| | | | | | |
| | | | ATTTTAT AAA GGGAAAGAG | | |
| | | | T C__ | | |
| GAM338 | NOTCH2 | 3' | GAGAATTAAAATATTTTA 2058 | T | |
| | | | TAAAATATTTT ATTCTC | | |
| | | | | | |
| | | | ATTTTATAAAA TAAGAG | | |
| | | | T | | |
| GAM338 | SIM1 | 3' | GAGAAAGAGAGAGATA 1181 | TAT | |
| | | | TATTTT TCTCTTCTC | | |
| | | | | | |
| | | | ATAGAG AGAGAAAGAG | | |
| | | | _____ | | |
| GAM338 | C11orf25 | 3' | AAAGAGAAAAATATTTTA 2193 | TAT | |
| | | | TAAAATATTTT TCTCTT | | |
| | | | | | |
| | | | ATTTTATAAAA AGAGAAA | | |
| | | | _____ | | |
| GAM338 | DKFZP564D116 | 3' | GAAAAGCAATAAAAATATTTTA 2938 | _ C | |
| | | | TAAAATATTTTATT CT TTTC | | |
| | | | | | |

ATTTTATAAAAATAA GA AAAG
 C _
 GAM338 DSCR6 3' GAGAAAGAGAAGGTCTATGTCA 1866 A TTTTA
 A ATAT TTCTCTTTCTC
 ||||| |||||
 A TGTA AAGAGAAAGAG
 C TCTGG
 GAM338 FLJ10006 3' GAGAAAGAAGATATTTTA 3152 A
 TAAAATATTTTT TTCTC
 ||||| |||||
 ATTTTATAGAAG AAGAG
 A
 GAM338 HTPAP 3' GAGAATAAAAAGATTTTA 2255 A
 TAAAAT TTTTATTCTC
 ||||| |||||
 ATTTTA AAAATAAGAG
 G
 GAM338 KIAA0979 3' AGAAAGATTTAAAGTATTTTA 1601 TATTC
 TAAAATATTTT TCTTTCT
 ||||| |||||
 ATTTTATGAAA AGAAAGA
 TTT_
 GAM338 KIAA1634 3' GAGAATAAAACTATTTTA 2657 T
 TAAAATA TTTTATTCTC
 ||||| |||||
 ATTTTAT AAAATAAGAG
 C
 GAM338 PTD012 3' GAGATTGGGAACAAAAATAT 1465 A TT
 ATATTTTT TTCTC TCTC
 ||||| |||||
 TATAAAAA AAGGG AGAG
 C TT
 GAM338 SAMHD1 3' AGAAAGAGAAAGAAATAT 2593 A
 ATATTTTT TTCTCTTTCT
 ||||| |||||
 TATAAAGA AAGAGAAAGA
 -
 GAM338 LOC196758 3' GAGAAAGAGCAGGTGAAATATT 3410 TATT_
 TT AAAATATTTT CTCTTTCTC
 ||||| |||||
 TTTTATAAAG GAGAAAGAG
 TGGAC
 GAM338 LOC219790 3' GAGAATAAAAATAATTTA 3520 A
 TAAA TATTTTTTATTCTC
 ||| |||||
 ATTT ATAAAAATAAGAG
 A
 GAM339 CAPN2 3' AAAACTTTATGAACTTCACCA 855 A _ AAA
 TG TGGAGT CGTAA AGTTTT
 || ||||| |||||

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|--------|-----------|----|-----------------------------|-----|-------|
| | | | AC ACTTCA GTATT TCAAAA | | |
| | | | C A _ | | |
| GAM339 | DAAM2 | 3' | AAAATTTTCTAAACTCCATC 3559 | CG | A |
| | A | | TGATGGAGT TA AAAAGTTTT | | |
| | | | | | |
| | | | ACTACCTCA AT TTTTAAAA | | |
| | | | AA C | | |
| GAM339 | SELE | 3' | AAACTCTCCTACACTTCCATT 747 | _ C | AAAA |
| | A | | TGATGGA GT GTA AGTTTT | | |
| | | | | | |
| | | | ATTACCT CA CAT TCAAAA | | |
| | | | T _ CCTC | | |
| GAM339 | KIAA0475 | 3' | AAAACCTTGCATTCCATCA 1570 | C | AAAA |
| | | | TGATGGAGT GTAA GTTTT | | |
| | | | | | |
| | | | ACTACCTTA CGTT CAAAA | | |
| | | | _ C _ | | |
| GAM339 | LOC222671 | 5' | GCTTCTACGACTCCGCCA 3582 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C _ | | |
| GAM339 | LOC254901 | 5' | AATTTCTTCACTGACTCCACCA 3699 | A | _ A A |
| | | | TG TGGAGTC GT AA AAGTT | | |
| | | | | | |
| | | | AC ACCTCAG CA TT TTAA | | |
| | | | C T C C | | |
| GAM339 | LOC257615 | 5' | GCTTCTACGACTCCGCCA 3749 | A | AAA |
| | | | TG TGGAGTCGTA AAGT | | |
| | | | | | |
| | | | AC GCCTCAGCAT TTCG | | |
| | | | C C _ | | |
| GAM340 | ADCY6 | 3' | TTGTACAATATTTTGTACAAAG 1617 | G | TTCAC |
| | A | | TCTTTG TACAAAAT ACAA | | |
| | | | | | |
| | | | AGAAAC ATGTTTTA TGTT | | |
| | | | _ TAACA | | |
| GAM340 | ADCY6 | 3' | TTGTACAATATTTTGTACAAAG 1933 | G | TTCAC |
| | A | | TCTTTG TACAAAAT ACAA | | |
| | | | | | |
| | | | AGAAAC ATGTTTTA TGTT | | |
| | | | _ TAACA | | |
| GAM340 | APBB2 | 5' | TGAGCTTTGTACCAAAGA 2946 | AT | |
| | | | TCTTTGGTACAAA TTCA | | |
| | | | | | |
| | | | AGAAACCATGTTT GAGT | | |
| | | | C _ | | |
| GAM340 | ATP8B2 | 3' | TGATTTTATACCAAAGA 2716 | C | TT |
| | | | TCTTTGGTA AAAA TCA | | |
| | | | | | |

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|--------|---------|----|-----------------------------|----------|
| | | | AGAAACCAT TTTT AGT | |
| | | | A T_ | |
| GAM340 | CEACAM1 | 3' | TGTGTGAACTAGCAAAGA 848 | G CAAAAT |
| | | | TCTTTG TA TTCACACA | |
| | | | | |
| | | | AGAAAC AT AAGTGTGT | |
| | | | G C_____ | |
| GAM340 | CHST1 | 3' | TGTGATATTTCTTTGTGCCAAA 1046 | ___ T |
| | | | TTTGGTACAAA AT TCACA | |
| | | | | |
| | | | AAACCGTGTTT TA AGTGT | |
| | | | CTT T | |
| GAM340 | FBXL7 | 3' | TGCGTGTTTTCCACCAAAGA 1425 | AC TTT A |
| | | | TCTTTGGT AAAA CAC CA | |
| | | | | |
| | | | AGAAACCA TTTT GTG GT | |
| | | | CC ___ C | |
| GAM340 | HOXC9 | 3' | TGCGTGCGAGATTTTGTAC 2592 | _ A |
| | | | GTACAAAATTT CAC CA | |
| | | | | |
| | | | CATGTTTTAGA GTG GT | |
| | | | C C | |
| GAM340 | IGF1 | 3' | TGTGGCATTGTACCAA 763 | ATT |
| | | | TTTGGTACAAA TCACA | |
| | | | | |
| | | | AAACCATGTTT GGTGT | |
| | | | AC_ | |
| GAM340 | ITGAL | 3' | TGTGAAATTCTGTCCAAA 907 | T A |
| | | | TTTGG ACA AATTCACA | |
| | | | | |
| | | | AAACC TGT TTAAAGTGT | |
| | | | _ C | |
| GAM340 | LBR | 3' | TGTACTGGATTGCACCAAGGA 2522 | A AAT C_ |
| | | | TCTTTGGT CAA TTCA ACA | |
| | | | | |
| | | | AGGAACCA GTT AGGT TGT | |
| | | | C ___ CA | |
| GAM340 | MIP | 3' | TGTGTGAAATCTTTCAAG 1399 | TACAAA |
| | | | TTTGG ATTCACACA | |
| | | | | |
| | | | GAACT TAAAGTGTGT | |
| | | | TTC_____ | |
| GAM340 | RLN2 | 3' | TGTTGGTTGTACCAA 1175 | AATT C |
| | | | TTTGGTACAA TCA ACA | |
| | | | | |
| | | | AAACCATGTT GGT TGT | |
| | | | _____ | |
| GAM340 | SART2 | 3' | TGATTTTCATACCAAAGA 1444 | CA TT |
| | | | TCTTTGGTA AAA TCA | |
| | | | | |

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|--------|----------|----|-----------------------------|------------|
| | | | AGAAACCAT TTT AGT | |
| | | | AC T_ | |
| GAM340 | TPK1 | 3' | AAATTTTGCTACCAAAGA 1987 | _ |
| | | | TCTTTGGTA CAAAATT | |
| | | | | |
| | | | AGAAACCAT GTTTTAAA | |
| | | | C | |
| GAM340 | TRIP12 | 3' | TGTGTGAAATTTAAAAAAGG 1094 | GGTACA |
| | | | TCTTT AAATTTACACACA | |
| | | | | |
| | | | GGAAA TTAAAGTGTGT | |
| | | | AAA__ | |
| GAM340 | BRD3 | 3' | GTGTGAGATTCGTACCGAAGA 1398 | AA |
| | | | TCTTTGGTAC AATTTACAC | |
| | | | | |
| | | | AGAAGCCATG TTAGAGTGTG | |
| | | | C_ | |
| GAM340 | FLJ13397 | 3' | GTGTGAAATTTACTAGCAAA 2116 | G CA |
| | | | TTTG TA AAATTTACAC | |
| | | | | |
| | | | AAAC AT TTAAAGTGTG | |
| | | | G CA | |
| GAM340 | FLJ22202 | 3' | TGTATCATTTTGTACCAA 2103 | TTC |
| | | | TTTGGTACAAAAT ACA | |
| | | | | |
| | | | AAACCATGTTTTA TGT | |
| | | | CTA | |
| GAM340 | GROS1 | 3' | TGTGTAGACAACCAAAGA 1986 | ACAAAATT _ |
| | | | TCTTTGGT TC ACACA | |
| | | | | |
| | | | AGAAACCA AG TGTGT | |
| | | | AC_____ A | |
| GAM340 | KIAA0981 | 3' | TGTGTAAAACTGCCAAGGA 2598 | CAAAA C |
| | | | TCTTTGGTA TTT ACACA | |
| | | | | |
| | | | AGGAACCGT AAA TGTGT | |
| | | | C_____ A | |
| GAM340 | KIAA1243 | 3' | TGTGACATGACCAAAGA 2978 | A AAATT |
| | | | TCTTTGGT CA TCACA | |
| | | | | |
| | | | AGAAACCA GT AGTGT | |
| | | | _ AC__ | |
| GAM340 | KIAA1462 | 3' | TTGTGTGAGAGGAACCCAAAGA 3524 | TACAAAA |
| | | | TCTTTGG TTTCACACAA | |
| | | | | |
| | | | AGAAACC AGAGTGTGTT | |
| | | | CAAGG__ | |
| GAM340 | MGC1136 | 3' | TTGTGTGAAACCCCTAGCATAG 2041 | T G CAAAA |
| | A | | TCT TG TA TTTCACACAA | |
| | | | | |

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|--------|-----------|----|-----------------------------|--------|------|
| | | | AGA AC AT AAAGTGTGTT | | |
| | | | T G CCCC_ | | |
| GAM340 | MSTP043 | 3' | TGTCTTTATTTTTACCAAAGA 2223 | C | TTC_ |
| | | | TCTTTGGTA AAAAT ACA | | |
| | | | | | |
| | | | AGAAACCAT TTTTA TGT | | |
| | | | _ TTTC | | |
| GAM340 | Nup43 | 3' | TGTGCAAAATTTTAGTATCAGA 2075 | _ | CA |
| | | | TTTGGTAC AAAATTT CACA | | |
| | | | | | |
| | | | AGACTATG TTTTAAA GTGT | | |
| | | | A AC | | |
| GAM340 | RPS6KA4 | 3' | TGTGCAATTACGTCCACCAAAG 1072 | _ | AA T |
| | A | | TCTTTGGT AC AATT CACA | | |
| | | | | | |
| | | | AGAAACCA TG TTAA GTGT | | |
| | | | CC CA C | | |
| GAM340 | SLC17A6 | 3' | TGAAACTTGTGCCACAGA 1911 | T | AA |
| | | | TCT TGGTACAA TTTCA | | |
| | | | | | |
| | | | AGA ACCGTGTT AAAGT | | |
| | | | C C_ | | |
| GAM340 | TERA | 3' | TGTATGAATAGTACCAAAG 1949 | AAAAT | C |
| | | | CTTTGGTAC TTCA ACA | | |
| | | | | | |
| | | | GAAACCATG AAGT TGT | | |
| | | | AT_ A | | |
| GAM340 | VAV3 | 3' | TTGTGTAGAGTTCTAATACCAA 1273 | CAA_ | TC |
| | AGA | | TCTTTGGTA AATT ACACAA | | |
| | | | | | |
| | | | AGAAACCAT TTGA TGTGTT | | |
| | | | AATC GA | | |
| GAM340 | LOC120892 | 3' | TGCAATTTTTTTTACCAAAGA 2987 | C_ | T |
| | | | TCTTTGGTA AAAATT CA | | |
| | | | | | |
| | | | AGAAACCAT TTTTAA GT | | |
| | | | TTT C | | |
| GAM340 | LOC155434 | 3' | TTGTGTGATTCGTACCAAA 3376 | A | TT |
| | | | TTTGGTAC AAA TCACACAA | | |
| | | | | | |
| | | | AAACCATG TTT AGTGTGTT | | |
| | | | C _ | | |
| GAM340 | LOC169966 | 3' | ATTTTGCCCTTTACCAAAGA 3252 | _____ | |
| | | | TCTTTGGTA CAAAAT | | |
| | | | | | |
| | | | AGAAACCAT GTTTTA | | |
| | | | TTCC | | |
| GAM340 | LOC221272 | 3' | TGTCTGCTCTGTACCAGAGA 3616 | AAATTT | C |
| | | | TCTTTGGTACA CA ACA | | |
| | | | | | |

AGAGACCATGT GT TGT
 CTC__ C
 GAM340 LOC221968 3' TTGTGTGAAATTTTGTGCGAA 3569 GT
 TTTG ACAAATTTTCACACAA
 ||| |||||
 AAGC TGTTTTAAAGTGTGTT

 GAM340 LOC86651 5' TTGTGTGAAAGATGTTTCATAC 2830 CA ____
 CAAGGA CTTTGGTA AAAT TTCACACAA
 ||||| ||| |||||
 GGAACCAT TTTG AAGTGTGTT
 AC TAGA
 GAM340 LOC90322 3' GAGATTCCATACTAAAGA 2632 CAA
 TCTTTGGTA AATTTC
 ||||| |||||
 AGAAATCAT TTAGAG
 ACC
 GAM341 MYO1E 5' ATGGAGTCCCCTCTAGGGTT 1168 ATC A A
 GACC GA GG GACTCCAT
 ||| ||| |||||
 TTGG CT CC CTGAGGTA
 GAT C _
 GAM341 ROCK2 3' ATGAAGTCTTTTAACAGTCTC 2737 CATCGA C
 GAGAC AGGAGACT CAT
 |||| ||||| |||
 CTCTG TTTTCTGA GTA
 ACAA__ A
 GAM341 MGC15937 5' GAGTTTCTTCTTCAAGGTCTCA 2383 ATC ____
 TGAGACC GAAGGAGA CTC
 ||||| ||||| |||
 ACTCTGG CTTCTTCT GAG
 AA_ TT
 GAM341 STK16 5' GAGCTCTTCGGTAGCCTCA 2937 ACC G A
 TGAG ATCGAAG AG CTC
 ||| ||||| |||
 ACTC TGGCTTC TC GAG
 CGA _ _
 GAM341 LOC148029 5' GGAGTCTCCATCCTCA 3116 ACCATC A
 TGAG GA GGAGACTCC
 ||| ||| |||||
 ACTC CT CCTCTGAGG
 ____ A
 GAM341 LOC169436 5' TGGAGTTCAATGAGCTCA 3261 AC C AGGAG
 TGAG CAT GA ACTCCA
 ||| ||| ||| |||||
 ACTC GTA CT TGAGGT
 GA A ____
 GAM341 LOC256267 3' ATGGAGTCTCCCTCTGTC 3713 CATC A
 GAC GA GGAGACTCCAT
 ||| ||| |||||

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|--------|--------------|----|-----------------------------|------|----|
| | | | CTG CT CCTCTGAGGTA | | |
| | | | T__ C | | |
| GAM341 | LOC257426 | 3' | GAGTCCTTCGGTGGCCTCA 2755 | A | GA |
| | | | TGAG CCATCGAAGGA CTC | | |
| | | | | | |
| | | | ACTC GGTGGCTTCCT GAG | | |
| | | | C _ | | |
| GAM341 | LOC92466 | 3' | ATGGAGTCTCCCTCTGTC 2858 | CATC | A |
| | | | GAC GA GGAGACTCCAT | | |
| | | | | | |
| | | | CTG CT CCTCTGAGGTA | | |
| | | | T__ C | | |
| GAM342 | MME | 3' | AAAAAAAGTTACAGAAATA 785 | AA | |
| | | | TATTTTGTGTA ACTTTTTTT | | |
| | | | | | |
| | | | ATAAAGACAT TGAAAAAAA | | |
| | | | _ | | |
| GAM342 | MME | 3' | AAAAAAAGTTACAGAAATA 1377 | AA | |
| | | | TATTTTGTGTA ACTTTTTTT | | |
| | | | | | |
| | | | ATAAAGACAT TGAAAAAAA | | |
| | | | _ | | |
| GAM342 | MME | 3' | AAAAAAAGTTACAGAAATA 1378 | AA | |
| | | | TATTTTGTGTA ACTTTTTTT | | |
| | | | | | |
| | | | ATAAAGACAT TGAAAAAAA | | |
| | | | _ | | |
| GAM342 | MME | 3' | AAAAAAAGTTACAGAAATA 1379 | AA | |
| | | | TATTTTGTGTA ACTTTTTTT | | |
| | | | | | |
| | | | ATAAAGACAT TGAAAAAAA | | |
| | | | _ | | |
| GAM342 | DKFZP434C212 | 3' | AAAAAGTACACAGAAATATT 2832 | AAA | |
| | | | AATATTTTGT ACTTTTT | | |
| | | | | | |
| | | | TTATAAAGACA TGAAAAA | | |
| | | | CA_ | | |
| GAM342 | FLJ11275 | 3' | TAAAATGGGATTTATAAAAATA 1821 | A | TT |
| | | TT | AATATTTTGTAAA CT TTTTA | | |
| | | | | | |
| | | | TTATAAAAATATTT GG AAAAT | | |
| | | | A GT | | |
| GAM342 | GOLPH3 | 3' | TAAAAAAGTTTTACTGCCATA 1981 | TTTT | |
| | | TT | AATAT GTAAACTTTTTTTA | | |
| | | | | | |
| | | | TTATA CATTTTGAAAAAAT | | |
| | | | CCGT | | |
| GAM342 | KIAA0563 | 5' | TAAAAAAGGAGCAAAAGTAT 1565 | AAAA | |
| | | | ATATTTTGT CTTTTTTA | | |
| | | | | | |

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|--------|--------------|----|---------------------------|------|
| | | | TATGAAAACG GAAAAAAAT | |
| | | | AG__ | |
| GAM342 | TAF2 | 3' | AGAAAGTTTGACAAAAATA 997 | A |
| | | | TATTTTTGT AAACTTTT | |
| | | | | |
| | | | ATAAAAACA TTTGAAAGA | |
| | | | G | |
| GAM342 | LOC147071 | 5' | TAAAAAAGGAGCAAAAGTAT 2965 | AAAA |
| | | | ATATTTTTGT CTTTTTTA | |
| | | | | |
| | | | TATGAAAACG GAAAAAAAT | |
| | | | AG__ | |
| GAM342 | LOC147639 | 5' | AAAAGTGCTGCAAAATATT 3110 | AA |
| | | | AATATTTTTGTA ACTTTT | |
| | | | | |
| | | | TTATAAAAACGT TGAAAA | |
| | | | CG | |
| GAM342 | LOC201173 | 5' | TAAAAAAGGAGCAAAAGTAT 3405 | AAAA |
| | | | ATATTTTTGT CTTTTTTA | |
| | | | | |
| | | | TATGAAAACG GAAAAAAAT | |
| | | | AG__ | |
| GAM342 | LOC201220 | 5' | TAAAAAAGGAGCAAAAGTAT 3406 | AAAA |
| | | | ATATTTTTGT CTTTTTTA | |
| | | | | |
| | | | TATGAAAACG GAAAAAAAT | |
| | | | AG__ | |
| GAM343 | MME | 3' | AAAAAAAGTTACAGAAATA 785 | AA |
| | | | TATTTTTGTA ACTTTTTT | |
| | | | | |
| | | | ATAAAGACAT TGAAAAAAA | |
| | | | — | |
| GAM343 | MME | 3' | AAAAAAAGTTACAGAAATA 1377 | AA |
| | | | TATTTTTGTA ACTTTTTT | |
| | | | | |
| | | | ATAAAGACAT TGAAAAAAA | |
| | | | — | |
| GAM343 | MME | 3' | AAAAAAAGTTACAGAAATA 1378 | AA |
| | | | TATTTTTGTA ACTTTTTT | |
| | | | | |
| | | | ATAAAGACAT TGAAAAAAA | |
| | | | — | |
| GAM343 | MME | 3' | AAAAAAAGTTACAGAAATA 1379 | AA |
| | | | TATTTTTGTA ACTTTTTT | |
| | | | | |
| | | | ATAAAGACAT TGAAAAAAA | |
| | | | — | |
| GAM343 | DKFZP434C212 | 3' | AAAAAGTACACAGAAATATT 2832 | AAA |
| | | | AATATTTTTGT ACTTTT | |
| | | | | |

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|--------|-----------|----|-----------------------------|------|-----|
| | | | TTATAAAGACA TGAAAAA | | |
| | | | CA_ | | |
| GAM343 | FLJ11275 | 3' | TAAAATGGGATTTATAAAAATA 1821 | A | TT |
| | | TT | AATATTTTTGTAAA CT TTTTA | | |
| | | | | | |
| | | | TTATAAAAATATTT GG AAAAT | | |
| | | | A GT | | |
| GAM343 | GOLPH3 | 3' | TAAAAAAGTTTTACTGCCATA 1981 | TTTT | |
| | | TT | AATAT GTAAACTTTTTTTA | | |
| | | | | | |
| | | | TTATA CATTTTGAAAAAAT | | |
| | | | CCGT | | |
| GAM343 | KIAA0563 | 5' | TAAAAAAGGAGCAAAAGTAT 1565 | AAAA | |
| | | | ATATTTTGT CTTTTTTA | | |
| | | | | | |
| | | | TATGAAAACG GAAAAAAT | | |
| | | | AG_ | | |
| GAM343 | TAF2 | 3' | AGAAAGTTTGACAAAATA 997 | A | |
| | | | TATTTTGT AAACTTTT | | |
| | | | | | |
| | | | ATAAAAACA TTTGAAAGA | | |
| | | | G | | |
| GAM343 | LOC147071 | 5' | TAAAAAAGGAGCAAAAGTAT 2965 | AAAA | |
| | | | ATATTTTGT CTTTTTTA | | |
| | | | | | |
| | | | TATGAAAACG GAAAAAAT | | |
| | | | AG_ | | |
| GAM343 | LOC147639 | 5' | AAAAGTGCTGCAAAAATATT 3110 | AA | |
| | | | AATATTTTGTACTTTT | | |
| | | | | | |
| | | | TTATAAAAACGT TGAAAA | | |
| | | | CG | | |
| GAM343 | LOC201173 | 5' | TAAAAAAGGAGCAAAAGTAT 3405 | AAAA | |
| | | | ATATTTTGT CTTTTTTA | | |
| | | | | | |
| | | | TATGAAAACG GAAAAAAT | | |
| | | | AG_ | | |
| GAM343 | LOC201220 | 5' | TAAAAAAGGAGCAAAAGTAT 3406 | AAAA | |
| | | | ATATTTTGT CTTTTTTA | | |
| | | | | | |
| | | | TATGAAAACG GAAAAAAT | | |
| | | | AG_ | | |
| GAM344 | MARK1 | 3' | TATAATAAACATGATTGCTTA 1857 | TA | TAC |
| | | A | TTA CGATC GTTTATTATA | | |
| | | | | | |
| | | | AAT GTTAG CAAAATAATAT | | |
| | | | TC TA_ | | |
| GAM345 | DKK1 | 3' | AAAATACTAGCTTATTTTCTGA 1417 | _ | TAA |
| | | | TCAGAAAG AGGTT TATTTT | | |
| | | | | | |


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AGTCTTTT TTCGA ATAAAA
A TC_
GAM345 KERA 3' AAAATATTGAATGCTTTCT 1349 AG
AGAAAG GTTTAATATTTT
||||| |||||||||
TCTTTC TAAGTTATAAAA
G_
GAM345 PPP1R12A 3' AAAATACTACATCTTTCTGG 931 G TTAA
TCAGAAAGA GT TATTTT
||||||| || |||||
GGTCTTTCT CA ATAAAA
A TC__
GAM345 S100B 3' AAAATTGAAAACCTCTTTC 1284 AAT
GAAAGAGGTTT ATTTT
||||||| |||||
CTTTCTCCAAA TAAAA
AGT
GAM345 DKFZP564I0422 3' AAAATATTGCATTCTTCTGAT 2196 A GTT
ATCAGAA GAG TAATATTTT
||||| ||| |||||||
TAGTCTT CTT GTTATAAAA
_ AC_
GAM345 EML4 3' AAAATGTTTCCTCTTTCT 1876 TTT
AGAAAGAGG AATATTTT
||||||| |||||||
TCTTTCTCC TTGTAAAA
T__
GAM345 FLJ21657 3' AAAATATTTTACTCTGCCTGAT 1990 AA GTTT
ATCAG AGAG AATATTTT
|||| ||| |||||||
TAGTC TCTC TTATAAAA
CG ATT_
GAM345 KIAA1054 3' AAAATGGTACCTCTTTC 2820 TTAA
GAAAGAGGT TATTTT
||||||| |||||
CTTTCTCCA GTAAAA
TG__
GAM345 SEMA3E 5' AAAATACAGCTTCTTCCTGA 1431 A TAA
TCAG AAGAGGTT TATTTT
||| ||||||| |||||
AGTC TTCTTCGA ATAAAA
C C__
GAM345 LOC130507 3' AAAATATTAAGATAACTTTCTG 3011 AGG_
CAGAAAG TTTAATATTTT
||||| |||||||||
GTCTTTC GAATTATAAAA
ATA
GAM345 LOC148145 5' AAAATATTAAACCTGGACCTGA 3296 AAAG
T ATCAG AGGTTTAATATTTT
||||| |||||||||

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| | | TAGTC TCCAAATTATAAAA | | | |
|--------|---------------|-----------------------|-----------------------------|------|------|
| | | CAGG | | | |
| GAM346 | DKK1 | 3' | AAAATACTAGCTTATTTTCTGA 1417 | _ | TAA |
| | | TCAGAAAG AGGTT TATTTT | | | |
| | | | | | |
| | | AGTCTTTT TTCGA ATAAAA | | | |
| | | A TC_ | | | |
| GAM346 | KERA | 3' | AAAATATTGAATGCTTTCT 1349 | AG | |
| | | AGAAAG GTTTAATATTTT | | | |
| | | | | | |
| | | TCTTTC TAAGTTATAAAA | | | |
| | | G_ | | | |
| GAM346 | PPP1R12A | 3' | AAAATACTACATCTTTCTGG 931 | G | TTAA |
| | | TCAGAAAGA GT TATTTT | | | |
| | | | | | |
| | | GGTCTTTCT CA ATAAAA | | | |
| | | A TC_ | | | |
| GAM346 | S100B | 3' | AAAATTGAAAACCTCTTTC 1284 | AAT | |
| | | GAAAGAGGTTT ATTTT | | | |
| | | | | | |
| | | CTTTCTCCAAA TAAAA | | | |
| | | AGT | | | |
| GAM346 | DKFZP564I0422 | 3' | AAAATATTGCATTCTTCTGAT 2196 | A | GTT |
| | | ATCAGAA GAG TAATATTTT | | | |
| | | | | | |
| | | TAGTCTT CTT GTTATAAAA | | | |
| | | _ AC_ | | | |
| GAM346 | EML4 | 3' | AAAATGTTTCCTCTTTCT 1876 | TTT | |
| | | AGAAAGAGG AATATTTT | | | |
| | | | | | |
| | | TCTTTCTCC TTGTAAAA | | | |
| | | T_ | | | |
| GAM346 | FLJ21657 | 3' | AAAATATTTTACTCTGCCTGAT 1990 | AA | GTTT |
| | | ATCAG AGAG AATATTTT | | | |
| | | | | | |
| | | TAGTC TCTC TTATAAAA | | | |
| | | CG ATT_ | | | |
| GAM346 | KIAA1054 | 3' | AAAATGGTACCTCTTTC 2820 | TTAA | |
| | | GAAAGAGGT TATTTT | | | |
| | | | | | |
| | | CTTTCTCCA GTAAAA | | | |
| | | TG_ | | | |
| GAM346 | SEMA3E | 5' | AAAATACAGCTTCTTCCTGA 1431 | A | TAA |
| | | TCAG AAGAGGTT TATTTT | | | |
| | | | | | |
| | | AGTC TTCTTCGA ATAAAA | | | |
| | | C C_ | | | |
| GAM346 | LOC130507 | 3' | AAAATATTAAGATAACTTTCTG 3011 | AGG_ | |
| | | CAGAAAG TTTAATATTTT | | | |
| | | | | | |

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|--------|---------------|----|------------------------|------|---------|
| | | | GTCTTTC GAATTATAAAA | | |
| | | | AATA | | |
| GAM346 | LOC148145 | 5' | AAAATATTAAACCTGGACCTGA | 3296 | AAAG |
| | | T | ATCAG AGGTTTAATATTTT | | |
| | | | | | |
| | | | TAGTC TCCAAATTATAAAA | | |
| | | | CAGG | | |
| GAM347 | DKK1 | 3' | AAAATACTAGCTTATTTTCTGA | 1417 | _ TAA |
| | | | TCAGAAAG AGGTT TATTTT | | |
| | | | | | |
| | | | AGTCTTTT TTCGA ATAAAA | | |
| | | | A TC_ | | |
| GAM347 | KERA | 3' | AAAATATTGAATGCTTTCT | 1349 | AG |
| | | | AGAAAG GTTTAATATTTT | | |
| | | | | | |
| | | | TCTTTC TAAGTTATAAAA | | |
| | | | G_ | | |
| GAM347 | PPP1R12A | 3' | AAAATACTACATCTTTCTGG | 931 | G TTAA |
| | | | TCAGAAAGA GT TATTTT | | |
| | | | | | |
| | | | GGTCTTTCT CA ATAAAA | | |
| | | | A TC__ | | |
| GAM347 | S100B | 3' | AAAATTGAAAACCTCTTTC | 1284 | AAT |
| | | | GAAAGAGGTTT ATTTT | | |
| | | | | | |
| | | | CTTTCTCCAAA TAAAA | | |
| | | | AGT | | |
| GAM347 | DKFZP564I0422 | 3' | AAAATATTGCATTCTTCTGAT | 2196 | A GTT |
| | | | ATCAGAA GAG TAATATTTT | | |
| | | | | | |
| | | | TAGTCTT CTT GTTATAAAA | | |
| | | | _ AC_ | | |
| GAM347 | EML4 | 3' | AAAATGTTTCCTCTTTCT | 1876 | TTT |
| | | | AGAAAGAGG AATATTTT | | |
| | | | | | |
| | | | TCTTTCTCC TTGTAAAA | | |
| | | | T_ | | |
| GAM347 | FLJ21657 | 3' | AAAATATTTTACTCTGCCTGAT | 1990 | AA GTTT |
| | | | ATCAG AGAG AATATTTT | | |
| | | | | | |
| | | | TAGTC TCTC TTATAAAA | | |
| | | | CG ATT_ | | |
| GAM347 | KIAA1054 | 3' | AAAATGGTACCTCTTTC | 2820 | TTAA |
| | | | GAAAGAGGT TATTTT | | |
| | | | | | |
| | | | CTTTCTCCA GTAAAA | | |
| | | | TG_ | | |
| GAM347 | SEMA3E | 5' | AAAATACAGCTTCTTCCTGA | 1431 | A TAA |
| | | | TCAG AAGAGGT TATTTT | | |
| | | | | | |

| | | | |
|--------|------------------|-----------------------------|---------|
| | | AGTC TTCTTCGA ATAAAA | |
| | | C C__ | |
| GAM347 | LOC130507 3' | AAAATATTAAGATACTTTCTG 3011 | AGG_ |
| | | CAGAAAG TTTAATATTTT | |
| | | | |
| | | GTCTTTC GAATTATAAAA | |
| | | AATA | |
| GAM347 | LOC148145 5' | AAAATATTAAACCTGGACCTGA 3296 | AAAG |
| | T | ATCAG AGGTTTAATATTTT | |
| | | | |
| | | TAGTC TCCAAATTATAAAA | |
| | | CAGG | |
| GAM348 | DKK1 3' | AAAATACTAGCTTATTTTCTGA 1417 | _ TAA |
| | | TCAGAAAG AGGTT TATTTT | |
| | | | |
| | | AGTCTTTT TTCGA ATAAAA | |
| | | A TC_ | |
| GAM348 | KERA 3' | AAAATATTGAATGCTTTCT 1349 | AG |
| | | AGAAAG GTTTAATATTTT | |
| | | | |
| | | TCTTTC TAAGTTATAAAA | |
| | | G_ | |
| GAM348 | PPP1R12A 3' | AAAATACTACATCTTTCTGG 931 | G TTAA |
| | | TCAGAAAGA GT TATTTT | |
| | | | |
| | | GGTCTTTCT CA ATAAAA | |
| | | A TC__ | |
| GAM348 | S100B 3' | AAAATTGAAAACCTCTTTC 1284 | AAT |
| | | GAAAGAGGTTT ATTTT | |
| | | | |
| | | CTTTCTCCAAA TAAAA | |
| | | AGT | |
| GAM348 | DKFZP564I0422 3' | AAAATATTGCATTCTTCTGAT 2196 | A GTT |
| | | ATCAGAA GAG TAATATTTT | |
| | | | |
| | | TAGTCTT CTT GTTATAAAA | |
| | | _ AC_ | |
| GAM348 | EML4 3' | AAAATGTTTCCTCTTTCT 1876 | TTT |
| | | AGAAAGAGG AATATTTT | |
| | | | |
| | | TCTTTCTCC TTGTAAAA | |
| | | T__ | |
| GAM348 | FLJ21657 3' | AAAATATTTTACTCTGCCTGAT 1990 | AA GTTT |
| | | ATCAG AGAG AATATTTT | |
| | | | |
| | | TAGTC TCTC TTATAAAA | |
| | | CG ATT_ | |
| GAM348 | KIAA1054 3' | AAAATGGTACCTCTTTC 2820 | TTAA |
| | | GAAAGAGGT TATTTT | |
| | | | |

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|--------|---------------|----|------------------------|--------|---------|-----|
| | | | CTTTCTCCA | GTAAAA | | |
| | | | TG__ | | | |
| GAM348 | SEMA3E | 5' | AAAATACAGCTTCTTCCTGA | 1431 | A | TAA |
| | | | TCAG AAGAGGTT TATTTT | | | |
| | | | | | | |
| | | | AGTC TTCTTCGA ATAAAA | | | |
| | | | C C__ | | | |
| GAM348 | LOC130507 | 3' | AAAATATTAAGATAACTTTCTG | 3011 | AGG_ | |
| | | | CAGAAAG TTTAATATTTT | | | |
| | | | | | | |
| | | | GTCTTTC GAATTATAAAA | | | |
| | | | AATA | | | |
| GAM348 | LOC148145 | 5' | AAAATATTAACCTGGACCTGA | 3296 | AAAG | |
| | | T | ATCAG AGGTTTAATATTTT | | | |
| | | | | | | |
| | | | TAGTC TCCAAATTATAAAA | | | |
| | | | CAGG | | | |
| GAM349 | DKK1 | 3' | AAAATACTAGCTTATTTTCTGA | 1417 | _ TAA | |
| | | | TCAGAAAG AGGTT TATTTT | | | |
| | | | | | | |
| | | | AGTCTTTT TTCGA ATAAAA | | | |
| | | | A TC_ | | | |
| GAM349 | KERA | 3' | AAAATATTGAATGCTTTCT | 1349 | AG | |
| | | | AGAAAG GTTTAATATTTT | | | |
| | | | | | | |
| | | | TCTTTC TAAGTTATAAAA | | | |
| | | | G_ | | | |
| GAM349 | PPP1R12A | 3' | AAAATACTACATCTTTCTGG | 931 | G TTAA | |
| | | | TCAGAAAGA GT TATTTT | | | |
| | | | | | | |
| | | | GGTCTTTCT CA ATAAAA | | | |
| | | | A TC__ | | | |
| GAM349 | S100B | 3' | AAAATTGAAAACCTCTTTC | 1284 | AAT | |
| | | | GAAAGAGGTTT ATTTT | | | |
| | | | | | | |
| | | | CTTTCTCCAAA TAAAA | | | |
| | | | AGT | | | |
| GAM349 | DKFZP564I0422 | 3' | AAAATATTGCATTCTTCTGAT | 2196 | A GTT | |
| | | | ATCAGAA GAG TAATATTTT | | | |
| | | | | | | |
| | | | TAGTCTT CTT GTTATAAAA | | | |
| | | | _ AC_ | | | |
| GAM349 | EML4 | 3' | AAAATGTTTCCTCTTTCT | 1876 | TTT | |
| | | | AGAAAGAGG AATATTTT | | | |
| | | | | | | |
| | | | TCTTTCTCC TTGTAAAA | | | |
| | | | T__ | | | |
| GAM349 | FLJ21657 | 3' | AAAATATTTTACTCTGCCTGAT | 1990 | AA GTTT | |
| | | | ATCAG AGAG AATATTTT | | | |
| | | | | | | |

| | | | | | | | |
|--------|---------------|----|-------------------------|------------|----------|--------|--|
| | | | | TAGTC TCTC | TTATAAAA | | |
| | | | | CG ATT_ | | | |
| GAM349 | KIAA1054 | 3' | AAAATGGTACCTCTTTC | 2820 | | TTAA | |
| | | | GAAAGAGGT TATTTT | | | | |
| | | | | | | | |
| | | | CTTTCTCCA GTAAAA | | | | |
| | | | TG__ | | | | |
| GAM349 | SEMA3E | 5' | AAAATACAGCTTCTTCCTGA | 1431 | A | TAA | |
| | | | TCAG AAGAGGTT TATTTT | | | | |
| | | | | | | | |
| | | | AGTC TTCTTCGA ATAAAA | | | | |
| | | | C C__ | | | | |
| GAM349 | LOC130507 | 3' | AAAATATTAAGATAACTTTTCTG | 3011 | | AGG_ | |
| | | | CAGAAAG TTTAATATTTT | | | | |
| | | | | | | | |
| | | | GTCTTTC GAATTATAAAA | | | | |
| | | | AATA | | | | |
| GAM349 | LOC148145 | 5' | AAAATATTAACCTGGACCTGA | 3296 | | AAAG | |
| | | T | ATCAG AGGTTTAATATTTT | | | | |
| | | | | | | | |
| | | | TAGTC TCCAAATTATAAAA | | | | |
| | | | CAGG | | | | |
| GAM350 | DKK1 | 3' | AAAATACTAGCTTATTTTCTGA | 1417 | _ | TAA | |
| | | | TCAGAAAG AGGTT TATTTT | | | | |
| | | | | | | | |
| | | | AGTCTTTT TTCGA ATAAAA | | | | |
| | | | A TC_ | | | | |
| GAM350 | KERA | 3' | AAAATATTGAATGCTTTCT | 1349 | AG | | |
| | | | AGAAAG GTTTAATATTTT | | | | |
| | | | | | | | |
| | | | TCTTTC TAAGTTATAAAA | | | | |
| | | | G_ | | | | |
| GAM350 | PPP1R12A | 3' | AAAATACTACATCTTTCTGG | 931 | | G TTAA | |
| | | | TCAGAAAGA GT TATTTT | | | | |
| | | | | | | | |
| | | | GGTCTTTCT CA ATAAAA | | | | |
| | | | A TC__ | | | | |
| GAM350 | S100B | 3' | AAAATTGAAAACCTCTTTC | 1284 | | AAT | |
| | | | GAAAGAGGTTT ATTTT | | | | |
| | | | | | | | |
| | | | CTTTCTCCAAA TAAAA | | | | |
| | | | AGT | | | | |
| GAM350 | DKFZP564I0422 | 3' | AAAATATTGCATTCTTCTGAT | 2196 | | A GTT | |
| | | | ATCAGAA GAG TAATATTTT | | | | |
| | | | | | | | |
| | | | TAGTCTT CTT GTTATAAAA | | | | |
| | | | _ AC_ | | | | |
| GAM350 | EML4 | 3' | AAAATGTTTTCTCTTTCT | 1876 | | TTT | |
| | | | AGAAAGAGG AATATTTT | | | | |
| | | | | | | | |

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|--------|------------------|-----------------------------|------|------|
| | | TCTTTCTCC TTGTA AAA | | |
| | | T__ | | |
| GAM350 | FLJ21657 3' | AAAATATTTTACTCTGCCTGAT 1990 | AA | GTTT |
| | | ATCAG AGAG AATATTTT | | |
| | | | | |
| | | TAGTC TCTC TTATAAAA | | |
| | | CG ATT_ | | |
| GAM350 | KIAA1054 3' | AAAATGGTACCTCTTTC 2820 | TTAA | |
| | | GAAAGAGGT TATTTT | | |
| | | | | |
| | | CTTTCTCCA GTAAAA | | |
| | | TG__ | | |
| GAM350 | SEMA3E 5' | AAAATACAGCTTCTTCCTGA 1431 | A | TAA |
| | | TCAG AAGAGGT TATTTT | | |
| | | | | |
| | | AGTC TTCTTCGA ATAAAA | | |
| | | C C__ | | |
| GAM350 | LOC130507 3' | AAAATATTAAGATAACTTTCTG 3011 | AGG_ | |
| | | CAGAAAG TTTAATATTTT | | |
| | | | | |
| | | GTCTTTC GAATTATAAAA | | |
| | | AATA | | |
| GAM350 | LOC148145 5' | AAAATATTAAACCTGGACCTGA 3296 | AAAG | |
| | T | ATCAG AGGTTTAATATTTT | | |
| | | | | |
| | | TAGTC TCCAAATTATAAAA | | |
| | | CAGG | | |
| GAM351 | DKK1 3' | AAAATACTAGCTTATTTTCTGA 1417 | _ | TAA |
| | | TCAGAAAG AGGTT TATTTT | | |
| | | | | |
| | | AGTCTTTT TTCGA ATAAAA | | |
| | | A TC_ | | |
| GAM351 | KERA 3' | AAAATATTGAATGCTTTCT 1349 | AG | |
| | | AGAAAG GTTTAATATTTT | | |
| | | | | |
| | | TCTTTC TAAGTTATAAAA | | |
| | | G_ | | |
| GAM351 | PPP1R12A 3' | AAAATACTACATCTTTCTGG 931 | G | TTAA |
| | | TCAGAAAGA GT TATTTT | | |
| | | | | |
| | | GGTCTTTCT CA ATAAAA | | |
| | | A TC__ | | |
| GAM351 | S100B 3' | AAAATTGAAAACCTCTTTC 1284 | AAT | |
| | | GAAAGAGGTTT ATTTT | | |
| | | | | |
| | | CTTTCTCCAAA TAAAA | | |
| | | AGT | | |
| GAM351 | DKFZP564I0422 3' | AAAATATTGCATTCTTCTGAT 2196 | A | GTT |
| | | ATCAGAA GAG TAATATTTT | | |
| | | | | |

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|--------|-----------|----|-----------------------------|---------|
| | | | TAGTCTT CTT GTTATAAAA | |
| | | | _ AC_ | |
| GAM351 | EML4 | 3' | AAAATGTTTCCTCTTTCT 1876 | TTT |
| | | | AGAAAGAGG AATATTTT | |
| | | | | |
| | | | TCTTTCTCC TTGTAAAA | |
| | | | T__ | |
| GAM351 | FLJ21657 | 3' | AAAATATTTTACTCTGCCTGAT 1990 | AA GTTT |
| | | | ATCAG AGAG AATATTTT | |
| | | | | |
| | | | TAGTC TCTC TTATAAAA | |
| | | | CG ATT_ | |
| GAM351 | KIAA1054 | 3' | AAAATGGTACCTCTTTC 2820 | TTAA |
| | | | GAAAGAGGT TATTTT | |
| | | | | |
| | | | CTTTCTCCA GTAAAA | |
| | | | TG__ | |
| GAM351 | SEMA3E | 5' | AAAATACAGCTTCTTCCTGA 1431 | A TAA |
| | | | TCAG AAGAGGTT TATTTT | |
| | | | | |
| | | | AGTC TTCTTCGA ATAAAA | |
| | | | C C__ | |
| GAM351 | LOC130507 | 3' | AAAATATTAAGATAACTTTCTG 3011 | AGG_ |
| | | | CAGAAAG TTTAATATTTT | |
| | | | | |
| | | | GTCTTTC GAATTATAAAA | |
| | | | AATA | |
| GAM351 | LOC148145 | 5' | AAAATATTAAACCTGGACCTGA 3296 | AAAG |
| | | T | ATCAG AGGTTTAATATTTT | |
| | | | | |
| | | | TAGTC TCCAAATTATAAAA | |
| | | | CAGG | |
| GAM352 | DKK1 | 3' | AAAATACTAGCTTATTTTCTGA 1417 | _ TAA |
| | | | TCAGAAAG AGGTT TATTTT | |
| | | | | |
| | | | AGTCTTTT TTCGA ATAAAA | |
| | | | A TC_ | |
| GAM352 | KERA | 3' | AAAATATTGAATGCTTTCT 1349 | AG |
| | | | AGAAAG GTTTAATATTTT | |
| | | | | |
| | | | TCTTTC TAAGTTATAAAA | |
| | | | G_ | |
| GAM352 | PPP1R12A | 3' | AAAATACTACATCTTTCTGG 931 | G TTAA |
| | | | TCAGAAAGA GT TATTTT | |
| | | | | |
| | | | GGTCTTTCT CA ATAAAA | |
| | | | A TC__ | |
| GAM352 | S100B | 3' | AAAATTGAAAACCTCTTTC 1284 | AAT |
| | | | GAAAGAGGTTT ATTTT | |
| | | | | |

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|--------|---------------|----|--------------------------|------|----------|
| | | | CTTTCTCCAAA TAAAA | | |
| | | | AGT | | |
| GAM352 | DKFZP564I0422 | 3' | AAAATATTGCATTCTTCTGAT | 2196 | A GTT |
| | | | ATCAGAA GAG TAATATTTT | | |
| | | | | | |
| | | | TAGTCTT CTT GTTATAAAA | | |
| | | | _ AC_ | | |
| GAM352 | EML4 | 3' | AAAATGTTTCCTCTTTCT | 1876 | TTT |
| | | | AGAAAGAGG AATATTTT | | |
| | | | | | |
| | | | TCTTTCTCC TTGTAAAA | | |
| | | | T__ | | |
| GAM352 | FLJ21657 | 3' | AAAATATTTTACTCTGCCTGAT | 1990 | AA GTTT |
| | | | ATCAG AGAG AATATTTT | | |
| | | | | | |
| | | | TAGTC TCTC TTATAAAA | | |
| | | | CG ATT_ | | |
| GAM352 | KIAA1054 | 3' | AAAATGGTACCTCTTTC | 2820 | TTAA |
| | | | GAAAGAGGT TATTTT | | |
| | | | | | |
| | | | CTTTCTCCA GTAAAA | | |
| | | | TG__ | | |
| GAM352 | SEMA3E | 5' | AAAATACAGCTTCTTCCTGA | 1431 | A TAA |
| | | | TCAG AAGAGGTT TATTTT | | |
| | | | | | |
| | | | AGTC TTCTTCGA ATAAAA | | |
| | | | C C__ | | |
| GAM352 | LOC130507 | 3' | AAAATATTAAGATAACTTTCTG | 3011 | AGG_ |
| | | | CAGAAAG TTTAATATTTT | | |
| | | | | | |
| | | | GTCTTTC GAATTATAAAA | | |
| | | | AATA | | |
| GAM352 | LOC148145 | 5' | AAAATATTAACCTGGACCTGA | 3296 | AAAG |
| | | | T ATCAG AGGTTTAATATTTT | | |
| | | | | | |
| | | | TAGTC TCCAAATTATAAAA | | |
| | | | CAGG | | |
| GAM353 | EFG1 | 3' | TGTCTATCTCAACTCTATT | 3661 | ATC TC |
| | | | AATAGAGTT GAT AGACA | | |
| | | | | | |
| | | | TTATCTCAA CTA TCTGT | | |
| | | | CT_ _ | | |
| GAM353 | PHYH | 3' | TCTGCTATAACTCTTTCA | 1281 | T CGATT |
| | | | TGAA AGAGTTAT CAGA | | |
| | | | | | |
| | | | ACTT TCTCAATA GTCT | | |
| | | | _ TC__ | | |
| GAM353 | SLC6A3 | 3' | TGTCTGTTGACCAATCTCTATT | 795 | TTA__ TT |
| | | | CA TGAATAGAG TCGA CAGACA | | |
| | | | | | |

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|--------|--------------|----|-------------------------|---------|--------------|---------|
| | | | ACTTATCTC | AGTT | GTCTGT | |
| | | | TAACC | ___ | | |
| GAM353 | H2AV | 3' | TGCCTGACAATTAGCTCTATTC | 2447 | TCGAT | A |
| | A | | TGAATAGAGTTA | TCAG | CA | |
| | | | | | | |
| | | | ACTTATCTCGAT | AGTC | GT | |
| | | | TAAC | _ | C | |
| GAM353 | HMP19 | 3' | GTCTGAACCGATATTTCT | 3408 | T | A |
| | | | AGAG | TATCG | TTCAGAC | |
| | | | | | | |
| | | | TCTT | ATAGC | AAGTCTG | |
| | | | T | C | | |
| GAM353 | KIAA1726 | 3' | TGTCTGAAAGCAACCCTACTC | 2786 | A | A ATCGA |
| | | | GA | TAG | GTT TTCAGACA | |
| | | | | | | |
| | | | CT | ATC | CAA AAGTCTGT | |
| | | | C | C | CGA | |
| GAM354 | SOX11 | 3' | GTCTCACTGTTTGATCAAACCTT | 992 | A | ATTTTT |
| | CT | | AGAGGTTT | AT | GTGAGAC | |
| | | | | | | |
| | | | TCTTCAA | TA | CACTCTG | |
| | | | C | GTTTGT | | |
| GAM354 | CAP350 | 3' | TCTTGTAATAGTTAAACCTC | 1554 | ATT | TG |
| | | | GAGGTTTAAT | TTG | AGA | |
| | | | | | | |
| | | | CTCCAAATTG | AAT | TCT | |
| | | | AT | _ | GT | |
| GAM354 | DKFZP564A022 | 3' | TCTCACAAATATAAAACC | 2174 | A | TT |
| | | | GTTTT | ATATT | TGTGAGA | |
| | | | | | | |
| | | | CCAA | TATAA | ACACTCT | |
| | | | A | _ | | |
| GAM354 | FLJ11730 | 3' | CTCACAAAGATAAACATC | 2005 | G | TAA |
| | | | GA | GTT | TATTTTTGTGAG | |
| | | | | | | |
| | | | CT | CAA | ATAGAAACACTC | |
| | | | A | _ | | |
| GAM354 | FLJ20686 | 5' | CTCACAGTCCTACTGAACCTC | 1765 | A | TTT |
| | | | GAGGTTTA | TA | TTGTGAG | |
| | | | | | | |
| | | | CTCCAAGT | AT | GACACTC | |
| | | | C | CCT | | |
| GAM354 | FRSB | 3' | GTCCCAGGGAGATATTAGACCT | 1236 | G | A |
| | CT | | AGAGGTTTAATATTTTT | TG | GAC | |
| | | | | | | |
| | | | TCTCCAGATTATAGAGG | AC | CTG | |
| | | | G | C | | |
| GAM354 | KIAA1600 | 3' | ACAAAAAGACTAAACCTCT | 2919 | ATA | |
| | | | AGAGGTTTA | TTTTTGT | | |
| | | | | | | |

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|--------|-----------|----|------------------------------|---|----------|
| | | | TCTCCAAAT AAAAACA | | |
| | | | CAG | | |
| GAM354 | LOC124801 | 3' | GTCTCACATTTGCCCCAAACCT 2996 | | AATATTTT |
| | | C | GAGGTTT TGTGAGAC | | |
| | | | | | |
| | | | CTCCAAA ACACTCTG | | |
| | | | CCCGGTTT | | |
| GAM354 | LOC221035 | 3' | TCCCAGTATTAAACCT 3593 | | TTTTG A |
| | | | AGGTTTAATAT TG GA | | |
| | | | | | |
| | | | TCCAAATTATG AC CT | | |
| | | | _____ C | | |
| GAM354 | LOC51611 | 3' | CGAAAATTAAACCTCT 1653 | | AT |
| | | | AGAGGTTTAAT TTTTG | | |
| | | | | | |
| | | | TCTCCAAATTA AAAGC | | |
| | | | _____ | | |
| GAM355 | AXUD1 | 3' | TTTATTCCATTTCTCTCT 2309 | | GA |
| | | | AGAGAGAAA GAATAAA | | |
| | | | | | |
| | | | TCTCTCTTT CTTATTT | | |
| | | | AC | | |
| GAM355 | BSN | 3' | ATTTTCTTTTGTTTCTCTCT 1024 | | G T |
| | | | AGAGAGAAA AGAA AAAAAT | | |
| | | | | | |
| | | | TCTCTCTTT TTTT TTTTAA | | |
| | | | G C | | |
| GAM355 | DPYSL2 | 3' | AATATTTTCGTGTCTGTCTCTC 822 | | A GA TA |
| | | T | AGAGAGA AGA A AAAATATT | | |
| | | | | | |
| | | | TCTCTCT TCT T TTTTATAA | | |
| | | | G G_ GC | | |
| GAM355 | EVA1 | 3' | AATGTGTTTACTCTCTTTTCCTT 1250 | A | A A |
| | | C | GAG GAAAGAGA TAAA ATATT | | |
| | | | | | |
| | | | CTT CTTTCTCT ATTT TGTAA | | |
| | | | C C G | | |
| GAM355 | PTMS | 3' | TTTGCTCTCTTTCTCCCT 959 | A | A |
| | | | AG GAGAAAGAGA TAAA | | |
| | | | | | |
| | | | TC CTCTTTCTCT GTTT | | |
| | | | C C | | |
| GAM355 | SELE | 3' | TTTTGTGGCTTTCTTTCT 748 | | AGA |
| | | | AGAGAGAAAG ATAAAA | | |
| | | | | | |
| | | | TCTTTCTTTC TGTTTT | | |
| | | | GG_ | | |
| GAM355 | SLC7A6 | 3' | AATATTTTGTACCTTTCTCCT 1076 | A | AGA |
| | | | AG GAGAAAG ATAAAAATATT | | |
| | | | | | |

TC CTCTTTC TGT TTTTATAA
 — CA—
 GAM355 TGFBR2 5' TTTCTTCTAGTTCTTTCT 1003 AG T
 AGAGAGAA AGAA AAA
 ||||| ||| ||
 TCTTTCTT TCTT TTT
 GA C
 GAM355 DKFZP586N0721 5' TTTTATTCCCTTTCCTCT 1627 A A
 AGAG GAAAG GAATAAAA
 ||| |||| |||||
 TCTC CTTTC CTTATTTT
 — C
 GAM355 DKFZp761J139 5' TTTATTCTCTCTGTCTCT 2242 GAA
 AGAGA AGAGAATAAA
 |||| |||||
 TCTCT TCTCTTATTT
 GTC
 GAM355 FLJ10468 3' TTTTATTCTCCTTTC 1779 AAA
 GAGAG GAGAATAAAA
 |||| |||||
 CTTTC CTCTTATTTT
 —
 GAM355 FLJ20485 3' AATATTTTTTAAAATCTCCTTTC 1874 AAA A—
 T AGAGAG GAGA TAAAAATATT
 |||| ||| |||||
 TCTTTC CTCT ATTTTATAA
 — AAA
 GAM355 H2BFQ 3' ATATTTACTCTTTCTGTC 2523 G AATAA
 GA AGAAAGAG AAATAT
 || ||||| |||||
 CT TCTTTCTC TTTATA
 G A—
 GAM355 KIAA0077 3' TTTTATTCTCTCTCCCTTT 2774 A A
 AGAG GA AGAGAATAAAA
 |||| || |||||
 TTTC CT TCTCTTATTTT
 C C
 GAM355 KIAA0295 3' TTTTTCCTTTCTCTCT 2807 A T
 AGAGAGAAAG GAA AAA
 ||||| ||| ||
 TCTCTCTTTC CTT TTT
 C T
 GAM355 KIAA0828 3' AATATTTTGCCTTCTTTCTTTC 3195 AATA
 T AGAGAGAAAGAG AAAATATT
 ||||| |||||
 TCTTTCTTTCTT TTTTATAA
 CCG—
 GAM355 KIAA1203 3' AATATTTTTATTCTTGAGTTAT 2921 GAGAAA
 CT AGA GAGAATAAAAAATATT
 ||| |||||

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|--------|-----------|----|-----------------------------|---------|-------|
| | | | TCT TTCTTATTTTATAA | | |
| | | | ATTGAG | | |
| GAM355 | OSBPL8 | 3' | TTTTTATTATCCTCCTCTCT 1928 | AAA | G |
| | | | AGAGAG GA AATAAAAA | | |
| | | | | | |
| | | | TCTCTC CT TTATTTT | | |
| | | | CTC A | | |
| GAM355 | PAK6 | 3' | AATATTTTtagattcttgct 1897 | _ | A AA |
| | C | | GAG AGAA GAG TAAAAATATT | | |
| | | | | | |
| | | | CTC TCTT CTT ATTTTATAA | | |
| | | | G _ AG | | |
| GAM355 | POLR3F | 3' | AATATTTTCACTGTTccttctt 2547 | A A | ___ |
| | TCT | | AGAGAGAA G GAATA AAAATATT | | |
| | | | | | |
| | | | TCTTTCTT C CTTGT TTTTATAA | | |
| | | | _ _ CAC | | |
| GAM355 | RNF11 | 3' | TTTATTCTCTTTCTTCT 1495 | G | |
| | | | AGA AGAAAGAGAATAAA | | |
| | | | | | |
| | | | TCT TCTTTCTCTTATTT | | |
| | | | - | | |
| GAM355 | SLC16A6 | 5' | TTTATTCTCTTCCCTTCT 1143 | AGA | |
| | | | AGAG AAGAGAATAAA | | |
| | | | | | |
| | | | TCTT TTCTCTTATTT | | |
| | | | CCC | | |
| GAM355 | LOC144321 | 3' | TTTTATTCCCTTCTCTC 3267 | A A | |
| | | | GAGAGAA G GAATAAAA | | |
| | | | | | |
| | | | CTCTCTT C CTTATTTT | | |
| | | | _C | | |
| GAM355 | LOC150951 | 5' | ATATTTTtattttcttcct 3336 | A | |
| | | | AG AAGAGAATAAAAATAT | | |
| | | | | | |
| | | | TC TTCTTTTATTTTATA | | |
| | | | C | | |
| GAM355 | LOC199920 | 5' | AATATTTTATTCTTTGATTCT 3435 | AA | |
| | T | | GAGAG AGAGAATAAAAATATT | | |
| | | | | | |
| | | | TTCTT TTTCTTATTTTATAA | | |
| | | | AG | | |
| GAM355 | LOC256435 | 3' | AATATTTTAAATGTTGTCTCT 3675 | AAGAGAA | |
| | CT | | AGAGAGA TAAAAATATT | | |
| | | | | | |
| | | | TCTCTCT ATTTTATAA | | |
| | | | GTTGTAA | | |
| GAM356 | ADAMTS5 | 3' | TATTTTCACAactactttctct 1352 | _ | AATA_ |
| | CT | | AGAGAGAAAG AG AAAATA | | |
| | | | | | |

TCTCTCTTTC TC TTTTAT
 A AACAC
 GAM356 ADAT1 3' TATTCCCAGCCTTTCTTTCTTC 1404 A____
 GAAGAGAGAAAG GAATA
 ||||| ||||
 CTTCTTTCTTTC CTTAT
 CGACC
 GAM356 ADCY2 3' TTTTATTTTCCTGTCTTC 2711 G AAA
 GAAGA AG GAGAATAAAA
 |||| || |||||
 CTTCT TC CTTTTATTTT
 G ____
 GAM356 AHR 3' ATTTTGTACTCTCTTC 840 _ A
 GAAGAGAG AA GAGAAT
 ||||| || |||||
 CTTCTCTC TT TTTTAA
 A G
 GAM356 BSN 3' ATTTTCTTTTGTTTCTCTCT 1025 G T
 AGAGAGAAA AGAA AAAAAT
 ||||| ||| |||||
 TCTCTCTTT TTTT TTTTAA
 G C
 GAM356 BSN 3' TCTCCCCCTTTCTCTCTTC 1026 ____
 GAAGAGAGAAA GAGA
 ||||| |||
 CTTCTCTCTTT CTCT
 CCCC
 GAM356 C7 3' TATTCCTTATTTCTCTTT 756 _ A
 GAAGAGAGA AAG GAATA
 ||||| ||| |||||
 TTTCTCTTT TTC CTTAT
 A _
 GAM356 CFTR 3' TATTCCTTTTTCTCTCCTC 753 A _
 GA GAGAGAAAGAG AATA
 || ||||| |||||
 CT CTCTCTTTTTTC TTAT
 C C
 GAM356 CHD2 3' ATATTTTTTCTGATCCCCACT 813 AA____ GAAT_ |||
 CTCTCTTC AGA GA AAAAATA T
 || || ||||| |
 TCT CT TTTTAT A
 CACCCC AGTCT |||
 GAM356 CKN1 3' TATTTTATTCTTTCTTC 703 AG
 GAAGAGAGAA AGAATA
 ||||| |||||
 CTTCTTTCTT TTTTAT
 A_
 GAM356 CTH 5' TGTTCTTTTCCTCTCTTC 867 A
 GAAGAGAG AAGAGAATA
 ||||| |||||

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|--------|--------|----|----------------------------|---------|--|
| | | | CTTCTCTC TTTTCTTGT | | |
| | | | C | | |
| GAM356 | EVA1 | 3' | ATTTTTATTTTATGTCTCTC 1251 | AA_ | |
| | | | GAGAGA GAGAATAAAAAT | | |
| | | | | | |
| | | | CTCTCT TTTTATTTTTA | | |
| | | | GTA | | |
| GAM356 | FBXL11 | 3' | TTGTTCCCCCTCTCTCTT 1426 | AAGA | |
| | | | GAAGAGAGA GAATAA | | |
| | | | | | |
| | | | TTTCTCTCT CTTGTT | | |
| | | | CCCC | | |
| GAM356 | GATA3 | 3' | TATTTTCCTTCTCTCTC 893 | A A | |
| | | | GA GAGAGAA GAGAATA | | |
| | | | | | |
| | | | CT CTCTCTT CTTTAT | | |
| | | | _ C | | |
| GAM356 | GDI2 | 5' | TTTTCCTCTCTTTCTCTT 832 | AT | |
| | | | GAGAGAAAGAGA AAAA | | |
| | | | | | |
| | | | TTCTCTTCTCT TTTT | | |
| | | | CC | | |
| GAM356 | HD | 3' | ATTCTCCCTTCTCTCTT 899 | A_ | |
| | | | GAAGAGAGAA GAGAAT | | |
| | | | | | |
| | | | TTTCTCTCTT CTCTTA | | |
| | | | CC | | |
| GAM356 | HTR2C | 3' | TATTTTGTCTCTCCCTCCCTTC 781 | A AAA A | |
| | | | GAAG GAG GAGA TAAAAATA | | |
| | | | | | |
| | | | CTTC CTC CTCT GTTTTAT | | |
| | | | C C_ C | | |
| GAM356 | LGR6 | 3' | TTCTCTTCCCCTCTCTTC 3302 | A_ | |
| | | | GAAGAGAG AAGAGAA | | |
| | | | | | |
| | | | CTTCTCTC TTCTCTT | | |
| | | | CCC | | |
| GAM356 | LRP8 | 3' | TCTCTTATTTCTCTTTTC 2326 | --- | |
| | | | GAAGAGAGAA AGAGA | | |
| | | | | | |
| | | | CTTTTCTCTT TCTCT | | |
| | | | TAT | | |
| GAM356 | LRP8 | 3' | TCTCTTATTTCTCTTTTC 1139 | --- | |
| | | | GAAGAGAGAA AGAGA | | |
| | | | | | |
| | | | CTTTTCTCTT TCTCT | | |
| | | | TAT | | |
| GAM356 | MEF2C | 5' | TTTTTTTTCTCTCTCTCTCT 926 | _ A T | |
| | C | | GA AGAGAGA AGAGAA AAAAA | | |
| | | | | | |

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|--------|---------|----|----------------------------|-------|--|
| | | | CT TCTCTCT TCTCTT TTTT | | |
| | | | C C T | | |
| GAM356 | MSR1 | 3' | TATTTTGGTTTCTCTCT 929 | — | |
| | | | AGAGAGAAA GAGAATA | | |
| | | | | | |
| | | | TCTCTCTTT TTTTAT | | |
| | | | GG | | |
| GAM356 | PCDH11X | 3' | TATTTTCACATTTTCTCTCT 2299 | — | |
| | | | AGAGAGAAA GAGAATA | | |
| | | | | | |
| | | | TCTCTCTTT CTTTAT | | |
| | | | TACA | | |
| GAM356 | PCDH11X | 3' | TATTTTCACATTTTCTCTCT 2301 | — | |
| | | | AGAGAGAAA GAGAATA | | |
| | | | | | |
| | | | TCTCTCTTT CTTTAT | | |
| | | | TACA | | |
| GAM356 | PCDH11Y | 3' | TATTTTCACATTTTCTCTCT 2303 | — | |
| | | | AGAGAGAAA GAGAATA | | |
| | | | | | |
| | | | TCTCTCTTT CTTTAT | | |
| | | | TACA | | |
| GAM356 | PCMT1 | 3' | TATCTTCTGCTCTTTCTTC 1205 | A_ GA | |
| | | | GAAGAGAGA AGA ATA | | |
| | | | | | |
| | | | CTTCTTTCT TCT TAT | | |
| | | | CG TC | | |
| GAM356 | PCNA | 3' | TATTTTTTTTCTCTATTC 939 | G | |
| | | | GAA AGAGAAAGAGAATA | | |
| | | | | | |
| | | | CTT TCTCTTTTTTTTAT | | |
| | | | A | | |
| GAM356 | PRELP | 3' | ATTCGTTTTCTCTCTCTC 950 | _ A | |
| | | | GA AGAGAGAAAG GAAT | | |
| | | | | | |
| | | | CT TCTCTCTTTT CTTA | | |
| | | | C G | | |
| GAM356 | PTMS | 3' | TTTGCTCTCTTTCTCCCT 958 | A A | |
| | | | AG GAGAAAGAGA TAAA | | |
| | | | | | |
| | | | TC CTCTTTCTCT GTTT | | |
| | | | C C | | |
| GAM356 | SLC4A4 | 3' | TATTTTATTCTCTTAAGTCTT 1054 | GAGA | |
| | T | | GAAGA AAGAGAATAAAAATA | | |
| | | | | | |
| | | | TTTCT TTCTCTTATTTTAT | | |
| | | | GAA_ | | |
| GAM356 | TRPS1 | 5' | TATTCCTTTCTCTTTCTCTCT 1471 | TAA | |
| | | | AGAGAGAAAGAGAA AAATA | | |
| | | | | | |

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|--------|---------------|----|----------------------------|---------|
| | | | TCTCTCTTTCTCTT TTTAT | |
| | | | TCC | |
| GAM356 | ARS2 | 5' | TTTTGTTCGCCTCTCTTC 1650 | AAAGA |
| | | | GAAGAGAG GAATAAAA | |
| | | | | |
| | | | CTTCTCTC CTTGTTTT | |
| | | | CG__ | |
| GAM356 | BRD4 | 3' | TATTTTAAATTCTCTCTTC 2368 | A_ |
| | | | GAAGAGAGAA GAGAATA | |
| | | | | |
| | | | CTTCTCTCTT TTTTAT | |
| | | | AA | |
| GAM356 | CAPN13 | 3' | TATTTTACCTGCCTCTCTTC 2485 | AA __ |
| | | | GAAGAGAG AG AGAATA | |
| | | | | |
| | | | CTTCTCTC TC TTTTAT | |
| | | | CG CA | |
| GAM356 | CECR6 | 3' | TTACCCTCTCCTCTCTTC 2218 | AA AA |
| | | | GAAGAGAG AGAG TAA | |
| | | | | |
| | | | CTTCTCTC TCTC ATT | |
| | | | C_ CC | |
| GAM356 | DKFZP434I0714 | 5' | TTTTTGTTTTTCCCCCTCTTC 3362 | AGAAA |
| | | | GAAGAG GAGAATAAAAA | |
| | | | | |
| | | | CTTCTC TTTTGTTTTT | |
| | | | CCCC_ | |
| GAM356 | DKFZP564G092 | 5' | TATTCCTCTTTCTTTTC 1639 | A A |
| | | | GAAGAGAGA AG GAATA | |
| | | | | |
| | | | CTTTTCTTT TC CTTAT | |
| | | | C _ | |
| GAM356 | DKFZp564K142 | 3' | TATCCTCTTAACCTTCTCTTC 2231 | A__ A |
| | | | GAAGAGAG AAGAG ATA | |
| | | | | |
| | | | CTTCTCTT TTCTC TAT | |
| | | | CCAA C | |
| GAM356 | DKFZp566D234 | 3' | TATTTTTTTTCTCTGTC 2612 | AG |
| | | | GA AGAGAAAGAGAATA | |
| | | | | |
| | | | CT TCTCTTTTTTTTAT | |
| | | | G_ | |
| GAM356 | DKFZP566I1024 | 3' | TTTAAATCTATTCTCTC 2878 | _ GAA |
| | | | GAGAGAA AGA TAAAA | |
| | | | | |
| | | | CTCTCTT TCT ATTTT | |
| | | | A AAA | |
| GAM356 | EPI64 | 3' | TATTTTGACATCTCTCTCTT 3681 | A GAATA |
| | C | | GAAGAGAGA AGA AAAATA | |
| | | | | |

CTTCTCTCT TCT TTTTAT
 C ACAG_
 GAM356 FLJ00012 3' TATTTTATCTCTATCTCCT 2985 A A A
 AG GAGA AGAGA TAAAAATA
 || ||| |||| |||||
 TC CTCT TCTCT ATTTTAT
 _ A _
 GAM356 FLJ10460 3' ATTTTATTCTACCTTTC 1778 AAAG
 GAGAG AGAATAAAAAT
 |||| |||||
 CTTTC TCTATTTTAA
 CA_
 GAM356 FLJ10687 3' TTTATTCATTTCTCTCCTC 1793 A GA
 GA GAGAGAAA GAATAAA
 || ||||| |||||
 CT CTCTCTTT CTTATTT
 C A_
 GAM356 FLJ10738 3' TATTTTACTCTCCCTCTTC 1799 AGAAA A
 GAAGAG GAGA TAAAAATA
 |||| ||| |||||
 CTTCTC CTCT ATTTTAT
 C__ C
 GAM356 FLJ13158 3' TTCTCTCCCTTTCTCTTC 2109 A_
 GAAGAGAGA AGAGAA
 ||||| |||||
 CTTCTCTTT TCTCTT
 CCC
 GAM356 FLJ20294 5' TATTCCTGTCTCCTCTTT 1747 _ A A
 GAAGAG AGA AG GAATA
 |||| ||| || |||||
 TTTCTC TCT TC CTTAT
 C G _
 GAM356 FLJ21657 3' TATTCTACTTCTCTCTTC 1991 AG
 GAAGAGAGAA AGAATA
 ||||| |||||
 CTTCTCTCTT TCTTAT
 CA
 GAM356 GT650 3' TATTCTGATTCTCCCTCTCTT 2341 AAA AA_
 C GAAGAGAG GAGAAT AAATA
 ||||| ||||| |||||
 CTTCTCTC CTCTTA TTTAT
 C__ GTC
 GAM356 HEY2 3' TATTCTCTTTTTTTTCTC 1420 AG
 GA AGAGAAAGAGAATA
 || ||||| |||||
 CT TTTTTTCTCTTAT
 CT
 GAM356 HIC2 3' ATTTTCTCTCTCTCTTTTC 2717 A T
 GAAGAGAGA AGAGAA AAAAAT
 ||||| ||||| |||||

CTTTTCTCT TCTTTT TTTTTA
 C _
 GAM356 HOOK3 3' ATTTTGAGGACTTTTTCTCTCT 2249 AATA_
 AGAGAGAAAGAG AAAAT
 ||||| ||||
 TCTCTCTTTTC TTTTA
 AGGAG
 GAM356 IL1RAPL1 5' TATTCTTATTTTCCCCTCTCTT 1488 AAA A
 T GAAGAGAG GAGAATAA AATA
 ||||| ||||| ||||
 TTTCTCTC CTTTATT TTAT
 CC_ C
 GAM356 KALI 3' TTTTGTTCTTGTCCCTCTC 2347 AAA_
 GAGAG GAGAATAAAA
 |||| |||||
 CTCTC TTCTTGTTTT
 CCTG
 GAM356 KIAA0077 3' TTTTATTCTCTCTCCCTTT 2773 A AA
 GAAG GAGA GAGAATAAAA
 ||| ||| |||||
 TTTC CTCT CTCTTATTTT
 C _
 GAM356 KIAA0089 3' ATTTTGTAGCCTCTTTTCTCTTC 2873 A AA
 GAAGAGAGAA GAG TAAAAAT
 ||||| ||| |||||
 CTTCTCTTTT CTC ATTTTTA
 _ CG
 GAM356 KIAA0286 3' TATTTTCACCCTCTTTTC 2814 AAA
 GAAGAGAG GAGAATA
 ||||| |||||
 CTTTCTC CTTTAT
 CCA
 GAM356 KIAA0295 3' TTTTTCCTTTTCTCTCT 2808 A T
 AGAGAGAAAG GAA AAA
 ||||| ||| |||
 TCTCTCTTTC CTT TTT
 C T
 GAM356 KIAA0342 3' TATTCTCATTACTTCTCTTT 2890 _ _ A
 GAAGAGA G AA GAGAATA
 ||||| || |||||
 TTTCTCT C TT CTCTTAT
 T A A
 GAM356 KIAA0564 3' TATTTTATTTTCTCCCTGCTC 2743 _ AA
 GAG AG AGAGAATAAAAATA
 ||| || |||||
 CTC TC TCTTTTATTTTAT
 G CC
 GAM356 KIAA0630 3' TATTTTAAAAAGTCTTTCTCT 3465 GAAT_
 CT AGAGAGAAAGA AAAAATA
 ||||| |||||

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|--------|----------|----|------------------------|--------|--------|----|
| | | | TCTCTCTTTCT | TTTTAT | | |
| | | | GAAAAT | | | |
| GAM356 | KIAA0662 | 3' | TGTTCTCTCTCTCTTT | 3215 | A | |
| | | | GAAGAGAGA AGAGAATA | | | |
| | | | | | | |
| | | | TTTCTCTCT TCTCTTGT | | | |
| | | | C | | | |
| GAM356 | KIAA0830 | 3' | TTTGCTTCTCTTTCTCCT | 2866 | A | — |
| | | | AG GAGAAAGAGAA TAAA | | | |
| | | | | | | |
| | | | TC CTCTTTCTCTT GTTT | | | |
| | | | — C | | | |
| GAM356 | KIAA0964 | 3' | ATTCTTATGTTTTTCTCTTTTC | 1579 | GA | A |
| | | | GAAGAGAGAAAGA ATAA AAT | | | |
| | | | | | | |
| | | | CTTTTCTCTTTT TATT TTA | | | |
| | | | G_ C | | | |
| GAM356 | KIAA1076 | 3' | TATTTTTTGCTTTTCTCTC | 2723 | AGAAT | |
| | | | GAGAGAAAG AAAAATA | | | |
| | | | | | | |
| | | | CTCTCTTTC TTTTAT | | | |
| | | | GT___ | | | |
| GAM356 | KIAA1181 | 3' | ATTCCTCTTCCTCTCTTC | 2817 | A | — |
| | | | GAAGAGAG AAGAG AAT | | | |
| | | | | | | |
| | | | CTTCTCTC TTCTC TTA | | | |
| | | | C C | | | |
| GAM356 | KIAA1319 | 3' | TATTTTTGTCTTCTTCCTTTC | 1925 | A | GA |
| | | | GAGAG AAGA ATAAAAATA | | | |
| | | | | | | |
| | | | CTTTC TTCT TGTTTTTAT | | | |
| | | | C TC | | | |
| GAM356 | KIAA1522 | 3' | ATTCTCTGACCTTTCTCTCT | 2708 | _____ | |
| | | | AGAGAGAA AGAGAAT | | | |
| | | | | | | |
| | | | TCTCTCTT TCTCTTA | | | |
| | | | TCCAG | | | |
| GAM356 | KIAA1906 | 3' | ATTTTTATTCTCTGCTT | 2971 | AA | |
| | | | GAG AGAGAATAAAAAAT | | | |
| | | | | | | |
| | | | TTC TCTCTTATTTTAA | | | |
| | | | G_ | | | |
| GAM356 | MAPK6 | 5' | TATTTTTCTTCTCCCTTT | 952 | A | AG |
| | | | GAAG GAGAA AGAATA | | | |
| | | | | | | |
| | | | TTTC CTCTT TTTTAT | | | |
| | | | C CT | | | |
| GAM356 | MGC13138 | 3' | TATTTTTATTCTTGTGACCCTC | 2332 | AGAAA_ | |
| | | | GAG GAGAATAAAAAATA | | | |
| | | | | | | |

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|--------|----------|----|-----------------------------|-----------|--|
| | | | CTC TTCTTATTTTAT | | |
| | | | CCAGTG | | |
| GAM356 | MGC2742 | 5' | TATTTCTTTTCTCTCTC 2040 | AG | |
| | | | GAAGAGAGAAAG AATA | | |
| | | | | | |
| | | | CTTCTCTCTTTT TTAT | | |
| | | | CT | | |
| GAM356 | MGC32043 | 3' | TATTCCTGTTTTCTCTTT 2486 | _ A | |
| | | | GAAGAGAGAA AG GAATA | | |
| | | | | | |
| | | | TTTCTCTTTT TC CTTAT | | |
| | | | G _ | | |
| GAM356 | NFAT5 | 3' | TATTCCCTTTTTCTCTTC 2452 | A | |
| | | | GAAGAGAGAAAG GAATA | | |
| | | | | | |
| | | | CTTCTCTTTTTTC CTTAT | | |
| | | | C | | |
| GAM356 | OSBPL8 | 3' | TTTTTATTATCCTCCTCTCTTC 1929 | AAA G | |
| | | | GAAGAGAG GA AATAAAAA | | |
| | | | | | |
| | | | CTTCTCTC CT TTATTTTT | | |
| | | | CTC A | | |
| GAM356 | RAB10 | 3' | TGTTCTGCTTTTCCTCCTC 3337 | A AG _ | |
| | | | GA GAG AAAG AGAATA | | |
| | | | | | |
| | | | CT CTC TTTC TCTTGT | | |
| | | | C CT G | | |
| GAM356 | RANBP1 | 3' | TATTTTCTTTTCCTCTCTTT 969 | — | |
| | | | GAAGAGAG AAAGAGAATA | | |
| | | | | | |
| | | | TTTCTCTC TTTCTTTTAT | | |
| | | | CT | | |
| GAM356 | RASSF2 | 3' | TATTTTCACAATCCTCTCTTC 1537 | AAA__ | |
| | | | GAAGAGAG GAGAATA | | |
| | | | | | |
| | | | CTTCTCTC CTTTTAT | | |
| | | | CTAACA | | |
| GAM356 | STK22D | 3' | TATTTTCATCAGCTTCTTCTCT 2226 | AG AATA__ | |
| | CT | | AGAGAGAA AG AAAATA | | |
| | | | | | |
| | | | TCTCTCTT TC TTTTAT | | |
| | | | CT GACTAC | | |
| GAM356 | SYNJ2 | 3' | ATTTTATAGGTTTTCTCTTC 2606 | AGAGAA | |
| | | | GAAGAGAGAA TAAAAAT | | |
| | | | | | |
| | | | CTTCTCTTTT ATTTTTA | | |
| | | | GG__ | | |
| GAM356 | TBLR1 | 3' | TATTCTTTTTTTCCCTTC 2079 | A | |
| | | | GAAG GAGAAAGAGAATA | | |
| | | | | | |

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|--------|-----------|----|-----------------------------|----|------|
| | | | CTTC CTTTTTTTCTTAT | | |
| | | | C | | |
| GAM356 | TM9SF1 | 3' | TATTGCTGTTCTCTCCCTTTCT 1296 | AA | AA |
| | | TC | GAAGAGAG AGAGAATA AATA | | |
| | | | | | |
| | | | CTTCTTTC TCTCTTGT TTAT | | |
| | | | CC CG | | |
| GAM356 | ULK2 | 3' | TATTCTATCCTCTCCTCTTC 1523 | _ | AAG_ |
| | | | GAAGAG AGA AGAATA | | |
| | | | | | |
| | | | CTTCTC TCT TCTTAT | | |
| | | | C CCTA | | |
| GAM356 | UNC5D | 3' | TTATTCTTTCTTCCTCTTC 2393 | A | _ |
| | | | GAAGAG GAA AGAGAATAA | | |
| | | | | | |
| | | | CTTCTC CTT TTTCTTATT | | |
| | | | _ C | | |
| GAM356 | LOC121219 | 5' | TTATTAACCTCTTCTCTCTTT 2988 | A | _ |
| | | | GAAGAGAGAA GAG AATAA | | |
| | | | | | |
| | | | TTTCTCTCTT CTC TTATT | | |
| | | | C AA | | |
| GAM356 | LOC128077 | 3' | ATTTGTTTTCTCTTTCTTTCCT 3006 | A | TAA |
| | | C | GA GAGAGAAAGAGAA AAAT | | |
| | | | | | |
| | | | CTCTTTCTTTCTCTT TTTA | | |
| | | | C TTG | | |
| GAM356 | LOC143451 | 3' | TTCTCTCCTTCTCTCTTC 3058 | _ | |
| | | | GAAGAGAGAA AGAGAA | | |
| | | | | | |
| | | | CTTCTCTCTT TCTCTT | | |
| | | | CC | | |
| GAM356 | LOC145125 | 3' | TTCTCTCCTTCTCTCTTC 3075 | _ | |
| | | | GAAGAGAGAA AGAGAA | | |
| | | | | | |
| | | | CTTCTCTCTT TCTCTT | | |
| | | | CC | | |
| GAM356 | LOC149351 | 3' | ATTTTTCAGATCTTTCTCTTT 3131 | | GAAT |
| | | | AGAGAGAAAGA AAAAAT | | |
| | | | | | |
| | | | TTTCTCTTTCT TTTTAA | | |
| | | | AGAC | | |
| GAM356 | LOC149722 | 5' | TATTCTTTCTTTCTCTTC 3312 | A | |
| | | | GAAGAGAGA AGAGAATA | | |
| | | | | | |
| | | | CTTCTCTTT TTTCTTAT | | |
| | | | C | | |
| GAM356 | LOC149837 | 5' | TATTCCTGTCTTTCTCTCT 3318 | _ | |
| | | | AGAGAGAAAGA GAATA | | |
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| | | TCTCTCTTTCT CTTAT | | |
| | | GTC | | |
| GAM356 | LOC150054 3' | TATTCTGTCTTTCTCCTC 3323 | — | — |
| | | GAG AGAAAGA GAATA | | |
| | | | | |
| | | CTC TCTTTCT CTTAT | | |
| | | C GT | | |
| GAM356 | LOC150150 5' | TTTTGTGCCTCTCTTTCTTC 3324 | AA | A_ |
| | | GAAGAGAGA GAG ATAAAA | | |
| | | | | |
| | | CTTCTTTCT CTC TGTTTT | | |
| | | — CG | | |
| GAM356 | LOC150225 3' | TATTTTGTTCCTCTTC 3327 | A | G |
| | | GAAGAG GAAA AGAATA | | |
| | | | | |
| | | CTTCTC CTTT TTTTAT | | |
| | | C G | | |
| GAM356 | LOC152816 3' | TATTTTATCCTCAACCTCTT 3364 | AAA | A |
| | | GAGAG GAG ATAAAAATA | | |
| | | | | |
| | | TTCTC CTC TATTTTAT | | |
| | | CAA C | | |
| GAM356 | LOC155038 3' | ATTGCGTTTCTCTTTCTCCTTC 3198 | A | TAAA |
| | | GAAG GAGAAAGAGAA AAT | | |
| | | | | |
| | | CTTC CTCTTTCTCTT TTA | | |
| | | — TGCG | | |
| GAM356 | LOC158629 3' | TATTTTCTTTCCCTCTC 3394 | A | A |
| | | GA GAG GAAAGAGAATA | | |
| | | | | |
| | | CT CTC CTTTCTTTTAT | | |
| | | — C | | |
| GAM356 | LOC158943 3' | TATTTTCTTTTCCTCTCTT 2572 | — | |
| | | GAAGAGAG AAAGAGAATA | | |
| | | | | |
| | | TTTCTCTC TTTCTTTTAT | | |
| | | CT | | |
| GAM356 | LOC170082 3' | ATTCTTTTCCCCTCTCTTTC 3254 | — | |
| | | GAAGAGAGA AAGAGAAT | | |
| | | | | |
| | | CTTTTCTCT TTTCTTA | | |
| | | CCCC | | |
| GAM356 | LOC199920 5' | TATTTTATTCTTTGATTCTTC 3436 | AGAA | |
| | | GAAGAG AGAGAATAAAAATA | | |
| | | | | |
| | | CTTCTT TTTCTTATTTTAT | | |
| | | AG_ | | |
| GAM356 | LOC219667 3' | ATTTTGTATCTCTCTTC 3516 | AAGAG | |
| | | GAAGAGAGA AATAAAAAT | | |
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|--------|--------------|------------------------|-------------|---------|
| | | CTTCTCTCT | TTGTTTTTA | |
| | | A_____ | | |
| GAM356 | LOC220279 5' | TATTTTCTTCCCCTACCTCTCT | 3653 | A_____ |
| | TC | GAAGAGAG | AAGAGAATA | |
| | | | | |
| | | CTTCTCTC | TTCTTTTAT | |
| | | CATCCCC | | |
| GAM356 | LOC221830 3' | TATTTTCTTTTCTTTCTTC | 3567 | — |
| | | GAAGAGAGAAA | GAGAATA | |
| | | | | |
| | | CTTCTTTCTTT | CTTTTAT | |
| | | T | | |
| GAM356 | LOC222166 3' | ATTTTACCTTCTCTCTTT | 3635 | AG_ |
| | | GAAGAGAGAA | AGAAT | |
| | | | | |
| | | TTTCTCTCTT | TTTTA | |
| | | CCA | | |
| GAM356 | LOC254440 3' | TTCTCTCCTTCTCTCTTC | 3729 | — |
| | | GAAGAGAGAA | AGAGAA | |
| | | | | |
| | | CTTCTCTCTT | TCTCTT | |
| | | CC | | |
| GAM356 | LOC51123 3' | ATTTTTATGCTGTTCCCTCTT | 2571 | A AG A |
| | | AAGAG GAA | AG ATAAAAAT | |
| | | | | |
| | | TTCTC CTT | TC TATTTTTA | |
| | | C G_ G | | |
| GAM356 | LOC51596 5' | TATTTTCCAAGTTTCTCTCTC | 1651 | A _____ |
| | | GA GAGAGAAA | GAGAATA | |
| | | | | |
| | | CT CTCTCTTT | CTTTTAT | |
| | | — | GAAC | |
| GAM356 | LOC84570 5' | TTTCGTTTTTCCTCTCTCTTC | 2257 | AA TA |
| | | GAAGAGAGA | GAGAA AAA | |
| | | | | |
| | | CTTCTCTCT | CTTTT TTT | |
| | | C_ GC | | |
| GAM356 | LOC92710 5' | TATTTTATGCCTCTGTCTC | 2885 | A A_ |
| | | GAGA AGAG | ATAAAAATA | |
| | | | | |
| | | CTCT TCTC | TATTTTAT | |
| | | G CG | | |
| GAM357 | FANCF 3' | GTCCCTTTAAAGCATTGA | 1997 | ATATAT |
| | | TCAATGTTTTAAA | GGAC | |
| | | | | |
| | | AGTTACGAAATTT | CCTG | |
| | | C_____ | | |
| GAM357 | GPR65 5' | TCCACCCTTTAAAGCATTGA | 2544 | A TATA |
| | | TCAATGTTTT AAA | TGGA | |
| | | | | |

AGTTACGAAA TTT ACCT
 A CCC_
 GAM357 LMNB1 3' TGTCCATACACTTTGTTGCA 1226 TT ATA
 TGT TAAA TATGGACA
 ||| ||| |||||
 ACG GTTT ATACCTGT
 TT CAC
 GAM357 MEN1 5' CATAATATTTTAAAACATT 3600 _
 AATGTTTTAAAATAT ATG
 ||||| |||
 TTACAAAATTTTATA TAC
 A
 GAM357 PLAG1 3' TGTCCATATACCAGATTTAAAA 944 A____
 TATT AATGTTTTAAA TATATGGACA
 ||||| |||||
 TTATAAAATTT ATATACCTGT
 AGACC
 GAM357 S100A11 3' TGTCAC TTTT TAAAACATGA 1231 A TATATG
 TCA TGTTTTAAAA GACA
 ||| ||||| |||
 AGT ACAAATTTT CTGT
 _ TTCA_
 GAM357 SLC9A6 3' TCCAGTTAGAACATTGA 1290 AATATA
 TCAATGTTTTAA TGGA
 ||||| |||
 AGTTACAAGATT ACCT
 G____
 GAM357 SOD2 3' TCCATATACTTTGGGGACTTG 766 T TA _
 CAA GTTT AAA TATATGGA
 ||| ||| ||| |||||
 GTT CAGG TTT ATATACCT
 _ GG C
 GAM357 BIRC2 5' TATATTTT TAAAACATTGA 2784 T
 TCAATGTTTTAAAA ATATG
 ||||| |||||
 AGTTACAAAATTTT TATAT
 _
 GAM357 CXorf1 5' TGTCCATAGAAAAAATATT 1145 AAAATA
 AATGTTTT TATGGACA
 ||||| |||||
 TTATAAAA ATACCTGT
 AAG_
 GAM357 KIAA0367 3' TGTCCCACAATGCCTAAAACAT 2787 AAATATAT_
 TGA TCAATGTTTTA GGACA
 ||||| |||
 AGTTACAAAAT CCTGT
 CCGTAACAC
 GAM357 KIAA1321 3' TCCTTGAGCTTTAAAGCATTGA 2627 ATATAT
 TCAATGTTTTAAA GGA
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|--------|-----------|----|------------------------|----------|-----------|---|
| | | | AGTTACGAAATTT | CCT | | |
| | | | CGAGTT | | | |
| GAM357 | KIAA1718 | 3' | TGTATTTTAAAATATTGA | 2686 | | |
| | | | TCAATGTTTTAAAATATA | | | |
| | | | | | | |
| | | | AGTTATAAAATTTTATGT | | | |
| GAM357 | KIAA1789 | 5' | TGTCCCTGCCCTAGAAACATTG | 2781 | AAAATATAT | |
| | A | | TCAATGTTTT | GGACA | | |
| | | | | | | |
| | | | AGTTACAAAG | CCTGT | | |
| | | | ATCCCGTC_ | | | |
| GAM357 | PRO2964 | 3' | CAAGTATTTTAAAACACTG | 1842 | A | A |
| | | | CA TGTTTTAAAATAT TG | | | |
| | | | | | | |
| | | | GT ACAAATTTTATG AC | | | |
| | | | C | A | | |
| GAM357 | SLC17A6 | 3' | TGTCCATACACAGAAACAT | 1912 | AAAATA | |
| | | | ATGTTTT | TATGGACA | | |
| | | | | | | |
| | | | TACAAAG | ATACCTGT | | |
| | | | ACAC_ | | | |
| GAM357 | TRAF3 | 5' | CATTTTATTTTAAAACGTTGA | 2542 | T_ | |
| | | | TCAATGTTTTTAAAATA ATG | | | |
| | | | | | | |
| | | | AGTTGCAAAATTTTAT TAC | | | |
| | | | TT | | | |
| GAM357 | LOC151361 | 3' | TGTCTGTGTTTTTAAAAC | 3344 | T | |
| | | | GTTTTAAAA ATATGGACA | | | |
| | | | | | | |
| | | | CAAAATTTT TGTGTCTGT | | | |
| GAM357 | LOC158714 | 3' | TCCACACATTTAAAACATTGA | 3224 | ATATA | |
| | | | TCAATGTTTTTAAA | TGGA | | |
| | | | | | | |
| | | | AGTTACAAAATTT | ACCT | | |
| | | | ACAC_ | | | |
| GAM357 | LOC219667 | 3' | TATACCTTAGAACATTGA | 3518 | AA | |
| | | | TCAATGTTTTTAA | TATA | | |
| | | | | | | |
| | | | AGTTACAAGATT | ATAT | | |
| | | | CC | | | |
| GAM357 | LOC91565 | 3' | TCCATTTTAAAACATT | 2749 | ATAT | |
| | | | AATGTTTTTAAA | ATGGA | | |
| | | | | | | |
| | | | TTACAAAATTT | TACCT | | |
| GAM358 | EHF | 3' | ATATTGTAGAAGGAAACACCAA | 1411 | T GGA | |
| | | | TTGGT GT TCTTCTACAATAT | | | |
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|--------|-----------|----|------------------------------|----------|
| | | | AACCA CA GGAAGATGTTATA | |
| | | | _ AA_ | |
| GAM358 | C9orf5 | 3' | ATATTGCAAAAACTACAGCTA 2225 | ATCTTCTA |
| | A | | TTGGTTGTGG CAATAT | |
| | | | | |
| | | | AATCGACATC GTTATA | |
| | | | AAAAAAC_ | |
| GAM358 | KIAA1546 | 3' | TTGAAAAGACCACAACCAA 2805 | A CTA |
| | | | TTGGTTGTGG TCTT CAA | |
| | | | | |
| | | | AACCAACACC AGAA GTT | |
| | | | _ AA_ | |
| GAM358 | LOC253263 | 3' | TGAGAAAAACCCACAATAA 3724 | ATC_ A |
| | | | TTGGTTGTGG TTCT CA | |
| | | | | |
| | | | AATCAACACC AAGA GT | |
| | | | CAAA _ | |
| GAM359 | BRCA1 | 3' | GCCATGAGCACAAAAATTATGGT 1380 | AGGGTA |
| | A | | TATCATAA TGCTCATGGC | |
| | | | | |
| | | | ATGGTATT ACGAGTACCG | |
| | | | AAAAC_ | |
| GAM359 | BRCA1 | 3' | GCCATGAGCACAAAAATTATGGT 1381 | AGGGTA |
| | A | | TATCATAA TGCTCATGGC | |
| | | | | |
| | | | ATGGTATT ACGAGTACCG | |
| | | | AAAAC_ | |
| GAM359 | BRCA1 | 3' | GCCATGAGCACAAAAATTATGGT 1382 | AGGGTA |
| | A | | TATCATAA TGCTCATGGC | |
| | | | | |
| | | | ATGGTATT ACGAGTACCG | |
| | | | AAAAC_ | |
| GAM359 | BRCA1 | 3' | GCCATGAGCACAAAAATTATGGT 1383 | AGGGTA |
| | A | | TATCATAA TGCTCATGGC | |
| | | | | |
| | | | ATGGTATT ACGAGTACCG | |
| | | | AAAAC_ | |
| GAM359 | BRCA1 | 3' | GCCATGAGCACAAAAATTATGGT 1384 | AGGGTA |
| | A | | TATCATAA TGCTCATGGC | |
| | | | | |
| | | | ATGGTATT ACGAGTACCG | |
| | | | AAAAC_ | |
| GAM359 | BRCA1 | 3' | GCCATGAGCACAAAAATTATGGT 1385 | AGGGTA |
| | A | | TATCATAA TGCTCATGGC | |
| | | | | |
| | | | ATGGTATT ACGAGTACCG | |
| | | | AAAAC_ | |
| GAM359 | BRCA1 | 3' | GCCATGAGCACAAAAATTATGGT 1386 | AGGGTA |
| | A | | TATCATAA TGCTCATGGC | |
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|--------|---------------|----|------------------------|---------------|--------|------|
| | | | ATGGTATT | ACGAGTACCG | | |
| | | | AAAAC_ | | | |
| GAM359 | BRCA1 | 3' | GCCATGAGCACAAAATTATGGT | 1387 | AGGGTA | |
| | A | | TATCATAA | TGCTCATGGC | | |
| | | | | | | |
| | | | ATGGTATT | ACGAGTACCG | | |
| | | | AAAAC_ | | | |
| GAM359 | BRCA1 | 3' | GCCATGAGCACAAAATTATGGT | 1388 | AGGGTA | |
| | A | | TATCATAA | TGCTCATGGC | | |
| | | | | | | |
| | | | ATGGTATT | ACGAGTACCG | | |
| | | | AAAAC_ | | | |
| GAM359 | BRCA1 | 3' | GCCATGAGCACAAAATTATGGT | 1389 | AGGGTA | |
| | A | | TATCATAA | TGCTCATGGC | | |
| | | | | | | |
| | | | ATGGTATT | ACGAGTACCG | | |
| | | | AAAAC_ | | | |
| GAM359 | BRCA1 | 3' | GCCATGAGCACAAAATTATGGT | 1391 | AGGGTA | |
| | A | | TATCATAA | TGCTCATGGC | | |
| | | | | | | |
| | | | ATGGTATT | ACGAGTACCG | | |
| | | | AAAAC_ | | | |
| GAM359 | PPP1CB | 3' | GCCATTTGACACCCTTTATGAT | 949 | ATGCTC | |
| | G | | TATCATAAAGGGT | ATGGC | | |
| | | | | | | |
| | | | GTAGTATTTCCCA | TACCG | | |
| | | | CAGTT_ | | | |
| GAM359 | TRPS1 | 3' | CATGCACACCCTCTCTGATA | 1470 | TAA | A TC |
| | | | TATCA | AGGGT TGC ATG | | |
| | | | | | | |
| | | | ATAGT | TCCCA ACG TAC | | |
| | | | CTC | C _ | | |
| GAM359 | FLJ23323 | 3' | GCCATGAATGGTGCCCTT | 2077 | GC_ | |
| | | | AAGGGTAT | TCATGGC | | |
| | | | | | | |
| | | | TTCCCGTG | AGTACCG | | |
| | | | GTA | | | |
| GAM359 | KIAA0057 | 3' | CCACAAGCATACCTATTAAGA | 1421 | A A | CA |
| | | | TC TAA | GGGTATGCT TGG | | |
| | | | | | | |
| | | | AG ATT | TCCATACGA ACC | | |
| | | | A A | AC | | |
| GAM359 | LOC145439 | 5' | GCCATGAGCTGCATCTTTAT | 3079 | _ | T |
| | | | ATAAAGG | GTA GCTCATGGC | | |
| | | | | | | |
| | | | TATTTCT | CGT CGAGTACCG | | |
| | | | A _ | | | |
| GAM360 | DKFZP434G1411 | 3' | TAGGTTGATACATGTATCA | 3554 | AA | |
| | | | TGATACATGTATTAA | TA | | |
| | | | | | | |

ACTATGTACATAGTT AT
 GG
 GAM360 DKFZP564I052 3' GAAAGTATTCCTATCATGTAT 2760 T TAA
 ATACATG AT AATACTTTC
 ||||| || |||||
 TATGTAC TA TTATGAAAG
 _ TCC
 GAM360 KLHL8 3' AAAGTATTTGTTACATAATCA 2639 AC TTA
 TGAT ATGTA AAATACTTT
 ||| |||| |||||
 ACTA TACAT TTTATGAAA
 A_ TG_
 GAM360 XLKD1 3' AAAGTGCCATTAACAAATGTAT 1323 GTA AA_
 CA TGATACAT TTAA TACTTT
 ||||| ||| |||||
 ACTATGTA AATT GTGAAA
 AAC ACC
 GAM360 LOC51003 3' GAGGCACTTAATACATGTAT 1658 AATA
 ATACATGTATTAA CTT
 ||||| |||
 TATGTACATAATT GAG
 CACG
 GAM361 GCNT2 5' TCTCGGGATGAAACGGAATCGA 831 _____ A
 TCGATTCCGT CC AGA
 ||||| || |||
 AGCTAAGGCA GG TCT
 AAGTAG C
 GAM361 BLP1 3' TTACCTTGCAGACGGAATGA 2222 G _ A
 TC ATTCCGTC CAAG TGA
 || ||||| ||| |||
 AG TAAGGCAG GTTC ATT
 _ AC C
 GAM361 BLP1 3' TTACCTTGCAGACGGAATGA 2371 G _ A
 TC ATTCCGTC CAAG TGA
 || ||||| ||| |||
 AG TAAGGCAG GTTC ATT
 _ AC C
 GAM361 LOC143914 5' TCACTCAAACGGAATCGA 3062 CCA A
 TCGATTCCGT AG TGA
 ||||| || |||
 AGCTAAGGCA TC ACT
 AAC _
 GAM361 LOC253891 5' CACTGGGACGGAATCGG 3654 A A
 TCGATTCCGTCC AG TG
 ||||| || |||
 GGCTAAGGCAGG TC AC
 G _
 GAM362 ADSS 3' GAAACAAATGATGAAAACAT 2925 CCTGTT
 ATGT TCATTTGTTTC
 ||| |||||

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|--------|-----------|----|-----------------------------|--------|-------|
| | | | TACA AGTAAACAAAG | | |
| | | | AAAGT_ | | |
| GAM362 | CASP6 | 3' | GAAACAAAATCCTCAGGAAATT 2305 | G | TTTCA |
| | A | | TAAT TCCTG TTTGTTTC | | |
| | | | | | |
| | | | ATTA AGGAC AAACAAAG | | |
| | | | A TCCTA | | |
| GAM362 | CASP6 | 3' | GAAACAAAATCCTCAGGAAATT 810 | G | TTTCA |
| | A | | TAAT TCCTG TTTGTTTC | | |
| | | | | | |
| | | | ATTA AGGAC AAACAAAG | | |
| | | | A TCCTA | | |
| GAM362 | CKTSF1B1 | 3' | AAGTGGATAAACAGAACATT 1445 | C | C TG |
| | | | AATGT CTGTTT ATT TTT | | |
| | | | | | |
| | | | TTACA GACAAA TAG GAA | | |
| | | | A _ GT | | |
| GAM362 | F2R | 3' | AAACAATGCAGTACAGGACAT 879 | TTCAT_ | |
| | | | ATGTCCTGT TTGTTT | | |
| | | | | | |
| | | | TACAGGACA AACAAA | | |
| | | | TGACGT | | |
| GAM362 | GPRK7 | 3' | GGAAACAAATGTTTCTGACATT 2476 | CTGTTT | |
| | | | AATGTC CATTTGTTTCC | | |
| | | | | | |
| | | | TTACAG GTAAACAAAGG | | |
| | | | TCTTT_ | | |
| GAM362 | NLGN1 | 3' | AAACAAATGAGATGGAC 1591 | T | |
| | | | GTCC GTTTCATTTGTTT | | |
| | | | | | |
| | | | CAGG TAGAGTAAACAAA | | |
| | | | — | | |
| GAM362 | APC10 | 5' | GGAAACTGTAACAGGACATT 1574 | T TTT | |
| | | | AATGTCCTGTT CA GTTTCC | | |
| | | | | | |
| | | | TTACAGGACAA GT CAAAGG | | |
| | | | T _ | | |
| GAM362 | C20orf139 | 3' | GGAACAAAAACAGGACATTA 3319 | CAT | |
| | | | TAATGTCCTGTTT TTGTTTC | | |
| | | | | | |
| | | | ATTACAGGACAAA AACAAAGG | | |
| | | | — | | |
| GAM362 | FLJ11186 | 3' | GAAGCCCGAAACAAGACATTA 1818 | C | ATTT |
| | | | TAATGTC TGTTTC GTTTC | | |
| | | | | | |
| | | | ATTACAG ACAAAG CGAAG | | |
| | | | A CC_ | | |
| GAM362 | FLJ22116 | 5' | GGAATTGCGGAAAACAGGAC 2073 | CA | _ |
| | | | GTCCTGTTT TTTGT TTCC | | |
| | | | | | |

CAGGACAAA AGGCG AAGG
 — TT
 GAM362 FLJ32978 3' AAACAAATGAAATCAACA 2487 CCT
 TGT GTTTCATTTGTTT
 ||| |||||
 ACA TAAAGTAAACAAA
 AC_

GAM362 KIAA1164 3' GGAAACAAAACAAAAC 2862 CC CA_
 GT TGTTC TTTGTTTCC
 || ||||| |||||
 CA ACAA AAACAAAGG
 AA ACA

GAM362 KIAA1762 3' AAAGAGAGAAACGGACA 2668 T A G
 TGTCC GTTTC TTT TTT
 ||||| ||||| ||| |||
 ACAGG CAAAG AGA AAA
 — — G

GAM362 KIAA1918 5' GAAAGGAGACAGAACATTA 2969 C ATTTG
 TAATGT CTGTTTC TTTC
 ||||| ||||| |||
 ATTACA GACAGAG AAAG
 A G____

GAM362 POPX1 3' GGAAACAAACTTCAGGTCA 1583 T TTCA
 TG CCTG TTTGTTTCC
 || ||||| |||||
 AC GGAC AAACAAAGG
 T TTC__

GAM362 PRO0800 3' AAACAAAGAGACAGGAATTA 1852 G A
 TAAT TCCTGTTTC TTTGTTT
 ||||| ||||| |||||
 ATTA AGGACAGAG AAACAAA

GAM362 LOC142779 3' GGAGTAACAAAATAGGACATTA 3050 CATT _
 TAATGTCCTGTTT TGTT TCC
 ||||| ||||| ||| |||
 ATTACAGGATAAA ACAA AGG
 — TG

GAM362 LOC143274 5' GGAAACAAACAAAAGGA 3053 G CA
 TCCT TTT TTTGTTTCC
 ||||| ||| |||||
 AGGA AAA AAACAAAGG
 — AC

GAM362 LOC154089 3' AAACAAATACTGAGACAG 3186 _
 CTGTTTCA TTTGTTT
 ||||| |||||
 GACAGAGT AAACAAA
 CAT

GAM362 LOC169679 3' AGCATATGAAGACAGGACAT 3404 _ T
 ATGTCCTGTTT CAT TGTT
 ||||| ||| |||

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|--------|-----------|----|-----------------------------|--------|-------|
| | | | TACAGGACAGA GTA ACGA | | |
| | | | A T | | |
| GAM362 | LOC202052 | 5' | GAAACAAATACCCAGAAGACA 3484 | __ | TTTC |
| | | | TGTC CTG ATTTGTTTC | | |
| | | | | | |
| | | | ACAG GAC TAAACAAAG | | |
| | | | AA CCA_ | | |
| GAM362 | LOC256021 | 3' | GAAACGAGAACAATGACATTA 3708 | C_ | CAT |
| | | | TAATGTC TGTTT TTGTTTC | | |
| | | | | | |
| | | | ATTACAG ACAAG AGCAAAG | | |
| | | | TA ____ | | |
| GAM362 | LOC91650 | 5' | AAACAAAACATCTCAGGACAT 2765 | TTTCA_ | |
| | | | ATGTCCTG TTTGTTT | | |
| | | | | | |
| | | | TACAGGAC AAACAAA | | |
| | | | TCTACA | | |
| GAM362 | LOC91752 | 5' | AAGTCAAATAAAACAGGACA 2777 | C _ | |
| | | | TGTCCTGTTT ATTTG TTT | | |
| | | | | | |
| | | | ACAGGACAAA TAAAC GAA | | |
| | | | A T | | |
| GAM363 | ARCN1 | 3' | CCCATTTCTCTCCAGTCA 844 | GAAGT | CA |
| | | | TGATTGGA AGGAAA GG | | |
| | | | | | |
| | | | ACTGACCT TCCTTT CC | | |
| | | | ____ AC | | |
| GAM363 | CTSK | 3' | TCCTACTTTGCTTCTCTCCACC 736 | AT | _____ |
| | CA | | TG TGGAGA AGTAGGA | | |
| | | | | | |
| | | | AC ACCTCT TCATCCT | | |
| | | | CC CTCGTT | | |
| GAM363 | HMG20A | 3' | TCCTATTTCCCTGCCATCA 1800 | T__ | A |
| | | | TGAT GG GAAGTAGGA | | |
| | | | | | |
| | | | ACTA CC CTTTATCCT | | |
| | | | CCGT _ | | |
| GAM363 | PRDM2 | 3' | TCCTGTTTCCCACCCAG 1415 | AGAA | A |
| | | | TTGG GT GGAAACAGGA | | |
| | | | | | |
| | | | GACC CA CCTTTGTCCT | | |
| | | | ____ C | | |
| GAM363 | RNMT | 3' | CCTGCCTATCCTCTCCGATCA 1060 | A_ | AAA |
| | | | TGATTGGAGA GTAGG CAGG | | |
| | | | | | |
| | | | ACTAGCCTCT TATCC GTCC | | |
| | | | CC ____ | | |
| GAM363 | SCAP1 | 3' | TCCCACCTCCCTACTTCTGCCA 1052 | _ | AAACA |
| | | | TGG AGAAGTAGG GGA | | |
| | | | | | |

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|--------|----------|----|-------------------------|------------|-----|---------|
| | | | ACC TCTTCATCC | CCT | | |
| | | | G | CTCAC | | |
| GAM363 | USH3A | 5' | CCTATTTTATTTCTCCATCA | 2355 | T | AAC |
| | | | TGAT GGAGAAGTAGGA | AGG | | |
| | | | | | | |
| | | | ACTA CCTCTTTATTTT | TCC | | |
| | | | — | A— | | |
| GAM363 | VAT1 | 3' | TCCTGTTTCCCACCTCCTTCTC | 1292 | TA— | |
| | C | | GGAGAAG | GGAAACAGGA | | |
| | | | | | | |
| | | | CCTCTTC | CCTTTGTCCT | | |
| | | | CTCCAC | | | |
| GAM363 | AIF1 | 5' | CCTGCTGAAAACCCTCCAGTCA | 2297 | A— | |
| | | | TGATTGGAG | AGTAGG | | |
| | | | | | | |
| | | | ACTGACCTC | TCGTCC | | |
| | | | CCAAAAG | | | |
| GAM363 | CPLX1 | 3' | CCTGTTTCTCCTCCATTCA | 1317 | T | AAGTA |
| | | | TGA TGGAG | GGAAACAGG | | |
| | | | | | | |
| | | | ACT ACCTC | TCTTTGTCC | | |
| | | | T | C— | | |
| GAM363 | CXYorf1 | 3' | CCTGTTCCTCCACCTCCCGGCTC | 3228 | — | A A A A |
| | | | GA TTGG GA GT GG AACAGG | | | |
| | | | | | | |
| | | | CT GGCC CT CA CC TTGTCC | | | |
| | | | C | — C C C | | |
| GAM363 | FLJ12221 | 3' | CCCACCCTTGCTCTCCAATTA | 2637 | A | AAACA |
| | | | TGATTGGAGA GTAGG | GG | | |
| | | | | | | |
| | | | ATTAACCTCT CGTTC | CC | | |
| | | | — | CCAC— | | |
| GAM363 | FLJ20207 | 3' | CCTGCCCTGCTTCCCCACCCA | 1741 | AT | A AAA |
| | | | TG TGG GAAGTAGG | CAGG | | |
| | | | | | | |
| | | | AC ACC CTTCGTCC | GTCC | | |
| | | | CC C | C— | | |
| GAM363 | FLJ22215 | 3' | CCTGCCCTTACCCTGTTCTCC | 3715 | — | AAA |
| | | | GGAGAA GTAGG | CAGG | | |
| | | | | | | |
| | | | CCTCTT CATCC | GTCC | | |
| | | | GTCC | CCC | | |
| GAM363 | FLJ31547 | 3' | TCCATAATTCTCCCGCAATC | 2511 | — | A— |
| | A | | TGATT GGAGAAGT | GGA | | |
| | | | | | | |
| | | | ACTAA CCTCTTTA | CCT | | |
| | | | CGC | ATAC | | |
| GAM363 | HSCBCIP1 | 3' | TCCTACCTATGTCTTCTCCAAT | 3449 | — | AAAC |
| | | | ATTGGAGAAG TAGG | AGGA | | |
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|--------|----------|----|-----------------------------|-------|-------|
| | | | TAACCTCTTC ATCC TCCT | | |
| | | | TGT A__ | | |
| GAM363 | KIAA0515 | 5' | TCCTACCAGAACTCCTCCGATC 2670 | A A__ | AAAC |
| | | A | TGATTGGAG AGT GG AGGA | | |
| | | | | | |
| | | | ACTAGCCTC TCA CC TCCT | | |
| | | | C AGA A__ | | |
| GAM363 | KIAA1514 | 3' | CCTGCTCAACTTCTCCA 1877 | A AAA | |
| | | | TGGAGAAGT GG CAGG | | |
| | | | | | |
| | | | ACCTCTTCA CT GTCC | | |
| | | | A C__ | | |
| GAM363 | KIAA1553 | 3' | TCCTCACTTCTCCATCCA 3544 | AT | _ |
| | | | TG TGGAGAAGT AGGA | | |
| | | | | | |
| | | | AC ACCTCTTCA TCCT | | |
| | | | CT C | | |
| GAM363 | KIAA1656 | 3' | CCCACTTCCTTCCAGTCA 2730 | _ | A |
| | | | TGATTGGA GAAGT GG | | |
| | | | | | |
| | | | ACTGACCT CTTCA CC | | |
| | | | TC C | | |
| GAM363 | KIAA1877 | 3' | CCTACCTTATTTCTCCAGCCA 2741 | AT | AAAC |
| | | | TG TGGAGAAGTAGG AGG | | |
| | | | | | |
| | | | AC ACCTCTTTATTC TCC | | |
| | | | CG CA__ | | |
| GAM363 | MTCH1 | 3' | CCCGTCTACCCCTCCAGTCA 1493 | AA | AAACA |
| | | | TGATTGGAG GTAGG GG | | |
| | | | | | |
| | | | ACTGACCTC CATCT CC | | |
| | | | CC GC__ | | |
| GAM363 | N-PAC | 3' | CCGCCCTCACCCCTCCAATC 2902 | AA _ | AAACA |
| | | | GATTGGAG GT AGG GG | | |
| | | | | | |
| | | | CTAACCTC CA TCC CC | | |
| | | | CC C CG__ | | |
| GAM363 | SEMA4B | 5' | CCTGTTTCCACCTCC 2839 | AA A | |
| | | | GGAG GT GGAAACAGG | | |
| | | | | | |
| | | | CCTC CA CCTTTGTCC | | |
| | | | _ C | | |
| GAM363 | SPRY1 | 3' | CCTGTTTCCACCTTCTCT 2709 | TA_ | |
| | | | GGAGAAG GGAAACAGG | | |
| | | | | | |
| | | | TCTCTTC CCTTTGTCC | | |
| | | | CAC | | |
| GAM363 | WS-3 | 5' | CCTGCCAGGCTCTCCAATC 1312 | A A_ | AAA |
| | | | GATTGGAGA GT GG CAGG | | |
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|--------|--------------|------------------------------|--------|----------|
| | | CTAACCTCT CG CC GTCC | | |
| | | GA | | |
| GAM363 | LOC123242 5' | TCTGTACCTTCTCCATCCA 3030 | AT | TAGGAA |
| | | TG TGGAGAAG ACAGG | | |
| | | | | |
| | | AC ACCTCTTC TGTCT | | |
| | | CT CA | | |
| GAM363 | LOC127702 3' | CCTGCCCACAACCTTCTCCAAAC 3024 | A | A__ AAA |
| | A | TG TTGGAGAAGT GG CAGG | | |
| | | | | |
| | | AC AACCTCTTCA CC GTCC | | |
| | | A ACA C | | |
| GAM363 | LOC146745 5' | TCCTGCCACCATTTCTCCAACC 3099 | A | A AAA |
| | A | TG TTGGAGAAGT GG CAGGA | | |
| | | | | |
| | | AC AACCTCTTTA CC GTCCT | | |
| | | C _ ACC | | |
| GAM363 | LOC147791 3' | CCCATTCCCTAACCTCCAATC 3294 | | AAG A CA |
| | | GATTGGAG TAGG AA GG | | |
| | | | | |
| | | CTAACCTC ATCC TT CC | | |
| | | CA_ C AC | | |
| GAM363 | LOC196892 3' | TCCTGGTGATTCTTCTCCAATC 3417 | | TAGGAAA |
| | A | TGATTGGAGAAG CAGGA | | |
| | | | | |
| | | ACTAACCTCTTC GTCCT | | |
| | | TTAGTG_ | | |
| GAM363 | LOC200093 3' | CCTGTTCCCCACCTCCCGGCTC 2648 | _ | A A A A |
| | | GA TTGG GA GT GG AACAGG | | |
| | | | | |
| | | CT GGCC CT CA CC TTGTCC | | |
| | | C _ C C C | | |
| GAM363 | LOC201243 5' | TCCTGCCACCATTTCTCCAACC 3426 | A | A AAA |
| | A | TG TTGGAGAAGT GG CAGGA | | |
| | | | | |
| | | AC AACCTCTTTA CC GTCCT | | |
| | | C _ ACC | | |
| GAM363 | LOC219404 3' | CCTGCTCCCTACTTCCTGGCA 3606 | A TG A | AAA |
| | | TG T G GAAGTAGG CAGG | | |
| | | | | |
| | | AC G C CTTTCATCC GTCC | | |
| | | _GT_ CTC | | |
| GAM363 | LOC222066 3' | TCCTGCAAACCACCTTCTCCAA 3574 | | TA AAA_ |
| | TCA | TGATTGGAGAAG GG CAGGA | | |
| | | | | |
| | | ACTAACCTCTTC CC GTCCT | | |
| | | CA AAAC | | |
| GAM363 | LOC253001 5' | TCTGTACCTTCTCCATCCA 3698 | AT | TAGGAA |
| | | TG TGGAGAAG ACAGG | | |
| | | | | |

AC ACCTCTTC TGTCT

CT CA_____

GAM363 LOC91040 3' CCTGTTCCCCACCTCCCGGCTC 2700 _ A A A A

GA TTGG GA GT GG AACAGG

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CT GGCC CT CA CC TTGTCC

C _ C C C